भाकृअनुप
ICAR

वार्षिक प्रतिवेदन
Annual Report
2024

भा.कृ.अनु.प. - भारतीय कृषि जैवप्रौद्योगिकी संस्थान
ICAR - Indian Institute of Agricultural Biotechnology
गढखटंगा, राँची - 834 003 (झारखण्ड)
Garhkhatanga, Ranchi - 834 003 (Jharkhand)

भाकृअनुप
ICAR

वार्षिक प्रतिवेदन
Annual Report
2024

IIAB

भा.कृ.अनु.प. - भारतीय कृषि जैवप्रौद्योगिकी संस्थान

ICAR - Indian Institute of Agricultural Biotechnology

गढखटंगा, राँची - 834 003 (झारखण्ड)

Garhkhatanga, Ranchi - 834 003 (Jharkhand)

Credit Line

Supervision & Guidance

Dr. Sujay Rakshit, Director

Dr. Vijai Pal Bhadana, Jt. Director (Research)

Editorial board

Dr. Kanaka KK

Dr. Sujit Kumar Bishi

Dr. Jayanta Layek

Dr. Soumajit Sarkar

Dr. Amit Kumar

Printed on : January, 2025

Acknowledgment

We acknowledge Dr. Kartik Sharma, for Hindi language editing and other scientific, administrative and supporting staff of the institute for their timely help.

IIAB Website : iiab.icar.gov.in

Note

Correct Citation

ICAR - Indian Institute of Agricultural Biotechnology. 2025. Annual Report 2024. ICAR - Indian institute of Agricultural Biotechnology, Garkhatanga, Ranchi - 834 003, Jharkhand, India pp: i-viii, 1-82.

Published by

Director, ICAR - Indian Institute of Agricultural Biotechnology, Ranchi

Contents

Preface

The agricultural sector, along with its allied industries, remains the backbone of India's economy, sustaining over 50% of the livelihood of Indian population. It is fundamentally shaping the socio-economic fabric of the nation. While agricultural production has seen remarkable progress, the sector confronts numerous challenges like climatic uncertainties, yield stagnation, decline in input use efficiency, deteriorating natural resources and pest and disease outbreaks. All these pose threats to sustainable agricultural growth especially in the vulnerable tribal belts like *Chotanagpur* plateau. In response to these challenges, ICAR-Indian Institute of Agricultural Biotechnology (ICAR-IIAB), Ranchi, an institution of excellence is committed to bring innovation driven agricultural growth by conducting basic and translational biotechnological research encompassing plants, animals, fishes and microbes in an integrated and wholistic approach. Through its comprehensive educational and trainings programmes, and entrepreneurship initiatives, ICAR-IIAB is working for building the next generation of human resources in the field of agricultural biotechnology for enhancing food and nutritional security and ecosystem health.

The institute has state-of-the-art facilities including specialized research centers for crops, livestock and fisheries, water harvesting units equipped with micro-irrigation facilities complemented by student accommodation to support its academic mission. More infrastructures are coming up. Current research initiatives focus on genomic resource development of crops (rice, winged bean, horse gram, mustard, chickpea, faba bean, amaranth), livestock (cattle, goat and chicken) and fisheries. Studies are underway for improving drought tolerance, nutrient use efficiency and biotic stress in different crops and profiling of microbial diversity of soil and coal void reservoir through metagenomic approach. Under genome editing initiative of ICAR, the institute has initiated targeted improvement of key crops (soybean, cotton, peanut, sunflower, rice, urd bean and maize). Efforts are also being made for development of cell surface biomarkers of cattle spermatozoa for sex-specific sperm segregation. Efforts are being made to standardize artificial insemination in goats to support the tribal economy. Works on nano-technology for treatment of jute retting waste-water, preparation of mineral mixture and green nano-particles for addressing micro-nutrient deficiency in animals are worth mentioning. Artificial intelligence is being used in genetic data simulation and analysis of time series data for drawing meaningful insights to assist biotechnological research. The institute is targeting to develop climate resilient self-sustaining farming models through a new initiative under a RKVY project.

The institute is leading the academic activities of ICAR-IARI Mega University Ranchi Hub, imparting degrees in undergraduate to post-doctoral levels. Students from across country with significant proportion of female students, as well as faculties from different parts of the country have brought national identity to the institute. The institute takes pride in outstanding performance of the students in national examinations. The institute maintains strong connections with the farming community through various outreach programmes which includes capacity building of the farming community through trainings on different areas of agriculture, input distribution initiatives and periodical health camps in the doorsteps of the farmers.

During the period under report the institute has made a good progress in research which can be gauged from the publication and recognition to its scientists in various fora. These scientists also succeeded in wining prestigious projects from various funding agencies. Commitment of the institute towards greening its campus and cleanliness drive has been recognized at national level by ICAR. The institute is committed not only to green its campus but the whole locality, under which it distributed ten thousand samplings to the local villagers, school children and gram panchayats.

I would like to express my sincere thanks to all our scientific, administrative, financial, field and supporting staff, students, research fellows and others of ICAR-IIAB, Ranchi and faculties from partner institutes for their hard work and contributions in various institutional activities. I also express my appreciation to the annual report editorial team for timely bringing out the publication.

I express my sincere gratitude to Dr. Himanshu Pathak, Secretary, DARE and Director General, ICAR for his inspiring guidance and all out support to our institute. I would also like to thank Dr. T. R. Sharma, DDG (Crop Science), ICAR and Dr. D.K. Yadava, ADG (Seeds), ICAR for their continuous guidance and encouragements.

Ranchi
January, 2025

(Sujay Rakshit)
Director
ICAR-IIAB

प्रस्तावना

कृषि एवं कृषि सम्बंधित क्षेत्र भारतीय अर्थव्यवस्था का एक महतवपूर्ण स्तम्भ है, जो 50 प्रतिशत से अधिक जनसंख्या के जीवनयापन का मुख्य स्रोत है और देश के सामाजिक-आर्थिक ढांचे के मूलभूत आकार का आधार हैं। कृषि उत्पादन में उल्लेखनीय प्रगति होने के बावजूद यह क्षेत्र कई चुनौतियों का सामना कर रहा है, जैसे जलवायु परिवर्तन के कारण होने वाली अनिश्चितता, उत्पादन वृद्धि में स्थिरता, इनपुट उपयोग दक्षता में कमी, प्राकृतिक संसाधनों का ह्रास और कीट तथा रोगों का प्रकोप इत्यादि। ये सभी चुनौतियाँ, विशेष रूप से छोटानागपुर पठार जैसे संवेदनशील आदिवासी बहुल क्षेत्रों में, सतत कृषि विकास के लिए खतरा पैदा करती हैं। इन चुनौतियों के निपटान हेतु, भ.कृ.अनु.प.- भारतीय कृषि जैव प्रौद्योगिकी संस्थान (आई.सी.ए.आर.-आई.आई.ए.बी.), रांची, एक उत्कृष्ट संस्थान, आधुनिक तकनीक आधारित कृषि विकास को बढ़ावा देने के लिए प्रतिबद्ध है। संस्थान में फसलों, पशुओं, मछलियों और सूक्ष्मजीवों से संबंधित मूलभूत और व्यावहारिक जैव प्रौद्योगिकी अनुसंधान को एकीकृत करने वाले शोधकार्य संचालित हैं। अपने व्यापक शैक्षणिक और प्रशिक्षण कार्यक्रमों तथा उद्यमिता पहल के माध्यम से भ.कृ.अनु.प.-भ.कृ.जै.प्रौ.सं. कृषि जैव प्रौद्योगिकी के क्षेत्र में अगली पीढ़ी के मानव संसाधन का निर्माण कर रहा है, ताकि खाद्य और पोषण सुरक्षा के अतिरिक्त पारिस्थितिकी तंत्र को भी सुदृढ़ किया जा सके।

संस्थान में अत्याधुनिक सुविधाएँ उपलब्ध हैं, जिनमें फसलों, पशुधन और मत्स्य पालन के लिए विशेष अनुसंधान केंद्र, माइक्रो-सिंचाई सुविधाओं से सुसज्जित जल-संग्रहण इकाइयाँ और संस्थान के शैक्षणिक उद्देश्यों की पूर्ति हेतु छात्र आवास सम्मिलित हैं। अतिरिक्त अधोसंरचनाएँ भी निर्माणाधीन हैं। वर्तमान शोध पहल फसलों (धान, सेम, कुल्थी, सरसों, चना, बाकला, राजगिरा) और पशुधन (गाय, बकरी, मुर्गी और मत्स्य) के जीनोमिक संसाधन विकास पर केंद्रित हैं। विभिन्न फसलों में सूखा सहनशीलता, पोषक तत्त्व उपयोग दक्षता और जैविक तनाव में सुधार के लिए अध्ययन चल रहे हैं, साथ ही मिट्टी और कोयला खदानों के जलाशय की सूक्ष्मजीव विविधता की प्रोफाइलिंग मेटाजीनोमिक दृष्टिकोण से की जा रही है। भ.कृ.अनु.प के जैव प्रौद्योगिकी विभाग की जीनोम संपादन पहल के अंतर्गत संस्थान ने प्रमुख फसलों (सोयाबीन, कपास, मूंगफली, सूरजमुखी, धान, उड़द और मक्का) के लक्षित सुधार की शुरुआत की है। गाय के शुक्राणुओं के लिंग-विशिष्ट पृथक्करण के लिए कोशिका सतह बायोमार्कर विकसित करने के प्रयास कार्यरत हैं। आदिवासी बहुल अर्थव्यवस्था को समर्थन देने के लिए बकरियों में कृत्रिम गर्भाधान को मानकीकृत करने का प्रयास भी जारी है। संस्थान जूट रेटिंग अपशिष्ट जल उपचार, खनिज मिश्रण निर्माण और पशुओं में सूक्ष्म पोषक तत्वों की कमी को दूर करने के लिए ग्रीन नैनोकणों के विकास में नैनो-प्रौद्योगिकी के उपयोग पर भी कार्य कर रहा है। कृत्रिम बुद्धिमत्ता का उपयोग आनुवंशिक डेटा सिमुलेशन और समय-श्रृंखला डेटा के विश्लेषण के लिए किया जा रहा है, ताकि जैव प्रौद्योगिकी अनुसंधान में उपयोगी अंतर्दृष्टि प्राप्त की जा सके। संस्थान राष्ट्रीय कृषि विकास योजना के अंतर्गत परिवर्तित जलवायु-लचीला/अनुकूल और आत्मनिर्भर कृषि मॉडल विकसित करने की और अग्रसर है।

संस्थान भ.कृ.अनु.प.-भ.कृ.अनु.सं. (आई.सी.ए.आर.-आई.ए.आर.आई.) मेगा यूनिवर्सिटी, रांची हब की शैक्षणिक गतिविधियों का नेतृत्व भी प्रभावी रूप से कर रहा है, जिसमे स्नातक से लेकर पोस्ट-डॉक्टोरल स्तर तक के शैक्षणिक कार्यक्रम सम्मिलित है। देशभर से छात्रों, जिनमें महिला छात्रों का महत्वपूर्ण अनुपात है, और विभिन्न क्षेत्रों से आए संकाय सदस्यों ने इस संस्थान को राष्ट्रीय पहचान प्रदान की है। संस्थान को राष्ट्रीय परीक्षाओं में छात्रों के उत्कृष्ट प्रदर्शन पर गर्व है। संस्थान विभिन्न प्रसार कार्यक्रमों के माध्यम से कृषक समुदाय की सहायता हेतु प्रतिबद्ध हैं। इसमें कृषि के विभिन्न क्षेत्रों में प्रशिक्षण के माध्यम से किसानों की क्षमता निर्माण, इनपुट वितरण पहल, और किसानों के लिए आयोजित होने वाले नियमित स्वास्थ्य शिविर शामिल हैं।

रिपोर्टिंग अवधि के दौरान संस्थान ने अनुसंधान के क्षेत्र में उल्लेखनीय प्रगति की है, जिसका आंकलन विभिन्न मंचों पर वैज्ञानिकों द्वारा प्रकाशित किए गए शोधपत्रो और मान्यताओं से किया जा सकता है। कार्यरत वैज्ञानिकों ने विभिन्न वित्त पोषण एजेंसियों से प्रतिष्ठित परियोजनाएँ प्राप्त करने में भी सफलता प्राप्त की है। संस्थान के परिसर को हरित बनाने और स्वच्छता अभियान के प्रति उसकी प्रतिबद्धता को आई.सी.ए.आ.र. द्वारा राष्ट्रीय स्तर पर मान्यता दी गई है। संस्थान केवल अपने परिसर को ही नहीं, अपितु पूरे क्षेत्र को हरित बनाने के लिए प्रतिबद्ध है। इस उद्देश्य से लगभग दस हजार पौधे स्थानीय ग्रामीणों, स्कूली बच्चों और ग्राम पंचायतों को वितरित किए गए।

मैं भ.कृ.अनु.प.- भारतीय कृषि जैव प्रौद्योगिकी संस्थान, रांची के सभी वैज्ञानिको, प्रशासनिक, वित्तीय, क्षेत्रीय अधिकारीयों एवं सहायक स्टाफ, छात्रों, शोध साथियों और अन्य कर्मचारियों के साथ-साथ संस्थान से जुड़े अन्य संस्थानों के संकाय सदस्यों को विभिन्न संस्थागत गतिविधियों में उनके कठिन परिश्रम और योगदान के लिए अपना हार्दिक धन्यवाद व्यक्त करता हूँ। साथ ही, वार्षिक रिपोर्ट संपादकीय टीम को समय पर प्रकाशन लाने के लिए हार्दिक बधाई देता हूँ।

मैं डॉ. हिमांशु पाठक, सचिव, कृषि अनुसंधान एवं शिक्षा विभाग तथा महानिदेशक, भारतीय कृषि अनुसंधान परिषद् का हमारे संस्थान को प्रेरणादायक मार्गदर्शन और पूर्ण समर्थन प्रदान करने के लिए हार्दिक आभार व्यक्त करता हूँ। मैं डॉ. टी. आर. शर्मा, उप-महानिदेशक (फसल विज्ञान), भ.कृ.अनु.प. और डॉ. डी. के. यादव, सहायक महानिदेशक (बीज), भ.कृ.अनु.प. का भी उनके निरंतर मार्गदर्शन और प्रोत्साहन के लिए धन्यवाद करता हूँ।

रांची
जनवरी, 2025

(सुजय रक्षित)
निदेशक
भाकृअनुप- भारतीय कृषि जैवप्रौद्योगिकी संस्थान

About the Institute

ICAR-Indian Institute of Agricultural Biotechnology (ICAR-IIAB), Ranchi, operates under the Indian Council of Agricultural Research as a premier national institute focused on agricultural biotechnology advancement. The institute strives to leverage cutting-edge technologies across agricultural biotechnology domains to boost agricultural productivity and national growth. Working at the convergence of plant, animal, fish, and microbial biotechnology, ICAR-IIAB conducts comprehensive research while maintaining high academic standards. The institute's core focus encompasses fundamental and strategic biotechnology research, alongside developing skilled professionals through various academic initiatives. It provides specialized education at master's, doctoral, and post-doctoral levels, covering diverse aspects of biotechnology and related fields. The institute's research portfolio includes innovative approaches like marker-assisted selection, gene identification, and regulatory region analysis from India's diverse biological resources. Significant emphasis is placed on genetically engineering crops for enhanced stress tolerance, improved productivity, and better nutrient utilization. ICAR-IIAB also develops molecular diagnostic tools for disease detection and management across plants, animals, and fish species.

A major milestone was achieved in 2021 when the institute relocated to its expansive new campus at Garhkhatanga, Ranchi Ring Road. The institute explores nanotechnology applications in pest detection and delivery systems for various agricultural inputs. As a biotechnology hub under NARES, it provides crucial technical support in areas including sequencing, bioinformatics, and safety studies. ICAR-IIAB continues to expand its scope as the Ranchi Hub coordinator of IARI Mega University, now offering programs from undergraduate to doctoral levels. The institute has enhanced its infrastructure with new student hostels and an upcoming main building. With growing scientific and administrative staff strength and increasing external collaborations through MOUs, ICAR-IIAB remains dedicated to addressing agricultural challenges and promoting food security through biotechnological innovations.

Executive Summary

- The genome editing work has been initiated in cotton, soybean, urdbean, peanut, and sunflower. The regeneration and *Agrobacterium*-mediated transformation protocols for peanut (*Arachis hypogaea* L.), soybean (*Glycine max*), and cotton (*Gossypium* spp.) have been optimized to facilitate subsequent ongoing genome editing studies.
- Marker-assisted selection is used to develop rice varieties that are tolerant to drought, low soil phosphorus, and blast diseases for rainfed conditions. It focuses on introgression key QTLs (qDTYs, *Pup1*) and resistance genes (*Pi2, Pi9, Pi54*). In *kharif* 2024, thousands of promising plants were selected from various generations and crosses based on their performance under direct-seeded conditions.
- Research on an F_3 rice population identified a few key SNPs linked to brown spot resistance. These single nucleotide polymorphisms (SNP) involve genes for chitinase-like and pentatricopeptide repeat proteins, which are critical for disease resistance.
- Out of 100 potential simple sequence repeat (SSR) markers, 49 polymorphic markers, including key markers on chromosome 4 near the *OsMed15a* gene region, were selected to aid in targeted rice genome analysis.
- F_2 populations from PB1121 × Badshabhog and PB1 × Badshabhog crosses showed significant grain size variations in F_3 seeds, with notable grain length and width differences compared to the parents in rice.
- From 100 potential SSR markers, 32 polymorphic markers were identified in IRCTN 91-84 and ISM parents, and F_4 populations from multiple crosses were advanced during Kharif 2024 for developing recombinant inbred lines (RILs).
- In winged beans, a study identified key genes, including transcription factor *MYB113* and *WAT1*-related protein, linked to seed coat color, revealing their role in anthocyanin production and genetic basis for breeding.
- The M_2 generation of winged beans exhibited significant genetic variation in qualitative and quantitative traits compared to the parental line, highlighting its potential for selecting desirable traits for breeding. Genotyping with 22 SSR markers revealed gamma radiation-induced genetic diversity identifying 31 unique alleles, and two major population clusters.
- The telomere-to-telomere assembly of 698 Mb winged bean genome and its 366 Kb mitochondrial genome indicated critical insights into genetic traits and bioenergetics.
- Cloned gRNA for *ZmFBL41* gene from maize in a binary vector pRGEB32-BAR based on restriction-based cloning utilizing the *BsaI* restriction site.
- For functional validation of Aldolase (*Os02g08030*) and CaM binding protein (*Os02g08120*) in rice, mutants were generated, and their agronomic characters were recorded.
- A total of 275 genotypes of finger millet were evaluated for tolerance to aluminum toxicity. A significant variation was observed in key traits leading to the identification of several promising genotypes. To enable high-throughput screening, hydroponic-based experiments and protocols were developed for selected varieties.
- RILs of chickpea derived from ICC 4958 and T-39-1 were assessed for seed protein content with the highest protein content (37.12%) recorded for RIL146.
- Genome-wide identification and *in-silico* characterization of polyphenol oxidase (*PPO*) genes and their promoter sequences was conducted in faba bean (*Vicia faba* L.) which are responsible for regulating L-3,4-dihydroxyphenylalanine (*L-DOPA*) accumulation. Through metabolite profiling, *PPO* gene expression, and associated enzyme activity, it is suggested that the redirection of metabolic flux at the precursor level may play a key role in regulating *L-DOPA* accumulation in leaf tissues.
- Protein domain analysis of aluminum toxicity tolerant proteins revealed that they contain bZIP_plant_ BZIP46, SAHH, and FACL_fum10p_ like domains. For plant disease resistant genes (R-genes), 199 encoded protein sequences were collected, with ongoing bioinformatics and compositional analysis.
- Four different fungal isolates of *Aspergillus* spp. were collected and characterized for their various morphological traits. The fungal isolates *Af*-1 and *Af*-4 were showing more greenish with having profuse conidia as compared to isolates *Af*-2 and *Af*-3 showing lesser in sporulation.
- Climate-resilient farming system models viz., integrated farming system, organic farming system, and natural farming system are being developed with the integration of water harvesting units,

micro-irrigation, diversified crops (cereals, pulses, oilseeds, vegetables, fruits, fodder crops), duck house, composting units etc. for enhancing soil health, system productivity, and nutritional security.

- Studies initiated on different nutrient (inorganic vs integrated vs organic) and management practices (residue retention vs removal, mulch vs no-mulch, conventional vs reduced tillage etc.) on soil microbial dynamics, nutrient use efficiency, and carbon sequestration for different cropping systems.
- Phosphorus solubilizing bacterial and fungal isolates (three each), potassium solubilizing bacterial and fungal isolates (one each), and zinc solubilizing bacterial fungal isolates (four each) were isolated from soil samples from the rhizosphere of plants grown in Ramgarh coal mine area and their characterization work is under progress.
- Application of machine learning to optimize management practices for improved performance of artificial insemination with sex-sorted semen (SSS) in dairy reveals that intensive management-based dairy production system benefits the most from the use of SSS through careful choice of breeds and parity of the cattle.
- Significant differences in copy number variation of the Y-chromosome specific genes (*HSFY1* and *ZNF280BY*) in different genetic backgrounds of cattle (indicine, taurine, and taurine × indicine) is observed revealing negative correlations with seminal attributes.
- Vaginal electrical resistance effectively detects estrus in Black Bengal goats, providing a practical alternative to buck-based methods.
- Using simulation study, suppressing meiotic recombination in parental lines of chicken significantly accelerated inbreeding, which offers enhancing heterosis in crossbreds while maintaining genetic fitness.
- Proteomic analysis of sheep and goat wool revealed distinct keratin protein profiles, emphasizing fiber quality and authenticity. The one-dimensional SDS-PAGE findings indicate the need for advanced techniques like two-dimensional SDS-PAGE for better differentiation of fiber types.
- Through molecular and biochemical analysis, a *Salmonella typhimurium* strain was characterized for further study.
- Study on bacterial pathogens in milk samples causing bovine mastitis in Ranchi, Jharkhand, identified major isolates like *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Escherichia coli*. Antimicrobial resistance profiling revealed multidrug-resistant strains, highlighting one health concern and the need for alternative therapeutic approaches.
- Herbal supplements for improving the bioavailability of nano-minerals viz., copper, zinc, and manganese in goats revealed improved hematological attributes viz., hemoglobin concentration, red blood cell indices, and white blood cell numbers.
- An *ex-situ* experiment was performed to assess the efficacy of zinc oxide nanoparticles (ZnO NPs) in degrading jute retting wastewater, with special consideration on microbial sustainability. The current metagenomics-based study revealed that a dosage of 750 ppm ZnO NPs enhanced microbial diversity, highlighting its non-toxic nature and ability to sustain microbial consortium along with higher efficacy in photocatalysis-induced remediation.
- A hybrid model combining CEEMDAN decomposition, MARS selection, and PSO optimization was developed to enhance the prediction accuracy of noisy time series data, outperforming individual models in forecasting weekly potato prices in India.
- Under various outreach activities such as Tribal Sub Plan (TSP), Scheduled Caste Sub Plan (SCSP), and North Eastern Himalayan (NEH) components, agricultural inputs have been distributed to about 6,600 farmers through 18 scientific programs and training sessions.
- Among 16 hubs of ICAR-IARI Mega University, IIAB-Ranchi Hub was the first to start the B. Tech Biotechnology degree program. During the academic year 2023-24 and 2024-25, a total of 20 and 21 students, respectively, have enrolled in the degree program. It has also started master's / doctoral programs in Genetics and Plant Breeding (GPB), Molecular Biology and Biotechnology (MBB), Agricultural Chemicals, and Agricultural Processing and Food Engineering (AE). A total of 16 courses for Master's programs have been taught by the faculties of Ranchi Hub (IIAB, NISA, ICAR-RCER-RC and NBPGR-RS). Currently, the hub hosts a diverse cohort of 110 students (69 in UG, 35 in PG, and 6 in Ph.D.) across the country, fostering a vibrant academic and research community.

कार्यकारी सारांश

- कपास, सोयाबीन, उड़द, मूंगफली और सूरजमुखी फसलों में जीनोम संपादन का कार्य प्रारंभ किया गया है। मूंगफली (*Arachis hypogaea* L.), सोयाबीन (*Glycine* max) और कपास (*Gossypium* spp.) के लिए पुनर्जनन और एग्रोबैक्टीरियम-मध्यस्थ रूपांतरण प्रोटोकॉल को अनुकूलित किया गया है, ताकि आगे चल रहे जीनोम संपादन कार्य को सरल बनाया जा सके।
- मार्कर-सहायित चयन का उपयोग ऐसे धान किस्मों के विकास के लिए किया जा रहा है जो सूखा प्रतिरोधी, मृदा में कम फॉस्फोरस उपलब्धता और ब्लास्ट रोग के प्रति सहनशील हों। यह शोध कार्य मुख्यता क्यूटीएल्स (qDTYs, Pup1) और प्रतिरोधी जीन (Pi2, Pi9, Pi54) के अंतर्ग्रहण पर केंद्रित है। खरीफ 2024 में, धान की सीधी बिजाई परिस्थितियों में प्रदर्शन के आधार पर विभिन्न पीढ़ियों और संकरणों से हजारों संभावित पौधों का चयन किया गया।
- एक ऍफ़ 3 धान जनसंख्या पर किए गए शोध में ब्राउन स्पॉट प्रतिरोध से जुड़े कुछ प्रमुख एस.एन.पी. (सिंगल न्यूक्लियोटाइड पॉलीमॉर्फिज़्म) की पहचान की गई। ये एस.एन.पी. काइतिनेज़ जैसे जीन और पेंटाट्रिकोपेप्टाइड रिपीट प्रोटीन से जुड़े हैं, जो रोग प्रतिरोधक क्षमता के लिए महत्वपूर्ण हैं। इन निष्कर्षों ने प्रतिरोधकता की विरासत को समझने में नई जानकारी प्रदान की है, जो मार्कर-सहायित चयन और सहनशील धान की किस्मों के विकास में सहायता करती है।
- 100 संभावित सरल अनुक्रम दोहराव (SSR) मार्करों में से, 49 बहुरूपी मार्करों का चयन किया गया, जिनमें क्रोमोसोम 4 पर OsMed15a जीन क्षेत्र के पास के प्रमुख मार्कर शामिल हैं, ताकि लक्षित धान जीनोम विश्लेषण में सहायता की जा सके।
- PB1121 × बदशाहभोग और PB1 × बदशाहभोग संकरणों से प्राप्त ऍफ़ 2 जनसंख्याओं ने ऍफ़ 3 बीजों में अनाज आकार में महत्वपूर्ण विविधताएँ दिखाई, जिनमें पैरेंट लाइन के मुकाबले दाने की लंबाई और चौड़ाई में उल्लेखनीय अंतर पाया गया।
- 100 संभावित एस.एस.आर. मार्करों में से, IRCTN 91-84 और ISM पेरेंट लाइन में 32 बहुरूपी मार्करों की पहचान की गई, और खरीफ 2024 के दौरान कई संकरणों से प्राप्त ऍफ़ 4 जनसंख्याओं को पुनः संयोजित इनब्रेड लाइनों (RILs) के विकास के लिए आगे बढ़ाया गया।
- वंशीय सेम में एक अध्ययन ने बीज आवरण के रंग से जुड़े प्रमुख जीनों की पहचान की, जिनमें ट्रांसक्रिप्शन फैक्टर MYB113 और WAT1-संबंधित प्रोटीन शामिल हैं। यह अध्ययन एंथोसाइनिन उत्पादन और प्रजनन के लिए इनके आनुवंशिक आधार को उजागर करता है।
- वंशीय सेम की M2 पीढ़ी ने पैरेंट लाइन रेखा की तुलना में गुणात्मक और मात्रात्मक लक्षणों में महत्वपूर्ण आनुवंशिक विविधता प्रदर्शित की, जो प्रजनन के लिए वांछनीय लक्षणों के चयन की संभावना को उजागर करती है। 22 एस.एस.आर. मार्करों का उपयोग करके जीनोटाइपिंग में गामा विकिरण से प्रेरित आनुवंशिक विविधता पाई गई, जिसमें 31 अद्वितीय एलील्स की पहचान की गई और डेंड्रोग्राम और संरचना विश्लेषण के माध्यम से दो प्रमुख जनसंख्या समूहों का निर्धारण किया गया।
- 698 Mb वंशीय सेम जीनोम और इसके 366 Kb माइटोकॉन्ड्रियल जीनोम के टीलोमिएर -से- टीलोमिएर असेंबली ने आनुवंशिक लक्षणों और जैव-ऊर्जाविज्ञान (बायोएनेरजेटिक्स) पर महत्वपूर्ण जानकारी प्रदान की।
- मक्का के ZmFBL41 जीन के लिए क्लोनित gRNA को बाइनरी वेक्टर pRGEB32-BAR में रेस्ट्रिक्शन-आधारित क्लोनिंग द्वारा BsaI रेस्ट्रिक्शन साइट का उपयोग करते हुए क्लोनित किया गया।
- धान में Aldolase (Os02g08030) और CaM बाइंडिंग प्रोटीन (Os02g08120) की कार्यात्मक सत्यापन के लिए म्यूटेंट्स उत्पन्न किए गए, और उनके कृषि संबंधी लक्षणों को रिकॉर्ड किया गया।
- एल्युमिनियम विषाक्तता के प्रति सहनशीलता के लिए कुल 275 फिंगर मिलेट के जीनोटाइप्स का मूल्यांकन किया गया। प्रमुख लक्षणों में महत्वपूर्ण विविधता देखी गई, जिससे कई संभावित जीनोटाइप्स की पहचान की गई। उच्च-प्रवाह स्क्रीनिंग को सक्षम करने के लिए, चयनित किस्मों के लिए हाइड्रोपोनिक-आधारित प्रयोग और प्रोटोकॉल विकसित किए गए।
- ICC 4958 और T-39-1 से प्राप्त चना फसल की पुनः संयोजित इनब्रेड लाइनों का बीज प्रोटीन उत्पादन के लिए मूल्यांकन किया गया, जिसमें RIL146 के लिए सबसे उच्च प्रोटीन उत्पादकता (37.12%) रिकॉर्ड की गई।
- फाबा बीज (*Vicia faba* L.) में पॉलीफिनोल ऑक्सीडेज़ (PPO) जीन और उनके प्रमोटर अनुक्रमों की जीनोम-व्यापी पहचान और इन-सीलिको विशेषता की गई, जो L-3,4-डिहाइड्रॉक्सीफेनाइलएलानिन (L-DOPA) संचय को नियंत्रित करने के लिए जिम्मेदार हैं। मेटाबोलाइट प्रोफाइलिंग, PPO जीन अभिव्यक्ति और संबंधित एंजाइम गतिविधि के माध्यम से यह सुझाव दिया गया है कि अग्रदूत स्तर पर मेटाबोलिक फ्लक्स का पुनर्निर्देशन पत्तियों में L-DOPA संचय को नियंत्रित करने में एक प्रमुख भूमिका निभा सकता है।
- प्रोटीन डोमेन विश्लेषण ने सरसों में एल्युमिनियम सहनशील प्रोटीनों में bZIP_plant_BZIP46, SAHH, और FACL_fum10p_ का पता लगाया। प्रतिरोधक जीनों के लिए, 199 सकारात्मक प्रोटीन अनुक्रम एकत्र किए गए, जिनका अनुक्रम लंबाई, अमीनो एसिड्स संरचना, और डोमेन का विश्लेषण किया जा रहा है।
- *ऐस्पेरजिलस स्पीशीज* के चार विभिन्न कवक आइसोलेट्स एकत्र किए गए और उनके विभिन्न रूपात्मक लक्षणों के लिए उनका विश्लेषण किया गया। कवक आइसोलेट्स Af-1 और Af-4 में Af-2 और Af-3 के मुकाबले अधिक हरा रंग और प्रचुर कोनिडिया पाया गया, जबकि

Af-2 और Af-3 में स्पोरुलेशन कम था।

- जलवायु-लचीले कृषि प्रणाली मॉडल, जैसे कि एकीकृत कृषि प्रणाली, जैविक कृषि प्रणाली, और प्राकृतिक कृषि प्रणाली, जल संचयन इकाइयों, सूक्ष्म-सिंचाई, विविध फसलों (अनाज, दलहन, तिलहन, सब्जियाँ, फल, चारा फसलें), बत्तख घर, खाद इकाइयाँ आदि के एकीकरण के साथ विकसित किए जा रहे हैं, ताकि मृदा स्वास्थ्य, प्रणाली की उत्पादकता और पोषण सुरक्षा को बढ़ाया जा सके।
- विभिन्न पोषक तत्वों (अकार्बनिक बनाम एकीकृत बनाम जैविक) और प्रबंधन प्रथाओं (अवशेष संरक्षण बनाम निकासी, मल्च बनाम बिना मल्च, पारंपरिक बनाम घटित जुताई आदि) पर मृदा सूक्ष्मजीवीय गतिकी, पोषक तत्व उपयोग दक्षता, और कार्बन संचयन पर विभिन्न फसल प्रणालियों के लिए अध्ययन शुरू किए गए हैं।
- फॉस्फोरस घुलनशील बैक्टीरियल और कवक आइसोलेट्स (प्रत्येक तीन), पोटेशियम घुलनशील बैक्टीरियल और कवक आइसोलेट्स (प्रत्येक एक), और जिंक घुलनशील बैक्टीरियल और कवक आइसोलेट्स (प्रत्येक चार) रामगढ़ कोयला खदान क्षेत्र में उगाए गए पौधों की राइजोस्पेयर से मृदा नमूनों से आइसोलेट किए गए और उनके विशेषण कार्य पर काम चल रहा है।
- दूध उत्पादन में सेक्स-पृथक किए गए शुक्राणु (SSS) के साथ कृत्रिम गर्भाधान के प्रदर्शन में सुधार के लिए प्रबंधन प्रथाओं को अनुकूलित करने हेतु मशीन लर्निंग का उपयोग करने से यह स्पष्ट हुआ है कि तीव्र प्रबंधन-आधारित डेयरी उत्पादन प्रणाली एस.एस. एस. के उपयोग से सबसे अधिक लाभ उठाती है, बशर्ते गायों की नस्ल और संतान संख्या का सावधानीपूर्वक चयन किया जाए।
- गायों के विभिन्न आनुवंशिक पृष्ठभूमियों (इंडिसिन, टॉरिन, और टॉरिन × इंडिसिन) में Y-क्रोमोसोम विशिष्ट जीन (HSFY1 और ZNF-280BY) की कॉपी संख्या विविधता में महत्वपूर्ण अंतर देखा गया, जिससे शुक्राणु लक्षणों के साथ नकारात्मक सहसंबंध सामने आए।
- ब्लैक बंगाल बकरियों में प्रजनन काल का पता लगाने के लिए योनि विद्युत प्रतिरोध प्रभावी रूप से काम करता है, जो बकरा-आधारित विधियों का एक व्यावहारिक विकल्प प्रदान करता है।
- मुर्गी की अभिभावक रेखाओं में मायोटिक पुनर्संयोजन को दबाने से इनब्रेडिंग में महत्वपूर्ण तेजी आई, जो क्रॉसब्रेड्स में हेटेरोसिस को बढ़ाने के साथ-साथ आनुवंशिक फिटनेस को बनाए रखने में मदद करती है।
- भेड़ और बकरी की ऊन का प्रोटियोमिक विश्लेषण ने विशिष्ट केराटिन प्रोटीन प्रोफाइल का खुलासा किया, जो फाइबर गुणवत्ता और प्रामाणिकता को उजागर करता है। एक-आयामी SDS-PAGE परिणामों से यह संकेत मिलता है कि फाइबर प्रकारों के बेहतर पृथक्करण के लिए उन्नत तकनीकों, जैसे दो-आयामी SDS-PAGE की आवश्यकता है।
- अनुसंधान के लिए आवश्यक साल्मोनेला टाइफीमुरियम स्ट्रेन की पहचान की गई, जीनोमिक डी.एन.ए. को पृथक किया, और invA जीन का उपयोग करके जैव रासायनिक परीक्षणों और PCR के माध्यम से स्ट्रेन की पुष्टि की।
- रांची, झारखंड में गायों में मैसटाईटिस का कारण बनने वाले बैक्टीरियल रोगजनकों पर अध्ययन में प्रमुख आइसोलेट्स जैसे स्टैफिलोकोकस ऑरियस, साइकोमोनस एरुजिनोसा और ई. कोलाई की पहचान की गई। एंटीमाइक्रोबियल प्रतिरोध प्रोफाइलिंग से मल्टीड्रग-प्रतिरोधी स्ट्रेन्स सामने आए, जो एक स्वास्थ्य चिंता को उजागर करते हैं और वैकल्पिक चिकित्सीय दृष्टिकोण की आवश्यकता को दर्शाते हैं।
- बकरियों में नैनो-मिनरल्स जैसे तांबा, जिंक और मैंगनीज की बायोएविलेबिलिटी सुधारने के लिए हर्बल सप्लीमेंट्स ने रक्तविज्ञान लक्षणों में सुधार दिखाया, जैसे कि हीमोग्लोबिन सांद्रता, लाल रक्त कणिका सूचकांक और श्वेत रक्त कणिका की संख्या।
- एक एक्स-सीटू प्रयोग किया गया था ताकि जूट रेटिंग अपशिष्ट जल को नष्ट करने में जिंक ऑक्साइड नैनोपार्टिकल्स (ZnO NPs) की प्रभावशीलता का मूल्यांकन किया जा सके, जिसमें सूक्ष्मजीवीय स्थिरता पर विशेष ध्यान दिया गया। वर्तमान मेटाजेनोमिक्स-आधारित अध्ययन से यह पता चला कि 750 ppm ZnO NPs की खुराक ने सूक्ष्मजीवी विविधता को बढ़ाया, जो इसके गैर-प्रतिकूल स्वभाव और सूक्ष्मजीवी कंसोर्टियम को बनाए रखने की क्षमता को उजागर करता है, साथ ही फोटोकैटालिसिस-प्रेरित सुधार में उच्च प्रभावशीलता को भी दर्शाता है।
- एक हाइब्रिड मॉडल विकसित किया गया, जिसमें CEEMDAN डिकम्पोज़िशन, MARS चयन और PSO अनुकूलन को जोड़ा गया, ताकि शोरयुक्त समय श्रृंखला डेटा की भविष्यवाणी सटीकता को बढ़ाया जा सके, जो भारत में साप्ताहिक आलू की कीमतों की भविष्यवाणी में व्यक्तिगत मॉडलों से बेहतर प्रदर्शन करता है।
- विभिन्न आउटरीच गतिविधियों जैसे कि जनजातीय उप योजना (TSP), अनुसूचित जाति उप योजना (SCSP), और उत्तर-पूर्वी हिमालयी (NEH) घटकों के तहत, 18 वैज्ञानिक कार्यक्रमों और प्रशिक्षण सत्रों के माध्यम से लगभग 6600 किसानों को कृषि सामग्री वितरित की गई है।
- रांची हब ने ICAR-IARI से संबद्ध B. Tech बायोटेक्नोलॉजी डिग्री प्रोग्राम की शुरुआत की है। यह कार्यक्रम 2022-23 शैक्षिक वर्ष में जनवरी से ऑनलाइन मोड में और अप्रैल से ऑफलाइन मोड में शुरू हुआ। शैक्षिक वर्ष 2023-24 और 2024-25 के दौरान, क्रमशः 20 और 21 छात्रों ने इस डिग्री प्रोग्राम में प्रवेश लिया है।
- आई.ए.आर.आई. मेगा यूनिवर्सिटी रांची हब ने जैनटिक्स और पौध संवर्धन (GPB), आणविक जीवविज्ञान और बायोटेक्नोलॉजी (MBB), कृषि रसायन, और कृषि प्रसंस्करण और खाद्य अभियांत्रिकी (AE) में मास्टर / डॉक्टोरल प्रोग्राम भी शुरू किए हैं। रांची हब (IIAB, NISA, ICAR-RCER-RC और NBPGR-RS) के संकायों द्वारा कुल 16 पाठ्यक्रम मास्टर प्रोग्राम के लिए पढ़ाए गए हैं।
- वर्तमान में, यह हब देश भर से 110 छात्रों (69 स्नातक, 35 स्नातकोत्तर, और 6 डॉक्टरल) का एक विविध समूह होस्ट करता है, जो एक जीवंत शैक्षिक और शोध समुदाय को बढ़ावा देता है।

Research Accomplishments

School of Basic and Social Sciences

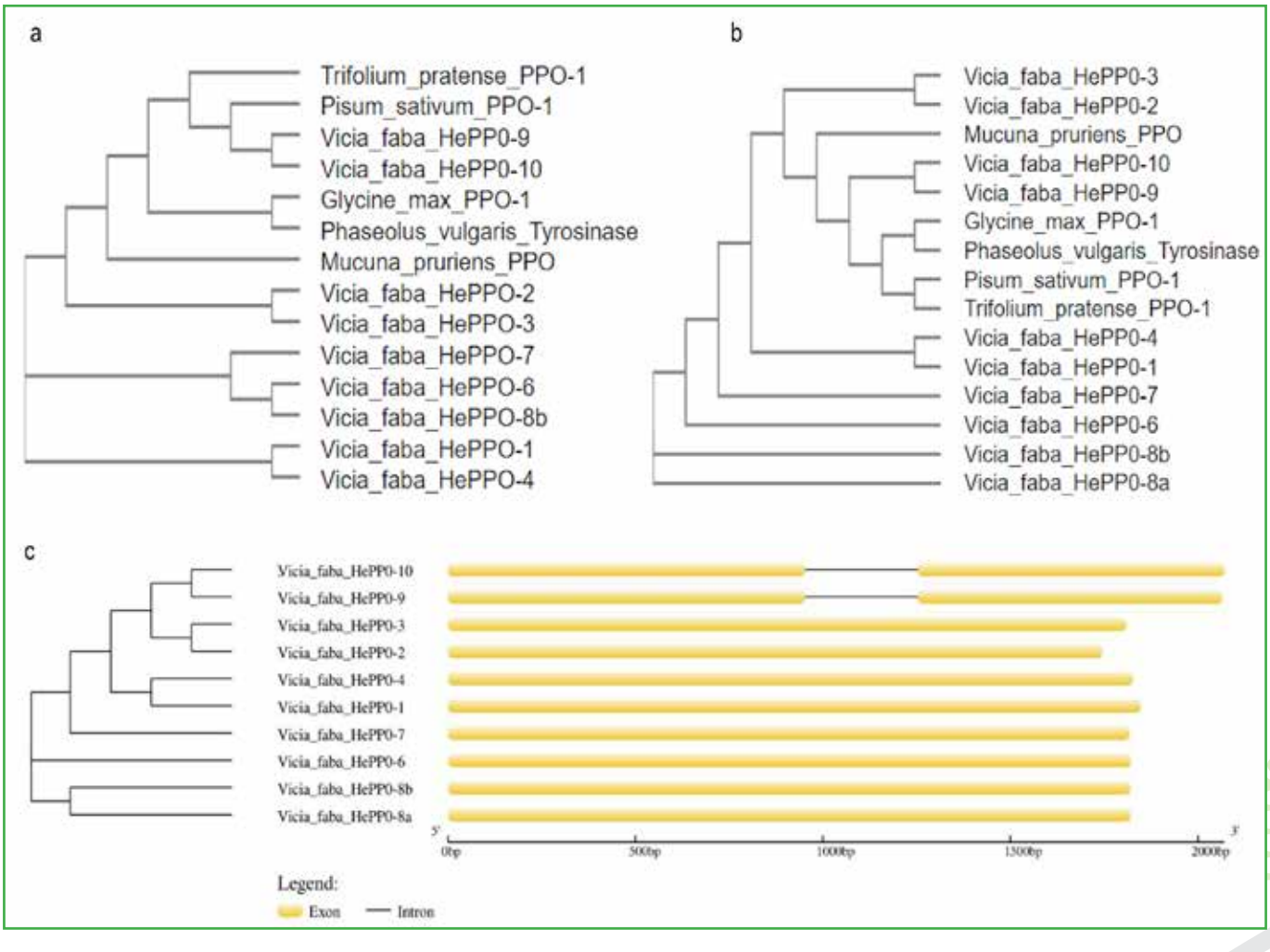
Understanding the biochemical and molecular regulation of L-DOPA and tannins biosynthesis in faba bean (*Vicia faba* L.)

Genome-wide identification and *in-silico* characterization of polyphenol oxidase (*PPO*) genes in faba bean

Genome-wide identification and characterization of polyphenol oxidase gene families are essential for understanding their functional roles in metabolism. In the current study, local blasts in the faba bean whole genome (nucleotide level and protein level) resulted in ten isoforms of polyphenol oxidase (PPO) genes, for both amino acid and nucleotide levels where one gene (*HePPO-8a*) showed 100% similarity with *HePPO-8b*. Thus, *HePPO-8a* was selected for further analysis. The local blast was best aligned with *Glycine max* (GM), *Pisum sativum* (PS), *Trifolium pratense* (TP) and *Phaseolus vulgaris* (PV). In case of amino acid sequence alignment (**Figure 1a**), *HePPO-9* and *HePPO-10* showed maximum similarity with TP and PS species while the *PPO* genes on the first chromosome showed maximum similarity with GM, PV, and MP. In case of nucleotide sequence alignment (**Figure 1b**) *PPO* genes on the fifth chromosome showed close relation with all other genera considered in the study. Faba bean *PPOs* were majorly single exon genes (**Figure 1c**) having six motifs, resembling similar structure as in related crops compared, except MP, where only four identical motifs were found (**Figure 1d**). Chromosome localization study revealed eight *PPO* genes (*HePPO-1* to 8) on 1q:1716-1720 Mb and two genes (*HePPO-9* and *HePPO-10*) on 5q:410 Mb (**Figure 1e**).

In-silico characterization of promoter sequence of polyphenol oxidase (*PPO*) genes

Analysis of promoter sequences provides valuable insights into the regulatory networks governing gene



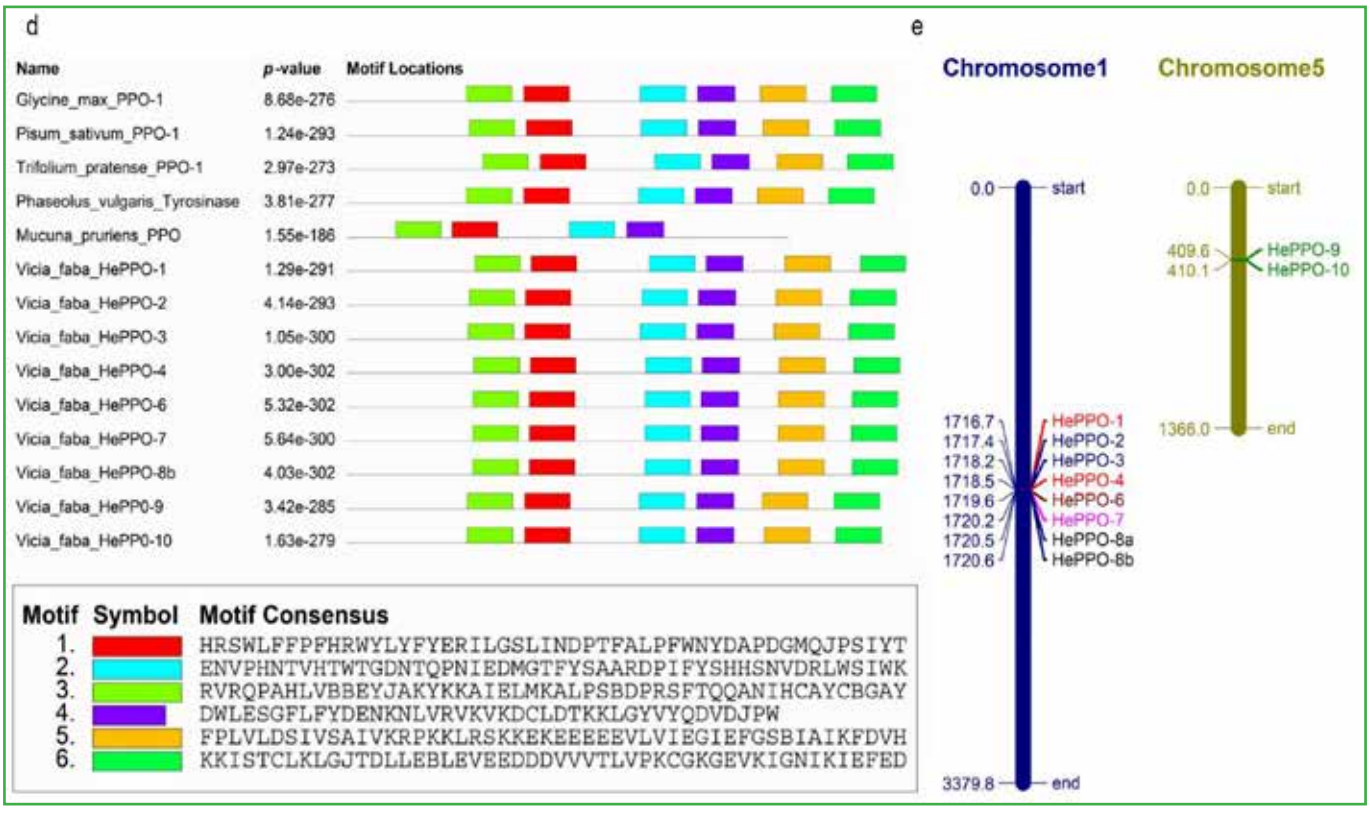


Figure 1: *In-silico* analyses of phylogenetic relationship (**a & b**), gene structure (**c**), motif composition (**d**) and chromosome localization (**e**) of faba bean polyphenol oxidase genes.

expression and their potential impact on metabolic pathways. Promoter analysis of two Kb upstream sequences of the polyphenol oxidase (*PPO*) genes reported 2,636 binding sites of 357 transcription factors (TFs), among them the top ten TFs with highest number of binding sites (**Figure 2a**) were Ethylene Responsive Factor (*ERF*), myeloblastosis (*MYB*), basic-helix-loop-helix (*bHLH*), *GATA*, *NAC*, Barley B Recombinant/Basic Penta Cysteine (*BBR-BPC*), *C2H2*-type zinc finger TF, basic leucine zipper (*bZIP*), DNA binding with one finger (*Dof*), and *MIKC*-type *MADS*-box TFs. A total of 272 potential regulatory interactions between 170 TFs and nine *PPO* genes were identified. The top five regulators of each *PPO* gene are represented in (**Figure 2b**). Transcription factor enrichment showed 43 TFs possessing over-represented targets in the *PPO* genes ($p \leq 0.05$). Transcription factors *viz*., *TCP, MYB, NAC, bHLH, MYB,* and *MIKC-MADS* were highly enriched (**Figure 2c**). Certain TF families, such as *ERF*, *MYB* and *bHLH* were the leading candidates for binding to *PPO* gene promoters, consistent with their roles in regulating secondary metabolism. *MYB* TF are well-known as flavonoid biosynthesis regulators, influencing crucial stages. Their abundance in the PPO gene promoters suggests a coordinated control of phenolic metabolism. Micro RNAs (miRNAs) prediction resulted in identification of 202 miRNAs having binding sites across the *PPOs*. Several unique miRNA sites were also observed on *HePPO-1* (miR172, miR4413a, miR5380c, miR5677); *HePPO-2* (miR1525 and miR1529), *HePPO-3* (miR9743); *HePPO-4* (miR4411); *HePPO-9* (miR1518, miR4342, miR4395a, miR9722); and *HePPO-10* (miR319p, miR482, miR5038, miR5041-5p) (**Figure 2d).** These TFs and miRNAs might be involved in the differential behavior of faba bean *PPOs* across tissues and developmental stages.

Redirection of metabolic flux regulates the L-DOPA accumulation in faba bean leaves

The regulation of metabolic pathways plays a crucial role in determining the tissue-specific and developmental stage-dependent accumulation of bioactive compounds in plants. Based on our earlier findings, a differential accumulation of L-DOPA and other catecholamines across various organs was observed in faba bean, with flowers and leaves identified as the primary sites of accumulation. It was also observed that L-DOPA content in both tissues declines as they mature. To explain the decreased L-DOPA levels in mature leaf tissues (ML) compared to very young leaves (VYL), a metabolic shift hypothesis has been proposed, where precursor molecules are diverted towards the synthesis of other metabolites in older tissues. To substantiate this hypothesis, a profiling of selected secondary metabolites and their associated enzyme activities was undertaken. The analysis revealed that VYL exhibit significantly higher polyphenol oxidases

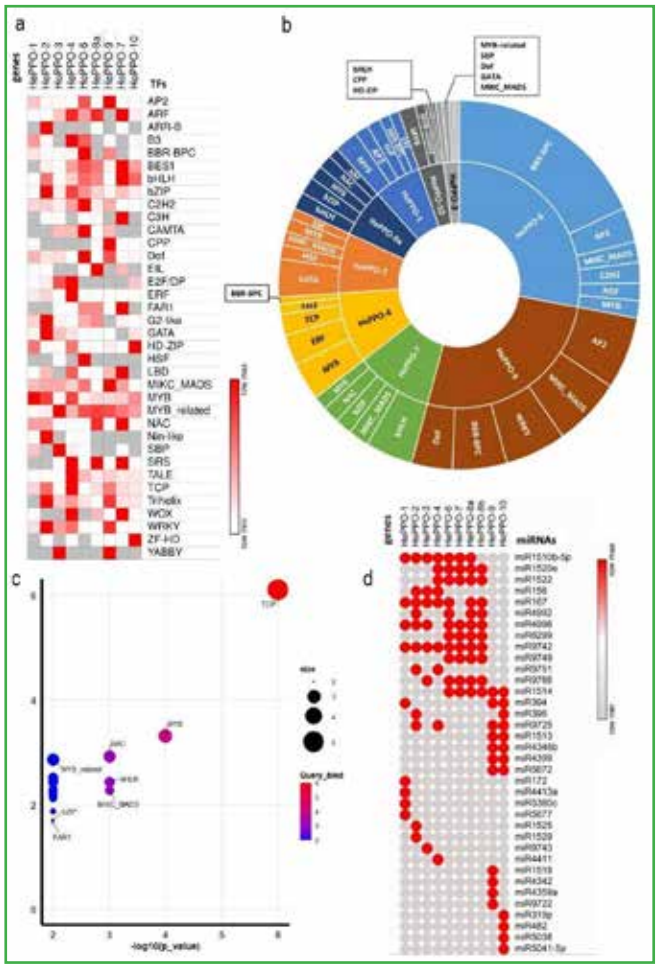


Figure 2: *In-silico* promoter analysis studies showing, (**a**) Transcription factor (TF) binding site prediction, (**b**) Top five regulatory TFs for each *PPO* gene, (**c**) TF enrichment, and (**d**) Predicted miRNAs from *Glycine max* having enriched binding sites on faba bean *PPO* genes. Highly enriched TFs are denoted by red color and bigger size (p-value) and grey color indicates absence of miRNAs enrichment.

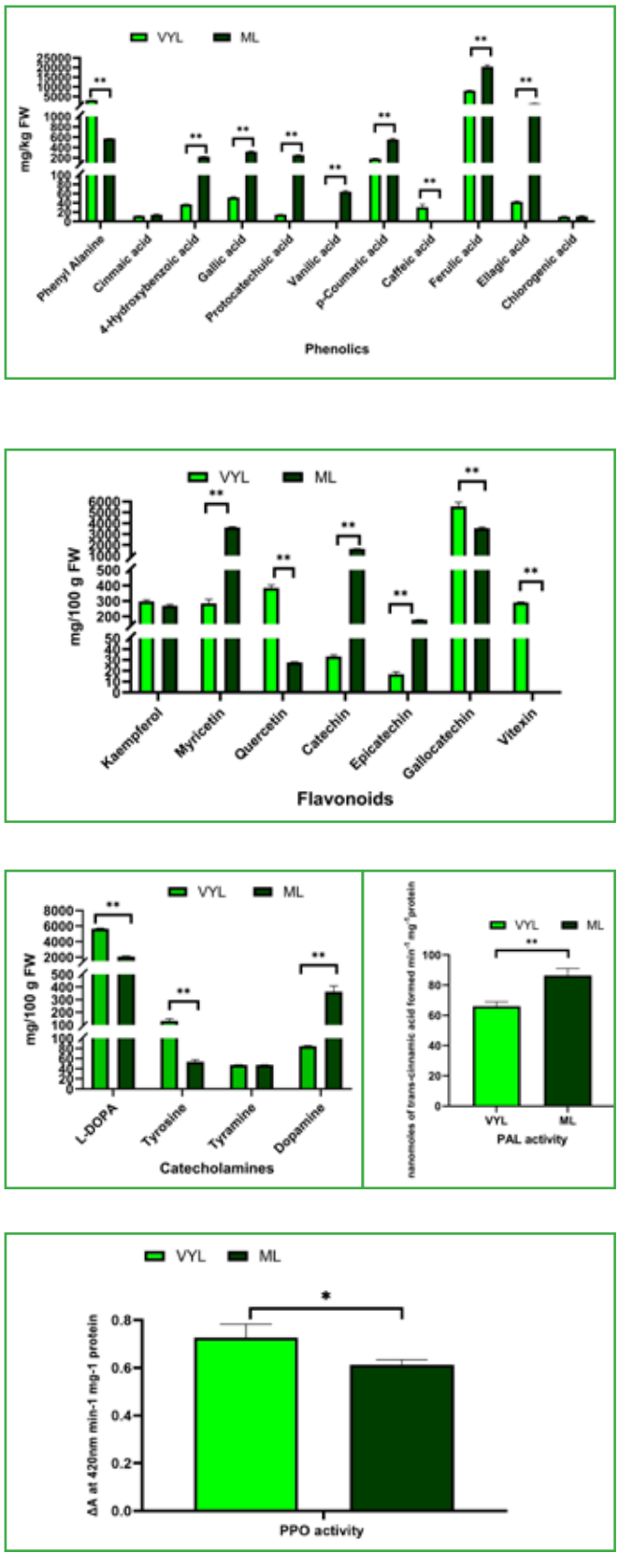


Figure 3: Metabolite content and enzymatic activities quantified in faba bean leaves at different developmental stages: VYL (Very Young Leaves) and ML (Mature Leaves). Asterisks (**) indicate highly significant differences in metabolite levels between VYL and ML.

(PPOs) enzymatic activity compared to ML, which may underpin their elevated L-DOPA accumulation. The increased abundance of phenylpropanoid pathway derived metabolites in mature faba bean leaves can be attributed to the upregulation of key enzymes, particularly phenylalanine ammonia-lyase (*PAL*). Additionally, other phenolic compounds derived from cinnamic acids, such as 4-hydroxybenzoic acid, protocatechuic acid, p-coumaric acid, ferulic acid, and ellagic acid, were also significantly more abundant in ML (**Figure 3**). These findings emphasize the need for a comprehensive understanding of the metabolic pathways and regulatory mechanisms underlying the differential accumulation of L-DOPA in faba bean tissues.

Bioprospecting plant microbe interactions in the coal mine area for higher nutrient use efficiency in rice under aerobic conditions

Screening of plant growth-promoting microbes from the rhizosphere of plants in coal mine area

The soil samples from the rhizosphere of plants grown in Ramgarh coal mine area were collected for the isolation of plant growth-promoting microbes. The samples were serially diluted and plated on the media plates of Aleaksandrow agar for potassium (K) solubilizing microbes, zinc (Zn) solubilizing agar for Zn solubilizing microbes, nutrient agar for bacteria, Rose Bengal agar for fungi, and Pikovaskaya agar for phosphate solubilizing microbes. The individual colonies showing zones of hydrolysis (**Figure 4**) on P, K and Zn solubilizing media were isolated and streaked on the fresh media plates for purification. The bacterial and fungal colonies obtained respectively on nutrient agar and Rose Bengal agar, were further screened for P, K and Zn solubilization potential on respective media plates. A total of three each, P solubilizing bacterial and fungal isolates, one each, K solubilizing bacterial and fungal isolates and four each Zn solubilizing bacterial fungal isolates were isolated.

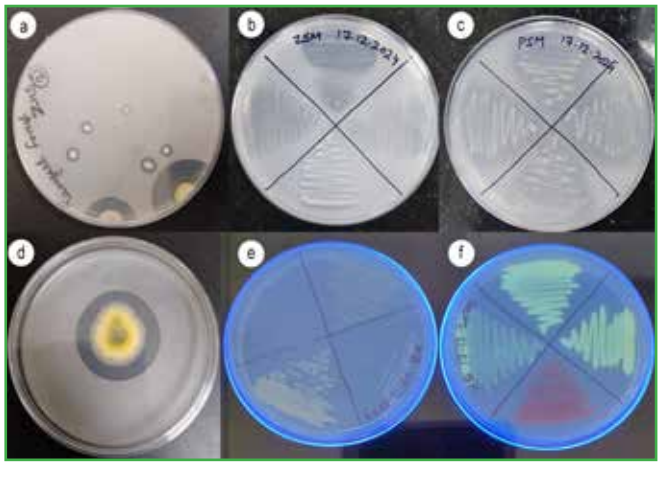


Figure 4: Colonies showing zones of hydrolysis in specific nutrient media by fungal (**a, d**) and bacterial isolates (**b, c, e & f**) isolated from the plant rhizosphere grown in coal mining areas of Ramgarh, Jharkhand.

Effect on different land use systems and management practices on microbial dynamics, soil health, and carbon sequestration in acidic soil

Assessing land use and management practices on soil microbial dynamics and health

Soil is one of the biggest reservoirs of microbial diversity, yet the processes that define the community dynamics are not fully understood. There is a need to characterize microorganisms and their byproducts for enhancing mineralization, mobilization and use efficiency of nutrients under abiotic stress *vis-a-vis* land use and management practices. A study has been initiated on different land use systems, management practices on microbial dynamics, soil health and carbon sequestration in acidic soil. Soil samples from different layers (0-15 and 15-30 cm) were taken from random places of the plots. Different nutrient management practices viz., 100% inorganic, integrated (50% inorganic and 50% inorganic), 100% organic are being evaluated on cereals (maize, finger millet), pulses and oilseeds (pea, French bean, mustard) and vegetables (tomato, brinjal) for productivity and physical, chemical and microbial properties of soil. Effect of conventional and conservation tillage were initiated to know the changes in soil microbiome in pea grown in rice fallow (**Figure 5**). Role of mulching (rice straw mulch, maize stalk mulch, Tephrosia sp. mulch and no-mulch) are being evaluated in pea, bean, vegetables etc. for documenting changes in microbial dynamics, soil health and carbon sequestration. Effect of crop residue management (standing residue, in-situ residue retention etc.) and organic vs inorganic pest/ disease management practices on different crops are being evaluated for soil health parameters. Cereal and legume intercropping systems showed higher bacterial populations compared to sole crops. Millet and soybean under organic recorded the highest bacterial (20.3 × 10^6 CFU/g) and fungal populations (26.9 × 10^3 CFU/g).

No-mulch vs straw mulch vs leaf mulch

Conventional tillage vs no-till

Figure 5: Different management practices on soil health and crop growth.

Crop diversification for enhancing food and nutritional security and soil fertility

Development of nutritional crop cafeteria and crop diversification model

A significant percentage of population in Jharkhand and adjoining states are faced with several nutritional deficiency and associated health issues. Keeping in mind the agro-climatic situation of *Chotanagpur* plateau region, food habits and resource availability a nutritional crop cafeteria has been developed in Farm-B of the institute (**Figure 6a**). The crop cafeteria developed in 1,000 m^2 area with diversified crops like cereals (maize, millets), pulses (lentil, chickpea, pea), oilseeds (rapeseed mustard, soybean, ground nut), vegetables (cauliflower, cabbage, pumpkin, spinach, fenugreek, amaranthus, basella, etc.), root vegetables (radish, beet root, carrot) and demonstrations to farming communities are being carried out (**Figure 6b**). A calendar for year-round growing of these different crops was prepared with inclusion of legumes in cropping system mode (in intercropping or in crop sequence). Sustainable agricultural practices like crop rotation, conservation tillage, residue recycling, mulching and drip and sprinkler irrigation etc. being followed for enhancing system productivity, profitability, water use efficiency and sustaining soil health. Major part of the "Pilot Project for Crop Diversification" was being implemented in the West Singhbhum district of Jharkhand. As part of the project, two training and awareness programs were conducted and various agricultural inputs, including seeds for paddy, mustard, finger millet, chickpea, and vegetables, were distributed to the farmers for enhancing their farm productivity and diversity index.

Figure 6: Diversified crop cafeteria developed in ICAR- IIAB (**a**). Demonstration and training being organized on crop diversification (**b**).

Development of climate resilient farming system models in Jharkhand for food and nutritional security and enhancing soil health

Development of climate resilient farming system models for sustainable agriculture

The primary land use in the *Chotanagpur* plateau is agriculture with low cropping intensity and subsistence type of agriculture. The soil is acidic with low organic carbon leading to nutrient deficiency and sub optimal crop productivity. To overcome these challenges, climate resilient farming system models *viz*., integrated farming system (IFS), integrated organic farming system (IOFS) and natural farming system were developed. Both the IFS and IOFS models (1.0 acre area each) are made up of different enterprises such as cereals (rice, maize. finger millet), pulses (French bean, pea, chickpea), oilseeds (soybean, groundnut, rapeseed-mustard), vegetable crops (French bean, tomato, brinjal, capsicum, carrot, okra, cabbage, potato, broccoli, cauliflower, chili, coriander, etc.), fruits (mango, banana, guava, custard apple, lemon, papaya, dragon fruit), fodder crops, central farm pond, duckery unit, farmyard manure pits and vermicomposting unit (**Figure 7**). A farm pond of 900 m^2 area with a depth of 3.0 m and lined with high density silpaulin was developed to cater drip and sprinkler irrigation irrigation of IFS and IOFS models along with duckery and aquaculture. Hedgerow species *Tephrosia* spp. was grown in bunds while guinea grass was planted at bund slopes for the supply of fodder. Integrated nutrient management for IFS and organic management for IOFS were being followed for crop production. Conservation agricultural practices like minimum tillage, mulching, residue retention, and organic pest management practices were also followed. Overall, these models will enhance system productivity, employment generation and nutritional security.

Figure 7: Different stages and components under IFS and IOFS models developed. (**a**) sowing of crops in lines, (**b**) water filled farm pond, (**c**) cereal + legume intercropping and (**d**) fruit orchard.

Identification of suitable mustard cultivars and standardization of management practices for enhancing phosphorus use efficiency in rice-fallow

Enhancing phosphorus use efficiency and productivity of mustard in acidic soil

Indian mustard (*Brassica juncea* L.) is an important oilseed crop in Jharkhand. The widespread occurrence of strong to slightly acidic soils, which account for 84.9% of the state's total geographical area, poses a significant abiotic stress on the productivity of rapeseed-mustard. In Jharkhand, out of the total cultivated area of 2.1 million hectares, 1.7 million hectares are left fallow under rice-fallow systems during the rabi season. The efficiency of phosphorus (P) fertilizers in acidic soils is notably low due to their adsorption and precipitation as aluminium-phosphates and iron-phosphates. Consequently, only 10–20% of the applied phosphorus is effectively utilized by crops. To overcome these challenges, a pilot study has been taken up, wherein paddy variety 'Sehbhagi Dhan' was cultivated through the direct-seeded method at the experimental site and harvested in November 2024 (**Figure 8a**). Observations on paddy yield and yield attributes were recorded, and soil samples from varying depths were collected for further analysis. Following the paddy crop, mustard cultivars were laid out in a split-plot experimental design (**Figure 8b**). The main plot treatments included different phosphorus levels along with phosphorus-solubilizing bacteria (PSB), liming and mulching, while the subplots were assigned with five different mustard cultivars. Comprehensive observations on crop performance and soil properties are being recorded and analysed for meaningful insights.

Figure 8: Cultivation of paddy through DSR method (**a**). Sowing and establishment of mustard cultivars under different phosphorus levels (**b**).

Quantifying gaps for sustaining agricultural production and assessing perception of biotechnology

Addressing technological gaps in enhancing agricultural productivity

The average monthly household income in Jharkhand is less than five thousand rupees, reflecting significant economic challenges despite advancements in agricultural technologies. Disparities in the adoption and implementation of modern practices hinder agricultural productivity in the state. Identifying and addressing the factors contributing to these technological gaps is critical to enhancing production efficiency. Furthermore, biotechnology, often equated solely with Bt/GM

crops, faces widespread environmental skepticism, exacerbated by misconceptions and limited awareness. This negative perception hampers its broader adoption and potential benefits in sustainable agriculture. The study is being conducted to explore these issues, assess the barriers to technology integration, and investigate strategies to rectify misconceptions about biotechnology to foster its acceptance and long-term impact on Jharkhand's agriculture. In this background, the research work has been initiated with a selection of areas and an inventory of technologies/ recommended practices in the selected area has been developed.

Sustainability of Farmer Producer Organizations (FPOs) in Eastern India

Farmer Producer Organizations (FPOs) are pivotal in empowering small and marginal farmers, enhancing market access, and fostering collective bargaining. However, their sustainability faces critical challenges, including inadequate capital, limited market linkages, and operational inefficiencies. The study examined the factors influencing the long-term viability of FPOs, emphasizing governance, capacity-building, and policy support. Initial findings based on a review of the literature reveal that a robust financial base, effective leadership, and institutional backing are central to sustaining FPOs. Additionally, innovative marketing strategies and the integration of digital technologies were identified as key enablers for resilience and scalability. An index is under development to map and quantify the sustainability of the FPOs in Eastern India.

Decipher the role of tetrathionate respiration on the colonization and virulence of *Salmonella typhimurium*

Characterization of plasmids for engineering tetrathionate pathways in *Salmonella* spp.

Salmonella typhimurium is a zoonotic pathogen affecting both humans and animals. Bacteria mainly spread through contaminated food and water and cause non-typhoidal salmonellosis (NTS). Studying the biofilm formation and colonization of this bacteria helps in designing preventive and therapeutic strategies. *Salmonella typhimurium* strain has been cultured and the strain lineage through biochemical tests and amplification *invA* gene. The plasmids like pKD46, pKD4, pCP20, pCas, and pTaregetF are being characterized to engineer tetrathionate-related pathways in the *Salmonella* spp. (**Figure 9**).

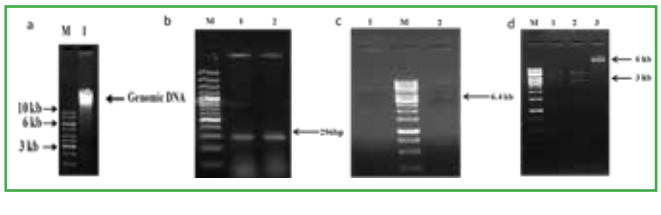


Figure 9: Characterization of *Salmonella typhimurium* and plasmids. (**a**) Agarose gel electrophoresis (0.8%) of *Salmonella typhimurium* genomic DNA. Lane M: 1 Kb DNA ladder; Lane 1: *Salmonella typhimurium* genomic DNA. (**b**) PCR confirmation of *Salmonella typhimurium* using the species-specific *invA* gene. Lane M: 100 bp DNA ladder; Lanes 1 and 2: amplification of the *invA* gene (296 bp). (**c**) Confirmation of the pKD46 plasmid. Lane M: 1 Kb DNA ladder; Lane 1: BamHI-digested pKD46 plasmid; Lane 2: undigested pKD46 plasmid. (**d**) Confirmation of the pCP20 plasmid. Lane M: 1 Kb DNA ladder; Lane 1: EcoRI-digested pCP20 plasmid; Lane 2: undigested pCP20 plasmid.

Understanding the morpho-physiology and molecular mechanism of seed shattering in grain amaranth (*Amaranthus spp.*)

Based on prior studies in other crops, key genes and transcription factors linked to seed-shattering tolerance were selected for this study. These genes influence abscission zone differentiation, cell wall reinforcement, and hormonal signaling. Genes such as *SHP1*, *SHP2*, and *qSH1* regulate abscission zone formation and lignification, while *NST1*, *NST2*, and *IDT* contribute to mechanical reinforcement and cell identity. Hormonal regulators, including ethylene (*ERFs*), auxin (*ARFs*), gibberellin (*GA20ox*, *GA3ox*), and cytokinin (*CKX*), play vital roles in balancing abscission and seed dispersal. Transcription factors like *NAC* and *MYB* are involved in cell wall remodeling and lignin biosynthesis. These genes and transcription factors were shortlisted from the *Amaranthus* database for real-time PCR-based expression analysis and validation. RNA isolated from spike tissues of contrasting genotypes was converted to cDNA to study the expression profiles of the selected genes. Gene-specific primers were designed and are being validated for their specificity.

Molecular breeding for development of rice varieties with inbuilt tolerance to drought, low soil phosphorus and blast

Marker-assisted selection in rice breeding for tolerance to drought, low soil phosphorus, and resistance to blast

Molecular breeding aimed at developing rice varieties with built-in tolerance to drought, low soil phosphorus, and blast diseases is essential due to the unpredictable monsoon patterns caused by climate change, which results in production losses in rainfed areas. To minimize losses from severe drought episodes, it is vital to cultivate rice varieties with appropriate growth duration that are tolerant to drought and other prevailing biotic stresses. Considering these challenges, the project focuses on breeding rice cultivars suitable for direct seeding. Introgression of key yield-related quantitative trait loci (QTLs) and genes: qDTYs for drought tolerance, *Pup1* for low soil phosphorus (P) tolerance, and *Pi2, Pi9,* and *Pi54* for blast resistance, using marker-assisted selection demonstrated promising solutions to address aforesaid challenges. In the Kharif 2024 season, 537 F_5 selections from eight crosses containing different combinations of DTYs and *Pup1* were evaluated under direct-seeded rainfed conditions. Based on their performance, 328 plants from these eight crosses were selected. Additionally, 3,100 plants from 170 complex crosses were chosen based on their performance from 4,032 F_4 plants associated with 326 evaluated crosses. Moreover, 114 F_3 populations segregating for QTLs related to drought and low phosphorus tolerances, as well as various blast resistance genes, were assessed, resulting in the selection of 1,480 plants exhibiting high-yielding traits (**Figure 10**).

Figure 10: Photograph representing rice field during *Kharif,* 2024.

Bulk segregant analysis revealed key polymorphisms to mitigate the impact of brown spot disease on rice performance

Brown spot disease poses a significant challenge to rice production, affecting yield and quality under diverse cultivation conditions. To address this issue, based on observations in *Kharif,* 2022 and 2023, an F_3 population was subjected to bulk segregant analysis a) to evaluate the impact of brown spot disease on rice performance under both direct-seeded and transplanted conditions, b) to investigate the inheritance patterns of resistance, and c) to identify genomic regions associated with brown spot resistance in rice. The analyses revealed that brown spot disease significantly impairs crop performance, affecting yield-contributing traits in susceptible plants. The top two SNPs with the highest ΔSNP index were located within coding regions of genes which are known to play crucial roles in disease resistance in various crop models. Inheritance studies suggested that major genes with supplementary interactions confer resistance to brown spot disease. The identification of specific SNPs associated with resistance provides a strong foundation for map-based cloning and marker-assisted selection to improve brown spot resistance in rice. This research offers valuable insights for breeding resistant rice varieties and developing effective disease screening strategies to mitigate the impact of brown spot disease on rice production.

Recombinant inbred lines for mapping of genomic regions translating for economically important traits in rice

Developing rice varieties that combine high yield with tolerance to abiotic and biotic stresses is crucial for sustainable rice production. In this context, recombinant inbred lines (RILs) serve as a powerful resource for mapping genomic regions associated with traits of economic importance, including drought tolerance, nutrient efficiency, and disease resistance. Four F_4 populations developed involving MTU1210, a high-yielding lowland variety possessing drought tolerance, were advanced through the single seed descent (SSD) method for developing RILs for mapping genomic regions conferring drought tolerance and their validation.

Improvement of rice yield under low light intensity

Improving rice yield under low light intensity is crucial for sustaining production in regions with prolonged cloudy conditions or shaded environments. In the current study, the identification of polymorphic markers and advancing mapping populations provided a foundation for uncovering genomic regions linked to enhanced adaptability and productivity under suboptimal light conditions (**Figure 11)**.

Figure 11: Evaluation of the F_4 rice population under low light conditions.

Out of 100 potential simple sequence repeats (SSR) markers, we identified 32 polymorphic SSR markers based on the band results observed in the parents IRCTN 91-84 and ISM. During *Kharif*, 2024 F_4 populations derived from the following crosses were cultivated: IRCTN 91-84 × ISM, IRCTN 91-84 × Rasi, IRCTN 91-84 × IIABR 48, IR 64 × Rhyllo Red, Danteshwari × MTU 1081, Danteshwari × MTU 1121, IRCTN 91-94 × Samba Mahsuri, MTU 1010 × IRCTN 91-84, MTU 1010 × Megha Rice-1, Rhyllo Red × Samba Mahsuri, Samba Mahsuri × IRCTN 91-94, Swarna × IRCTN 91-84, Swarna × Mahisugandha, Swarna × Rhyllo Red, Swarnprabha × MTU 1081, and Swarnprabha × MTU 1153. From each plant, single panicles were harvested for generation advancement. Single seeds were collected from these plants across all mentioned families for further generation advancement in the next season, aiming at mapping key genomic regions for targeting in genetic improvement of rice (**Figure 11**).

Deciphering and deploying low phosphorus tolerance and nitrogen use efficiency in rice using targeted genomics approach

Targeted genomics for enhancing low phosphorus tolerance and nitrogen use efficiency in rice

This study focused on deploying targeted genomics to enhance low phosphorus tolerance and nitrogen use efficiency in rice, leveraging CRISPR/Cas9-mediated gene editing and advanced breeding approaches. The two genic candidates Aldolase (*Os02g08030*) and CaM binding protein (*Os02g08120*) were targeted for deciphering the role in low phosphorus (P) tolerance in rice. For each gene, two sets of guide RNA (gR1, gR2) were designed using CRISPR direct software and were cloned separately in pCAMBIA1302CRISPR/Cas9-U6sgRNA vector. The sgRNA was cloned in CRISPR/Cas9 plant transformation vector containing hygromycin (*hpt*) selection marker. Further, the editing construct was mobilized in *Agrobacterium tumefaciens* strain LBA4404 and genetically edited rice. MTU-1010 lines were generated using plant tissue culture methods of seed sterilization, callus induction, *Agrobacterium* infection, selection, shoot regeneration, and root formation. A total of 27 MTU-1010 plants hardened putative genome-edited plants were grown in soilrite mixture in pots to maturity in the greenhouse facility. T0 plants showed a good response, and each individual was fertile and able to produce T1 seeds. Genomic DNA was isolated from individual leaves of each plant and putative transgenic plants were subjected to molecular analysis the hpt-positive plants were selected (**Figure 12**) and their agro-morphological characters were recorded (**Table 1**). Advanced breeding lines through biparental crosses involving best lines were identified (seven F_5 and 67 F_2 crossed lines) for nitrogen use efficiency and low P tolerance and multi-locational evaluation in deficient soils for enhancing genetic gain (**Figure 13**).

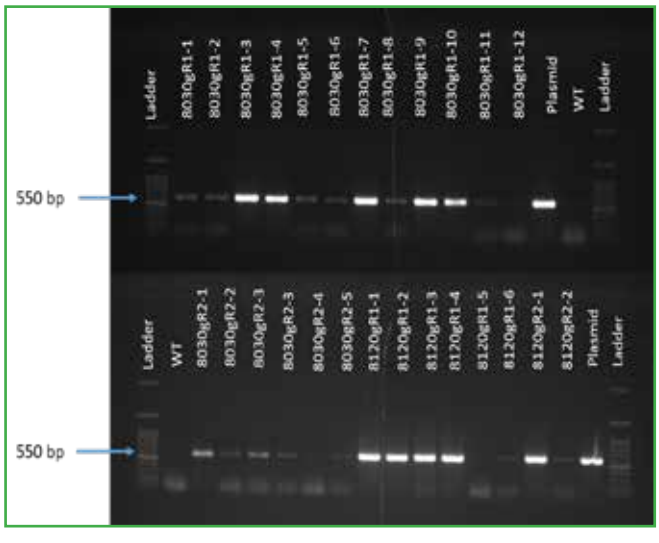


Figure 12: Gel photograph of PCR amplified product using hygromycin (*hpt*) specific primers, DNA templates isolated from rice T0 lines.

Figure 13: Rice F_2 Populations in the field during *Kharif*, 2024.

Table 1: Agronomic traits of putative T0 mutant rice lines.

Sl. No.	Genotype (MTU1010)	Plant height (cm)	Tiller numbers	Panicle length (cm)	Total grain/ panicle	Filled grain/ panicle	Empty grain/ panicle
1.	Wild Type	80.2	13	20.5	256.7	222.5	34.2
2.	8030gR1-1	73.2	10	18.3	201.3	101.1	100.2
3.	8030gR1-2	66.1	8	16.4	129.4	31.1	98.3
4.	8030gR1-3	72.3	14	20.0	135.2	55.1	80.1
5.	8030gR1-4	68.2	12	17.3	117.6	53.7	63.9
6.	8030gR1-5	71.7	11	15.1	131.9	60.5	71.4
7.	8030gR1-6	70.1	11	14.9	128.7	26.1	102.6
8.	8030gR1-7	69.1	9	17.2	111.3	54.8	56.5
9.	8030gR1-8	65.3	8	13.6	109.7	38.9	70.8
10.	8030gR1-9	64.7	10	16.3	85.8	20.7	65.1
11.	8030gR1-10	62.6	7	15.4	96.1	30.2	65.9
12.	8030gR1-11	70.5	11	15.6	102.8	62.6	40.2
13.	8030gR1-12	72.1	12	17.8	137.5	70.5	67.0
14.	8030gR2-1	60.0	10	13.5	80.6	31.4	49.2
15.	8030gR2-2	58.9	8	11.4	86.7	35.8	50.9
16.	8030gR2-3	65.2	8	16.7	100.8	46.7	54.1
17.	8030gR2-4	63.8	6	11.9	113.6	76.5	37.1
18.	8030gR2-5	66.1	7	14.3	96.7	40.1	56.6
19.	8030gR2-6	66.0	13	13.8	118.1	50.9	67.2
20.	8030gR2-7	68.6	9	16.1	105.6	51.5	54.1
21.	8120gR1-1	70.5	10	17.3	112.3	60.1	52.2
22.	8120gR1-2	74.1	11	18.7	213.4	104.3	109.1
23.	8120gR1-3	68.4	10	15.4	93.9	57.4	36.5
24.	8120gR1-4	67.1	12	13.7	84.3	32.7	51.6
25.	8120gR1-5	63.8	8	12.2	96.7	43.2	53.5
26.	8120gR2-1	72.3	11	17.9	169.5	70.5	99.0
27.	8120gR2-2	74.6	12	18.2	201.9	108.3	93.6

Gene editing and engineering of mediator subunit *Med15* to modulate grain size/weight trait in rice

Characterization of F_2 and F_3 rice populations for grain size variations through the use of polymorphic SSR markers was carried out. A total of 49 out of 100 potential simple sequence repeat (SSR) markers were selected based on polymorphism for the donor (PB1 & PB1121) parent and recipient (Badshabhog & Malbhog) parent. In the targeted gene *OsMed15a,* located on 4p:1.75Mb-1.76Mb of the rice genome several markers were prioritized based on polymorphic associations viz., Rice27, Rice33, Rice40, Rice41, Rice42, Rice51, Rice53, Rice54, RM201, RM161, RM162, RM236, RM237, RM408, RM431, RM452, RM514, RM518, RM495, RM316, RM6100, RM655, RM16335, RM16338, RM16355, RM16353, RM16393 and RM16424 (**Figure 14a**). Variations in seed size were observed within the F_2 populations (PB1121 x Badshabhog). Significant differences in the grain size traits of the F_3 seeds compared to their respective parents were evaluated. These seeds' grain length (GL) varied from 5.74 mm to 13.09 mm, while the grain width (GW) ranged from 1.64 mm to 2.96 mm (**Figure 14b**). Whereas in the F_2 population, GL ranged from 7 mm to 10 mm, and the GW varied from 1.7 mm to 3.25 mm (**Figure 14c**).

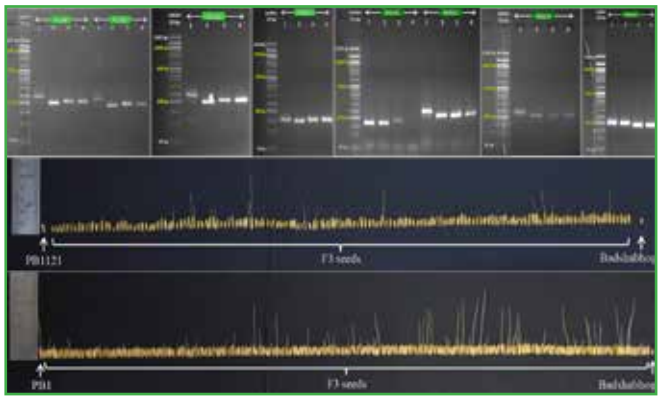


Figure 14: Polymorphism of Simple sequence repeat markers (Rice40-42, 51, 161, 162, 219, and 236) in parental lines. Lanes 1, 2, 3, and 4 represent PB1, PB1121, Badshabhog, and Malbhog, respectively (**a**). Variations in grain morphology phenome of seeds of crossbred F_3 populations in comparison to parental populations (**b & c**).

Molecular mapping and transcript analysis of seed protein content, digestibility and aluminium toxicity in chickpea (*Cicer arietinum* L.)

Evaluation of seed protein content and QTL mapping in recombinant inbred lines of chickpea

Chickpea production in India reached 13.75 million tons, contributing to over 50% of India's total pulse production and serving as a significant source of plant-based protein. Typically, chickpea varieties contain 18-22% seed protein content (SPC), but germplasm lines like T39-1 have been found to have higher protein content (>28%). During the 2024-25 cropping season, 231 Recombinant Inbred Lines (RILs) derived from the cross of ICC 4958 and T-39-1 were evaluated for seed protein content.

Figure 15: Chickpea cultivation during the 2024-2025 season in the institute field (**a**). Total protein content in the recombinant inbred lines of chickpea (**b**).

A well-known chickpea repository i.e., CHNS, revealed a wide range of protein content (8-38%) within the population. Remarkably, some lines, such as RIL146, showed protein content as high as 37.125% (**Figure 15**). Although both parent lines have high protein content, the fixed RIL population exhibited the highest protein levels. Genotyping the RIL population is being used to locate quantitative trait loci responsible for the elevated seed protein content for downstream applications.

Comprehensive characterization of winged bean mutant population (M_2) through morphological and molecular studies

Morphological and molecular characterization of M_2 winged bean mutant population for genetic diversity analysis

The winged bean, often called the "one species supermarket" due to its completely edible parts, has the potential for genetic improvement. Genetic variation within this crop population is essential for selecting desirable traits.

Figure 16: Variation in seed size (**a**) and tuber length (**b**) in mutant winged bean.

Our studies analyzed 147 families, consisting of 873 individual M_2 plants, using 30 agro-morphological descriptors (both qualitative and quantitative). The M_2 generation displayed considerable variation in most qualitative characters compared to the parental line (AKWB1) as we observed two to four distinct traits for a single character (**Figure 16**). Regarding quantitative characters, the M_2 generation exhibited a wider range, higher standard deviation, and more significant variance than the parental line. The mutants genotyped using

22 polymorphic simple sequence repeats (SSR) markers produced a total of 85 alleles, with the number of alleles per locus ranging from two to six and an average of 3.86 alleles per locus. The average polymorphic information content was 0.4727, ranging from 0.1886 to 0.7382. A total of 31 unique alleles were identified across 21 SSR loci. The Neighbor-joining dendrogram identified two major clusters, which was in agreement with the results of admixture modeling (**Figure 17**). These findings suggest that gamma radiation effectively induced significant genetic diversity in the winged bean.

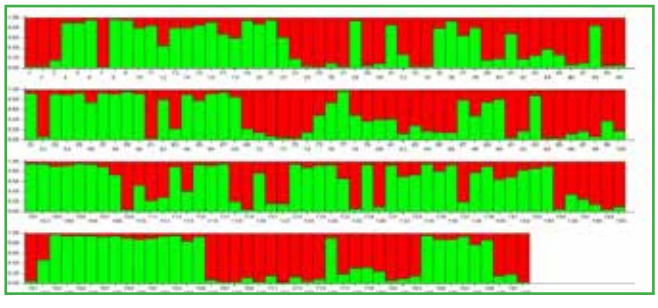


Figure 17: Population structure (K=2) based on simple sequence repeat markers in 192 M_2 winged bean germplasm.

Creation of variability, genome analysis and identification of genotypes/QTL for trait of importance in winged bean

Identification of the gene for seed coat color in winged bean

The seed coat color in winged beans ranges from white to brown to purple, serving as an essential marker for breeding and indicating the plant's antioxidant properties. Seed coat color-related QTLs *qSdc1.1* and *qsdc3.1* were analyzed using flanking marker information and a chromosome-level reference genome sequence. Gene prediction from these QTL regions identified 127 genes for *qSdc1.1* and 24 for *qSdc3*. *In-silico* annotation of these genes using the NCBI database highlighted four key seed coat color with its different paralogous genes: *qSdc1.1-9, qSdc1.1-12, qSdc1.1-15, qSdc1.1-16, qSdc1.1-17, qSdc1.1-18, qSdc1.1-25, qSdc1.1-28* (*UDP*-glycosyltransferase 83A1), *qSdc1.1-74, qSdc1.1-78, qSdc1.1-79* (transcription factor *MYB113*), from QTL *qSdc1.1*. Similarly, from QTL *qSdc3.1* the selected genes were *qSdc3.1-3* (G-box-binding factor 4), *qSdc3.1-12, qSdc3.1-13, qSdc3.1-16, qSdc3.1-18* (*WAT1*-related protein). Expression analysis of genes in different winged bean genotypes revealed that *qSdc1.1-78* (transcription factor *MYB113*) and *qSdc3.1-13* (*WAT1*-related protein) are upregulated in purple and semi-purple genotypes but not in white seed colored genotypes. This suggests their role in seed coat coloration. The study provides insights into the genetic basis of seed coat color and identifies key genes involved in anthocyanin production in the winged bean.

Deciphering mechanism conferring tolerance to aluminum toxicity in finger millets

Evaluation of morphological traits and hydroponic screening for aluminum toxicity tolerance in finger millet genotypes

A set of 275 genotypes of finger millet (*Eleusine coracana*), including advanced breeding lines received from ICAR-IIMR, Hyderabad, India were evaluated under an experimental plot inheriting aluminum toxicity stress (78.75 ppm), while the other set was on a control plot treated with lime to mitigate soil acidity during cropping season of 2024-25. Post-germination, approximately 15 traits were recorded during the growth period until harvest, including days to flowering, days to maturity, plant height, culm branching, leaf dimensions, finger length, and chlorophyll content. Significant variations in finger length and chlorophyll content across the two experimental conditions were observed. Morphological observations revealed several promising genotypes with desirable traits and variations (**Figure 18a**). Simultaneously, hydroponics research focused on optimizing aluminum toxicity doses optimization and standardizing germination protocols for BM-3 and PR-202 varieties. Growth parameters at the 3-4 leaf stage (21 days) were evaluated in Hoagland solutions with aluminum concentrations ranging from 100-200 µM at pH 4.5 (**Figure 18b**). Initial trials provided insights into aluminum stress responses, with recorded parameters including plant height, chlorophyll content, root and shoot biomass, and leaf count. Preparations are underway for extended hydroponic experiments involving 275 genotypes and aluminum concentrations ranging from 100-500 µM. These studies aim to refine aluminum stress tolerance screening protocols, thereby advancing the development of resilient finger millet varieties for acid-stressed soils.

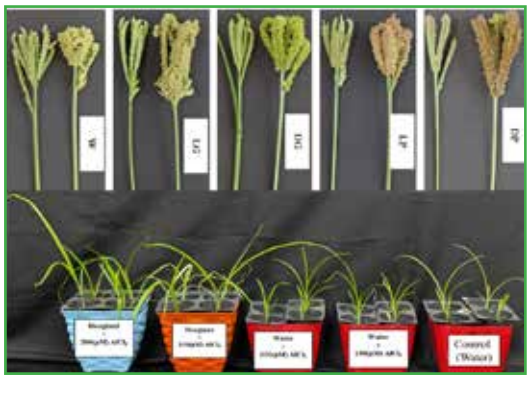


Figure 18: Diversity in glume color of finger millets: W- White, LG- Light Green, DG- Dark Green, LP-Light Pink, DP- Dark Pink (**a**). Evaluation of growth parameters at 3-4 leaf stage in Hoagland solutions with aluminum concentrations ranging from 100-200 µM at pH 4.5 (**b**).

Creation of variability, genome analysis and identification of genotypes/QTL for trait of importance in winged bean

Telomere-to-telomere chromosome-scale whole genome sequencing of winged bean (*Psophocarpus tetragonolobus* L.)

Winged bean, a diploid legume (2n=2x=18), is a neglected and underutilized crop with remarkable potential due to its high protein content and adaptability to tropical environments. Despite its high nutritional value, with protein content ranging from 34.3 to 40.7% and oil content from 16.4 to 21.3%, winged bean lacks comprehensive genomic resources. To bridge the gap, measures were taken to build a reference assembly for genetic improvement. The genome size of the winged bean was estimated to be 710 Mb based on flow cytometry analysis. Whole genome sequencing was performed using the PacBio Sequel-II platform, generating a total of 990 Gb of raw data. Hi-C data and Bionano optical mapping were used for scaffolding and chromosome-level assembly. The final assembly covered 697 Mb, organized into 15 scaffolds, with the largest scaffold measuring 111Mb. The assembly had an N50 value of 85.9 Mb and an N90 value of 41.7 Mb, with 27.47 N's per 100 Kb (**Table 2**). The assembly was assessed using BUSCO analysis with the Fables database and results indicated C: 97.61% (S: 94.5%, D: 3.11%), F: 0.42%, M: 1.9%, n: 5366 (**Figure 19a**). Of the assembled scaffolds, nine were large and corresponded to the individual chromosomes of winged bean. The analysis of telomere sequences from the scaffolds revealed that chromosomes 1, 2, 3, 4, 5, and 7 have telomeres at both ends, while chromosomes 6, 8, and 9 were missing a telomere at one end (**Figure 19b**). A total of 49,431 genes were predicted from the assembled genome using the Braker pipeline. This fully annotated assembly will have downstream application, which can be streamlined to genetic improvement of winged bean.

Table 2: Assembly statistics of the winged bean genome, highlighting the accuracy of the built reference assembly.

Statistic	Number	Statistic	Number
Scaffold (>= 0 bp)	15	NG50	$85.97x10^7$
Scaffold (>= 1000 bp)	15	NG90	$11.16x10^7$
Total length (>= 0 bp)	$69.76x10^7$	auN	$83.73x10^6$
Total Scaffold	15	auNG	$83.45x10^{12}$
Largest Scaffold	$11.16x10^7$	L50	4
Total length	$69.76x10^7$	L90	8
Estimated reference length	700	LG50	1
GC (%)	31.08	LG90	1
N50	$85.97x10^6$	N's per 100 Kb	27.47
N90	$41.78x10^6$		

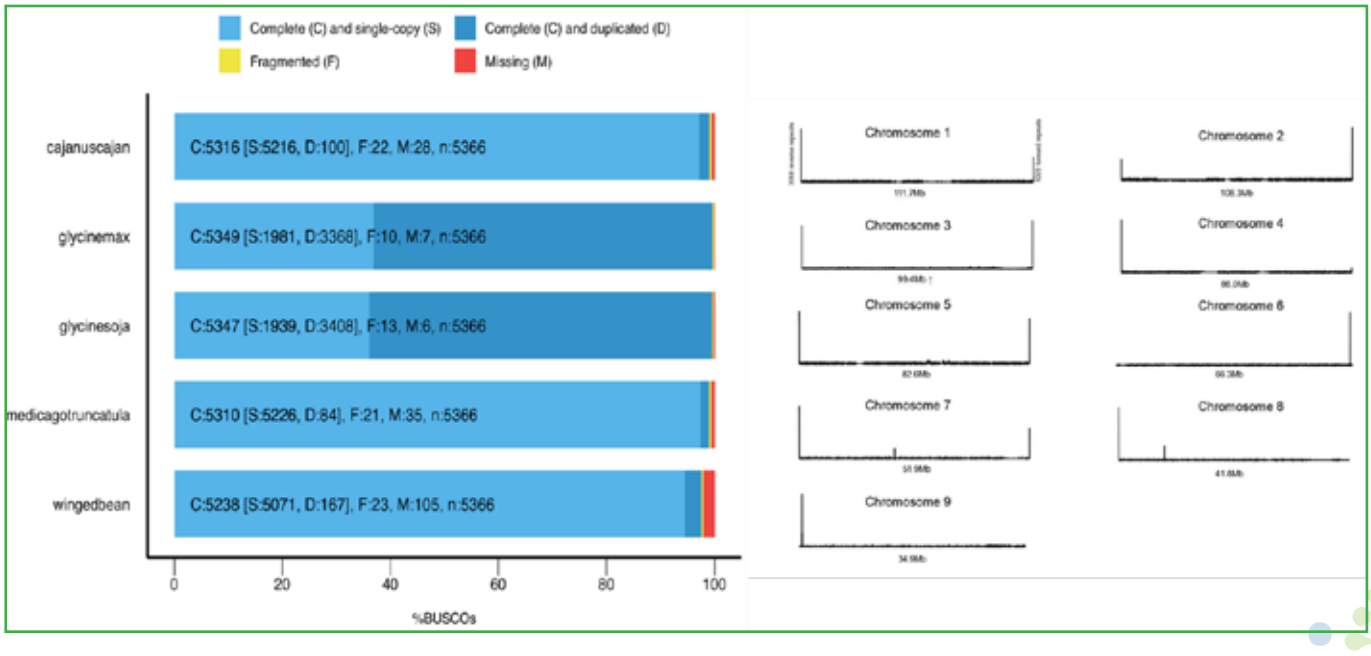


Figure 19: Completeness analysis of the winged bean genome using BUSCO with the Fables database. C = Complete, S = Single copy, D = Duplicate, F = Fragmented, M = Missing, n = Total number of BUSCOs (**a**). Telomere prediction from the assembled chromosomes of the winged bean genome (**b**). Vertical lines represent the telomere signals.

Assembly of the mitochondrial genome of winged bean

The mitochondrial genome of *Psophocarpus tetragonolobus* was successfully assembled using high-quality Illumina short reads and PacBio long reads, yielding a circular genome structure with a length of 366,925 bp (**Figure 20**). The average read coverage depth was 450.805X, ensuring high confidence in the accuracy of base calls across the genome. The base composition of the genome was as follows: A (27.63%), T (26.93%), C (22.72%), and G (22.72%).

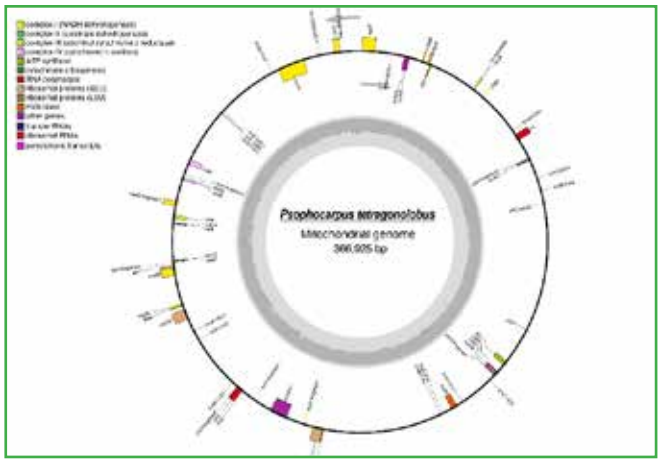


Figure 20: Circular representation of the mitochondrial genome of winged bean.

The annotated mitochondrial genome consisted of 124 genes, including 65 protein-coding genes, 37 tRNA genes, and 22 rRNA genes. Additionally, 20 distinct transfer RNAs were identified, transporting 18 amino acids, with some tRNAs (e.g., *trnM-CAT* and *trnM-CAU*) covering synonymous codons for the same amino acid. Also, a total of 25 simple sequence repeats (SSRs) and 19 variable number tandem repeats (VNTRs) were identified from the assembled mitochondrial genome. The distribution of SSR types included 12% mononucleotide repeats, 36% dinucleotide repeats, and 52% trinucleotide repeats.

Phylogenetic analysis of winged bean using mitochondrial markers

The phylogenetic analysis of the mitochondrial genome revealed strong clustering within the Fabaceae family, with species like *Medicago truncatula*, *Lotus japonicus*, *Phaseolus vulgaris*, and *Glycine* spp. Forming well-supported clades (**Figure 21**). Non-legume species clustered separately, indicating evolutionary divergence, including *Solanum tuberosum, Ipomoea batatas*, and *Brassicaceae* members. Notably, domesticated and wild species of *Glycine* showed genetic diversity linked to domestication. The analysis also highlighted convergent evolution between Ipomoea batatas and *Manihot esculenta*, suggesting shared adaptive traits. These results provide insights into plant evolutionary relationships and genetic diversity.

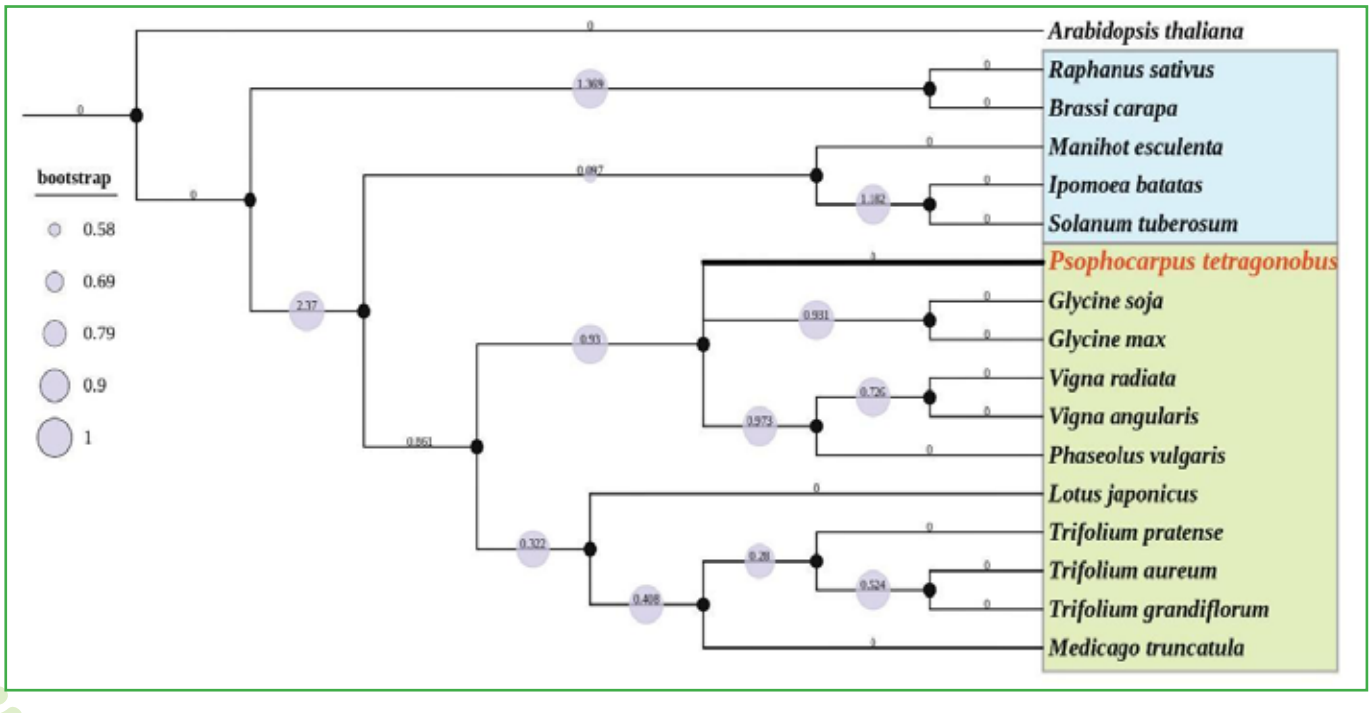


Figure 21: Phylogenetic analysis of the winged bean mitochondrial genome in relation to other legume and tuber species.

Genomic exploration of lesser-known chicken populations and development of improved germplasm

Genetic simulation to explore strategies for heterosis maximization in crossbreeding programs

Inbreeding is a crucial tool in agriculturally important species and laboratory animals for developing homozygous lines to increase heterosis and biomedical research, respectively. But traditional methods require ~20 generations of full sib mating to achieve desired levels. This study investigated a novel approach to expedite inbreeding by suppressing meiotic recombination during gamete formation in chickens. Using stochastic simulation, we compared random mating with recombination (control scenario) to those with blocked recombination in meiosis I (test scenario). A total of 1,000 founder population was simulated using python programming, followed by selection based on genomically estimated breeding value (GEBV) with 20% selection intensity. Random mating of selected parents were done for ten generations in both the scenarios and runs of homozygosity based inbreeding coefficients were analyzed in each generation. The suppression of recombination resulted in accelerated inbreeding accumulation compared to the control scenario, and reached 100% in just nine generations of random mating of selected individuals. We also evaluated the impact of inbreeding on economically important traits including egg production, body weight, and immune response indicators (cell-mediated and antibody-mediated immunity) using real genetic architecture and population parameters (**Figure 22**).

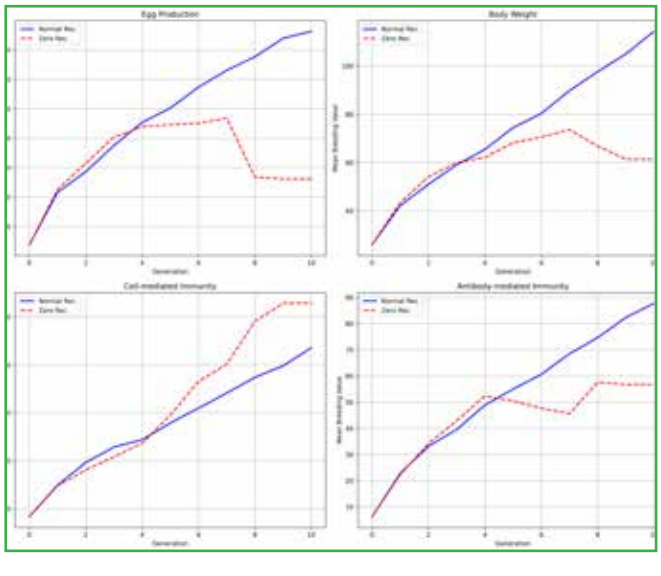


Figure 22: *In-silico* tracking of population and quantitative genetic metrics in conventional and crossover suppressed chicken. Mean breeding values of production, reproduction and fitness traits (cell mediated and antibody mediated immunity) under consideration.

The trends of mean breeding value for the traits did not differ much until the sixth generation, except for cell mediated immunity which performed better compared to control scenarios, even in tenth generation. This approach offers a potential strategy for heterosis maximization by crossing specialized inbred parental lines in chicken, and can be extrapolated to other agriculturally important species and laboratory animals. By reducing the time and resources in inbred lines breeding, the project outcomes are to advance sustainable development goals, mitigation of climate change and 4R (Replace, Reduce, Refine and Responsibility) principles of laboratory animal ethics.

CEEMDAN-based hybrid machine learning models for time series forecasting using MARS algorithm and PSO-optimization

Accurate prediction of time series data is essential for informed decision-making and economic growth, yet remains challenging due to irregular patterns and complex trends. To address this, a CEEMDAN-based hybrid machine learning algorithm was developed, integrating stochastic models to capture weekly potato price volatility in major Indian markets. Smooth decomposed components were modeled using stochastic techniques, while coarser components, identified *via* MARS, were processed using two machine learning algorithms (**Figure 23**). The final predictions were optimized using particle swarm optimization, with performance metrics confirming that the combined model significantly outperformed its individual components.

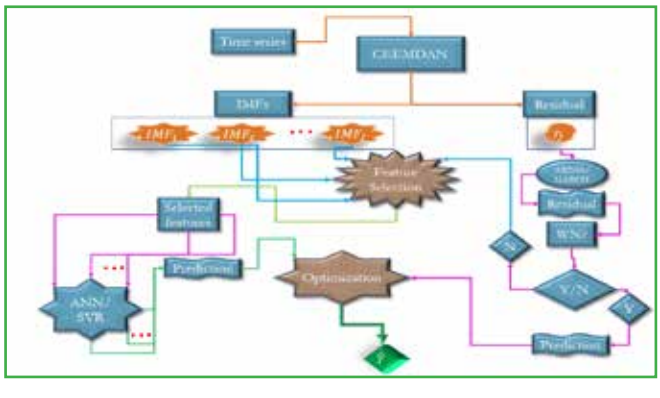


Figure 23: Machine learning algorithm developed and optimized for time series data analysis.

Establishment of information resource and prediction servers for the genes related to yield traits, biotic stress, and abiotic stress in agriculturally important crops

Decoding genetic elements conferring tolerance to aluminum toxicity

The soil acidity (pH <5) poses significant challenges for agriculture, as it often leads to aluminum (Al) toxicity.

It became a serious factor limiting crop productivity as it rapidly inhibits root growth and disrupts root morphology. Certain plant species exhibit natural resistance to Al toxicity, offering the opportunity to catalogue Al toxicity resistance genes for crop improvement. Thus, to develop a machine learning based tool for Al toxicity tolerance genes, initially, 503 protein sequences and 461 DNA sequences were collected as the positive datasets (Al tolerance) and approximately 1,500 sequences of both protein and DNA were collected as negative datasets (non-Al tolerance) (**Figure 24**). The preliminary homology analysis revealed more than 80% similarity in both positive and negative datasets. Sequence length distribution, composition of amino acid (protein), domain composition, nucleotide composition, overall GC content in both of the datasets were analyzed. Though, most of the amino acids in the protein dataset were found to be equally distributed, the percentage of alanine and glycine were more abundant in the positive dataset. Further, in the DNA dataset, GC content was found more in the positive-set than the negative-set. The domain analysis of the protein dataset revealed the abundance of bZIP_plant_BZIP46, SAHH and FACL_fum10p_like domains while in the negative dataset, the domains like GT1_Gtf-like, 7tmC_V2R_pheromone, PBP1_pheromone_receptor were found most abundant. Additionally, domains such as DPBB_EXPA_N, malate_synt_A, S-AdoMet_synt, ABC_MTABC3_MDL1_MDL2, and homeodomain were commonly observed in both the positive and negative datasets. The sequences are currently being encoded to train the MLA models for developing a prediction server.

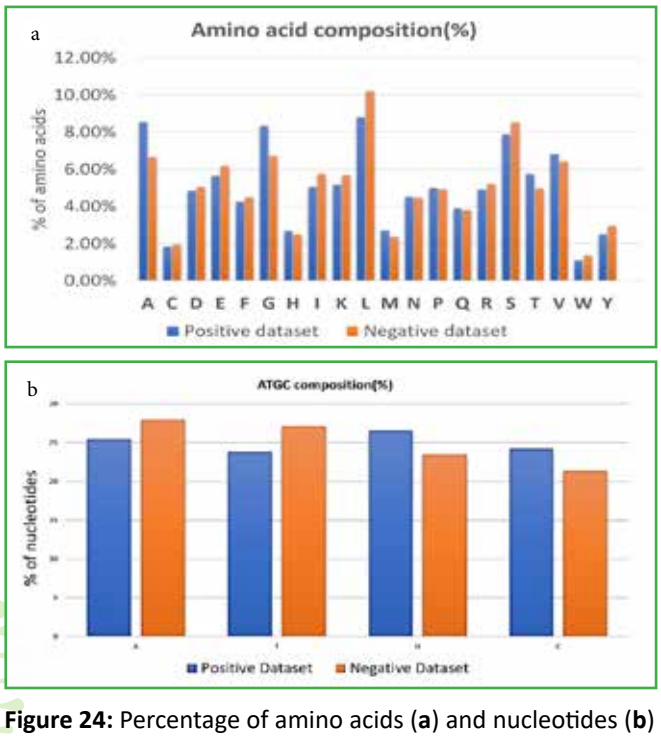


Figure 24: Percentage of amino acids (**a**) and nucleotides (**b**) in the protein datasets.

Prioritization of important genes in important crops for genetic engineering

Success of genome editing depends on the choice of genes to be edited and identification of paralogues. In the Urd bean (*Vigna mungo*) genome, one paralogous gene to the *FNS* (Flavonoid Synthase) gene was identified. *FNS* gene found to have the domains like *CYP93* and *PLN02687*, which belong to the cytochrome *P450* family. For the *F3H* (Flavanone 3-hydroxylase) gene, no paralogous gene was identified. The gene was found to contain conserved domains for oxygenase activity and secondary metabolite biosynthesis, such as the oxidoreductase *2OG-Fe (II)* oxygenase family protein and isopenicillin N synthase. In Sunflower (*Helianthus annuus*) genome, for acyl-lipid (9+3)-(E)-desaturase (*FAD2-1*) gene, no significant paralogue was found. In the crop Soybean (*Glycine max*), for gene *E1Lb* (photoperiod insensitivity gene), two paralogous genes i.e., *E1* (chr-6) and *E1La* (chr-4) were identified. A total of 12 genes associated with photoperiod insensitivity in soybean. In case of Cotton (*Gossypium hirsutum*), jointless gene from tomato (responsible for abscission layer formation) was selected as the target gene. Five orthologs of the gene were found, which are *MADS*-box protein *AGL 24*-like (Gene ID: 107921301), *MADS*-box protein *SVP* (Gene ID: 107924315), MADS-box protein SVP-like (Gene ID: 107945005), *MADS*-box protein *SVP*-like (Gene ID: 121218207). A phylogenetic analysis of these genes with the jointless gene of tomato revealed the better closeness of *MADS*-box protein *AGL* (Gene ID: 107920922) with the jointless gene of tomato. Thus, *MADS*-box protein *AGL* was selected for guide RNA designing. In Maize *(Zea mays)* genome, for *zmDST* (drought and salt tolerance), one paralogous gene was identified on chromosome 1 (Gene ID: 100274943) having a length of 1437 bp and a single exon. For all these genes prioritised, guide RNA's were designed using CRISPOR and CRISP-Pv2.0 tools, for deploying in genetic engineering.

Deciphering the role of microbiome including extremophiles in water bodies and surrounding phylloplane in coal mining areas in the perspective of intensive cage aquaculture system

Metagenomic study of plant leaves revealed microbial abundance in the coal mining environment

Plant Leaf samples were collected from the new and old mine sites of the Ramgarh coal mine and Getalsud (control site) to study the microbial community structure. The control site represents a baseline for microbial diversity and ecological variability. The analysis of phyllosphere microbial community structures across control, new, and old mine sites at the phylum level revealed significant ecological and environmental distinctions. *Cyanobacteriota* was found to be the most dominant phylum in all samples (**Figure 25**). *Pseudomonadota* was another prevalent phylum, though with slightly lower relative abundance compared to *Cyanobacteriota*. The dominance of these two phyla highlights their ecological importance in the mine environments. The new mine site shows signs of ecological adaptation, with distinct microbial communities forming in response to the environment. The old mine site reflects a more stabilized and less diverse ecosystem, potentially due to prolonged exposure to mining activities or environmental changes.

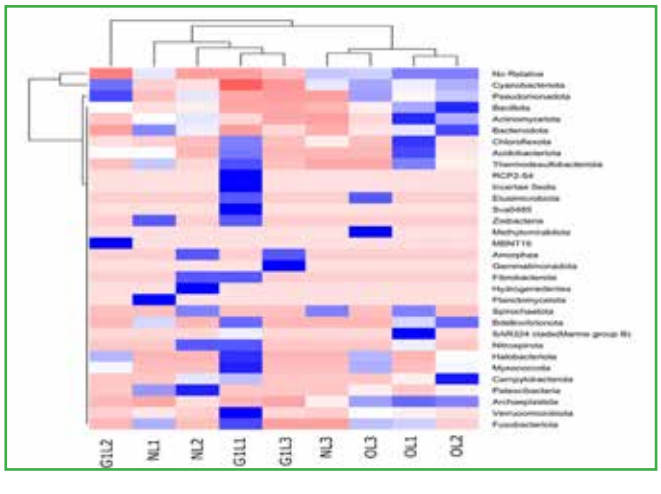


Figure 25: Relative abundance of microbial communities in the control site (Getalsud, G1L1, G1L2, and G1L3), new mine site (Ramgarh new coal mine site, NL1, NL2 and NL3) and old mine site (Ramgarh old coal mine site, OL1, OL2 and OL3).

Formulation and evaluation of nano-inspired mineral mixture for improving productivity and gut health in livestock and poultry

Exploring herbal supplements for improving the bioavailability of nano-minerals in goats

This project aims to address the low bioavailability of minerals and food animal-origin antibiotic resistance. This synthesis of nano-minerals namely copper (Cu), zinc (Zn), and manganese (Mn) is underway through employing both chemical and biological synthesis at laboratory scale and will be followed by large-scale synthesis of these minerals. The nano-minerals synthesized by the chemical method may pose environmental concerns; consequently, the biological method of nano-mineral synthesis is explored. On this line, the plant products employed in nano-mineral synthesis by biological method were evaluated in goats for their possible improvement in feed efficiency through modulating the health and rumen fermentation in goats. Goats are reared primarily by marginal and landless farmers who barely feed the goats with concentrate feed except under commercial setup. Consequently, newer strategies for improving feed efficiency through modulating the health and rumen fermentation. Herbal feed additives are explored due to their potential to address these aspects in sustainable and cost-effective ways. Therefore, a trial was conducted in adult goats with an herbal formulation comprising four herbs (i.e. *Tinospora cordifolia* stems- 2 parts, *Aloe barbadensis* miller pulp- 2 parts, *Curcuma longa* rhizome- 1 part, *Trigonella foenum-graecum* seeds- 1 part) at 0.2% of concentrate feed. The feeding trial was conducted for six weeks followed by one week of digestion trial. There was a significant improvement in adult body weight gain in herbal formulation-fed goats compared to control. Further, the blood analysis revealed that the incorporation of herbs in the diet of goats improved hematological attributes namely hemoglobin concentration, red blood cell indices, and white blood cell number (**Figure 26**).

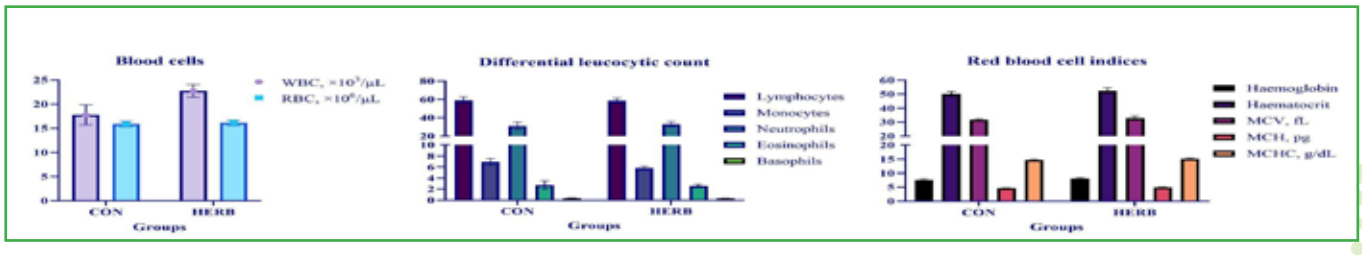


Figure 26: Hematological attributes of goats fed on herbal supplements (HERB) rich diet highlights rise of white blood cells as compared to control groups (CON).

Isolation, identification, and antimicrobial resistance patterns of bacterial pathogens causing bovine clinical and subclinical mastitis

Characterization of bacterial pathogens from bovine mastitis milk samples

The present study aimed to characterize the bacteriome isolated from bovine mastitis. The cases of clinical mastitis were chosen based on local inflammation of the udder, changes in the milk, and general symptoms like reduced milk yield, fever, and hard/ painful mammary glands. The cases of sub-clinical mastitis were assessed based on the California mastitis test and a total of 62 milk samples were screened. Bacterial strains up to the species level were identified based on the culture characteristics in selective and differential media such as MacConkey's, EMB, cetrimide, and blood agar. Different biochemical tests were performed using indole and methyl red Voges Prauskar reagent, citrate, urease, nitrate, and catalase. Also, gram staining and PCR-based characterization of bacterial DNA were done. Results of the bacteriological experiments are depicted in **Figure 27**, where the **a series** represents *Escherichia coli* and the **b series** represents *Pseudomonas aeruginosa*. The prevalent isolated bacteria were identified as *Staphylococcus aureus* (18/62; 29.03%), *Streptococcus pyogenes* (10/62; 16.12%), *P. aeruginosa* (8/62; 12.90%), *E. coli* (5/62; 8.06%), *Shigella* spp. (1/62; 1.61%), *Klebsiella* spp. (2/62; 3.22%), and *Salmonella* spp. (2/62; 3.22%). Overall, this study identified and characterized the prevalence of several bacterial pathogens associated with bovine clinical and subclinical mastitis.

Antimicrobial resistance profiling of bacterial isolates from bovine mastitis

Antimicrobial resistance (AMR) profiles were phenotyped using the Kirby Bauer disc diffusion method of antimicrobial susceptibility test as per the guidelines of the Clinical and Laboratory Standards Institute. Higher susceptibility of gram-negative bacteria against beta-lactam antibiotics was found except for *P. aeruginosa*, which showed resistance against cefuroxime, cefixime, and amoxicillin/clavulanic acid combination. However, *P. aeruginosa* was found to be susceptible against aminoglycoside antibiotics except for streptomycin. The *E. coli* isolates were found susceptible against all the beta-lactam antibiotics, but fairly strong resistance was noted against tetracycline, clindamycin, and sulphonamide groups of antibiotics (**Table 3**). The study revealed the presence of multi-drug-resistant pathogenic bacterial isolates in mastitis milk, such as methicillin-resistant *Staphylococcus aureus* and vancomycin-resistant *Streptococcus bovis*.

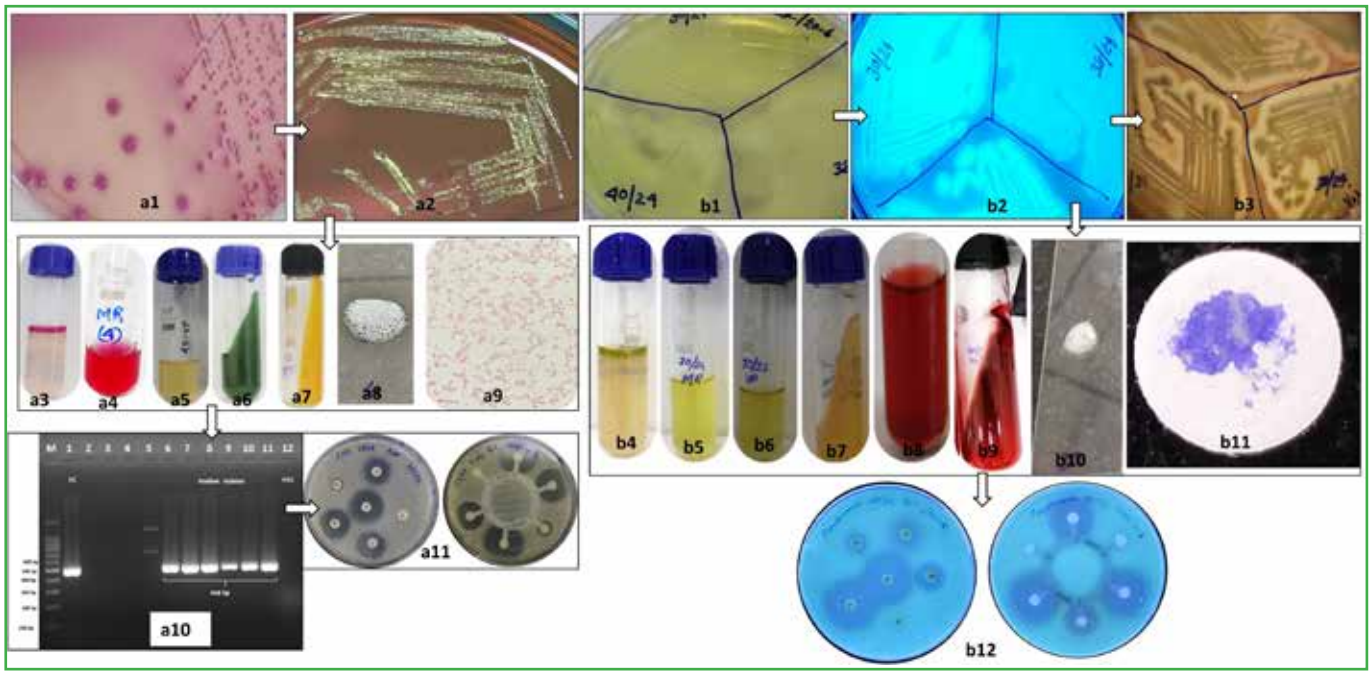


Figure 27: Isolation, identification, and AST study of *E. coli* (**a series**) and *P. aeruginosa* isolates (**b series**). Agarose gel electrophoresis showing specific amplification of 468 bp *phoA* gene segment of *E. coli* (**a10**). *E. coli* (**a11**) and *P. aeruginosa* (**a12**) isolate showing multidrug resistance in antibiotic sensitivity test.

Table 3: The trend of resistance profile of different antibiotics against *E. coli* and *P. aeruginosa* isolates from bovine mastitis.

Antibiotics (concentration in µg)	*E. coli*		*P. aeruginosa*		
	Isolate 1	Isolate 2	Isolate 1	Isolate 2	Isolate 3
Beta-lactam antibiotics					
Ceftazidime/Clavulanic acid (30/10)	53.6	54.0	29.1	27.3	28.2
Cefotaxime (30)	58.8	60.3	30.0	26.9	26.0
Cefotaxime/Clavulanic acid (30/10)	58.7	61.6	26.7	29.1	28.0
Cefpodoxime (10)	50.5	50.1	30.7	29.6	28.6
Cefpodoxime/Clavulanic acid (10/5)	52.4	52.1	31.4	29.6	30.5
Ceftazidime (30)	55.0	55.4	29.2	28.3	29.4
Cefuroxime (30)	50.6	27.5	R	R	R
Cefoperazone (75)	53.1	29.8	27.8	28.4	27.8
Cefotaxime/Clavulanic acid (30/10)	55.9	57.9	18.5	16.8	16.9
Cefixime (5)	18.7	27.1	R	R	R
Amoxiclin/Clavulanic acid (20/10)	44.6	17.5	R	R	R
Fluoroquinolone antibiotics					
Ofloxacin (10)	48.5	22.8	27.1	23.0	26.0
Ofloxacin (5)	20.9	17.4	30.1	22.6	28.5
Tetracycline antibiotics					
Tetracycline (20)	35.0	R	23.6	19.4	18.5
Tetracycline (30)	R	R	18.9	20.0	18.0
Aminoglycoside antibiotics					
Gentamicin (10)	51.5	55.5	38.9	27.9	28.3
Gentamicin (10)	49.5	21.5	28.8	21.7	22.7
Amikacin (30)	19.6	18.9	28.5	24.1	28.2
Streptomycin (10)	16.6	16.2	18.6	R	R
Polymyxin antibiotics					
Colistin sulphate (10)	15.6	15.6	17.8	17.1	17.2
Lincomycin antibiotics					
Clindamycin (2)	R	R	R	R	R
Sulphonamide antibiotics					
Co-trimoxazole (25)	R	R	23.7	29.7	25.9

*R - Resistant

Evaluating the nano-inspired degradation of aquatic pollutants with special reference to lac dye and Jute retting waste-water

Assessment of microbial profiling via metagenomics analysis of nano-remediated jute wastewater to evaluate the sustainability of microorganisms

A semi-pilot scale field study was conducted *ex-situ* to evaluate the effectiveness of zinc oxide nanoparticles (ZnO NPs) in degrading jute-retting wastewater, focusing on microbial sustainability. Experimental trials were conducted by suspending 8 kg of jute in 80 litre (L) of water within a 100 L FRP tank (5 FRP) and supplementing it with a microbial consortium i.e., *CRIJAF SONA* applied at a recommended dose of 15 g/kg of jute. ZnO NPs were synthesized and characterized by dynamic light scattering (DLS) and Fourier transform infrared spectroscopy (FTIR) for the study. Jute wastewater (12 L) was divided into five treatments in triplicates: treatment 1 (500 ppm ZnO NPs), treatment 2 (750 ppm ZnO NPs), treatment 3 (1000 ppm ZnO NPs), and a positive control and control group. All treatments, including the control, were exposed to sunlight, stirred hourly, and observed for color changes. The results indicated that all treatments effectively degraded jute waste water within 144 hours, with treatment 2 (750

ppm ZnO NPs) showing the highest efficiency. Nano-treated wastewater from all treatment sets was collected and pooled for metagenomic profiling using the MiSeq platform. Results highlighted the influence of nano-treatments on the relative abundance and microbial diversity, which has been significantly influenced in the treatment groups as compared to the positive control reflected in the rarefaction curve plot and taxonomical barplot (**Figure 28**). The treatment dosage of 750 ppm ZnO NPs demonstrated enhanced microbial diversity whereas in the positive control decline in microbial populations was observed, indicating its non-toxicity and its potential to sustain the microbial consortium associated with the jute retting process.

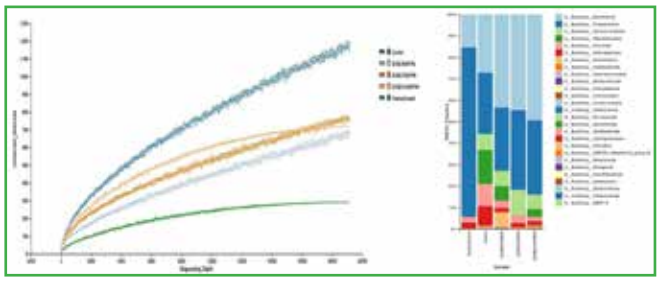


Figure 28: Rarefaction curve showing the relative abundance among the treatment and control groups (**a**). Taxonomical barplot showing the comparative analysis of microbial diversity among the treatment and control groups (**b**).

Exploring the influence of temperature and water activity on the growth, sporulation and aflatoxin production of *Aspergillus* spp. and bioprospecting of associated genes

Studying the growth, sporulation, and aflatoxin production of *Aspergillus flavus*

Four *Aspergillus flavus* fungal cultures (Af-1, Af-2, Af-3, and Af-4) were sub cultured in Potato Dextrose Agar (PDA) media in 90mm petri plate and glass tube slants at 26±2^{0}C to study radial growth rate. The full-grown fungal culture grown on PDA media was cut into small circular plugs with the help of a hollow circular cork borer and placed on the middle of the freshly prepared PDA plates (90 mm diameter) and incubated at 26±2^{0}C for periodic observation. The radial growth was measured on the third, seventh, and ninth-day post incubation. In the initial stages, the mycelial color of *A. flavus* was seen to be white. After a period of three days of incubation, the *A. flavus* colony exhibited the formation of olive green conidia, influencing the overall appearance of the colony. The colonies exhibited a flat morphology at their peripheries while displaying a raised structure at the center on 13 dpi (**Figure 29a**). All isolates of *A. flavus* generated exudates (droplets) that were either brown in hue or devoid of color. Furthermore, the average diameter of the colonies ranged from 77 to 88 mm (**Figure 29b**), encircled by a white halo. The underside of the colonies exhibited a pale coloration. The cultured isolates Af-1 and Af-4 were more greenish with having profuse conidia as compared to isolates Af-2 and Af-3. Further transcriptional profiling of fungal isolates for growth and sporulation have to be carried out to mine genes involved in aflatoxin biosynthesis, which ultimately offers biotechnological remedies for aflatoxicosis.

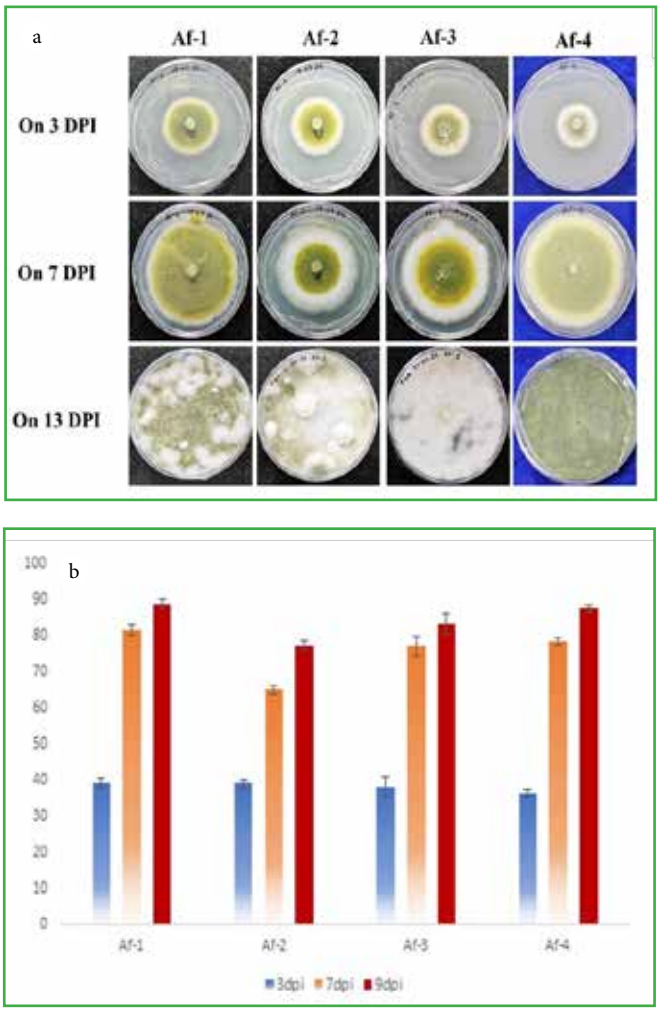


Figure 29: Colony morphology of *Aspergillus flavus* isolates (Af-1, Af-2, Af-3 and Af-4) grown in potato dextrose agar medium (**a**). Radial growth of different isolates of *A. flavus* studied (**b**).

Effect of ice recrystallization inhibitors on cryopreservation of goat semen

Evaluating the efficacy of vaginal electrical resistance for estrus detection

Black Bengal is a major goat breed found in eastern India, known for its important economic traits, such as high fecundity, excellent meat quality, and its distinctive black color. Detection of estrus is an important managerial activity for making apt breeding decisions and higher productivity of farms. Detecting estrus in goats becomes challenging in the absence of male goats. To address this, the present study aims to evaluate the efficacy of vaginal electrical resistance (VER) as a method for detecting estrus in goats. A total of six female goats were used, with their estrus cycles synchronized using progesterone sponges (Awikesil-S®).

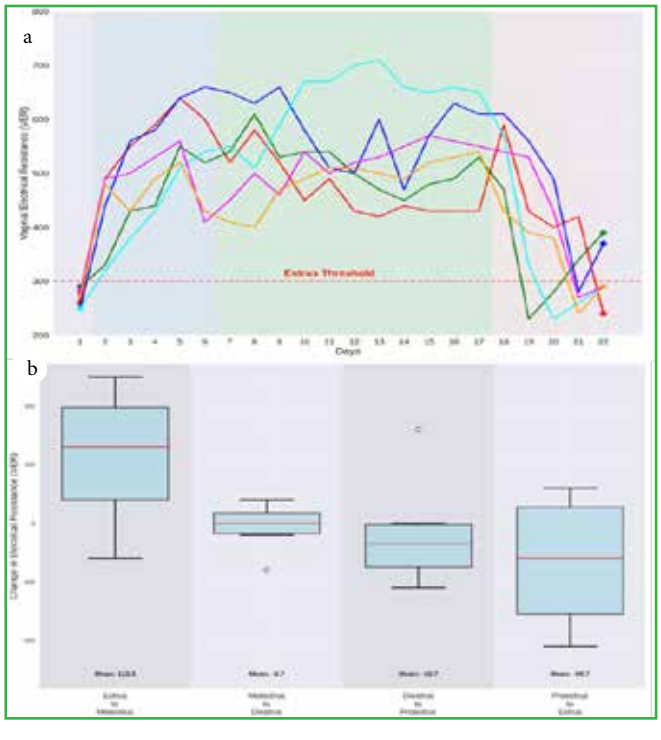


Figure 30: Trend of vaginal electrical resistance (VER) (in units) in individual goats (**a**) and phase-wise in the experimental goats (**b**).

Behavioral and physiological signs of estrus (*viz*. buck interest, cervical mucus, and vulvar oedema) and VER were monitored over 22 days, extending through the subsequent estrus cycle. The results indicated that the VER values were significantly lower ($p<0.05$) during estrus compared to other phases of the estrus cycle (**Figure 30a**). Also, VER across the estrus phases found strongly correlated with the physiological and behavioral estrus signs (**Figure 30b**). Principal Component Analysis identified VER and buck interest as key features explaining variations in estrus (**Figure 31**). Based on these findings, we conclude that a reference minimum VER value of 300 units could be used for estrus detection in Black Bengal and other small-sized goats.

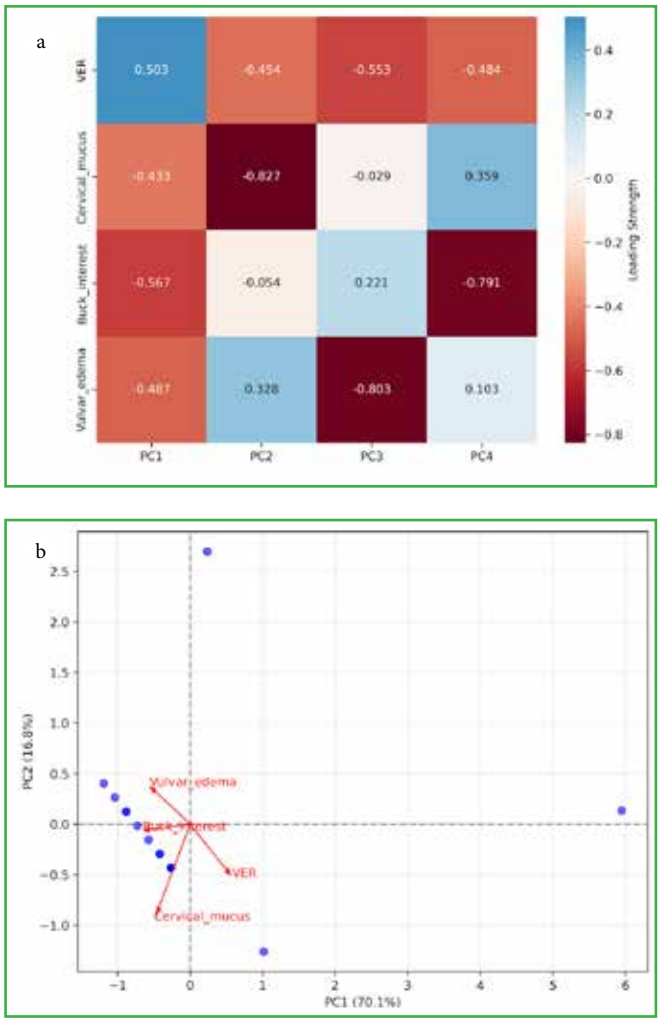


Figure 31: Principal Component Analysis identified key features explaining variations in estrus (**a & b**).

Characterization of sheep wool and pashmina proteins for quality enhancement and pashmina authentication

India ranked third in sheep production by having 74.26 million sheep and ranked ninth in wool production. Pashmina, known for its softness, warmth, and luxury, holds immense cultural and economic importance, serving as a source of livelihood for communities in Ladakh. Therefore, there is an urgent need to highlight indigenous wool and curb adulteration of pashmina with cheaper fibers. The proteomic analysis of wool and pashmina fibers were carried out, with the aim to identify unique biomarkers for wool quality to prevent adulteration. Wool and pashmina samples were collected from the Reasi sheep farm and *Changthang*

region of Ladakh, followed by proteomic and biochemical analyses. The results revealed distinct protein bands, with dominant keratin fractions at 40 kDa and 65 kDa, indicating the structural integrity and quality of the fibers. SDS-PAGE analysis of wool samples from various sheep breeds, along with pashmina and guard hair controls, showed similar fractionation profiles, with no significant differences in the number or intensity of protein bands. Prominent bands at approximately 40 kDa and 60 kDa corresponded to keratin proteins, while thinner bands near 30 kDa indicated keratin-associated proteins (KAPs) (**Figure 32a**). Densitometric analysis revealed consistent peak patterns across wool samples, with more prominent peaks compared to controls, reflecting higher protein content (**Figure 32b**). However, the uniformity observed suggests that 1D SDS-PAGE lacks the resolution to distinguish between different breeds or fiber types. To achieve greater differentiation and detect subtle differences among different types of wool samples, the next phase will employ more advanced techniques such as 2D-PAGE and LC-MS/MS analysis for deeper proteomic analysis.

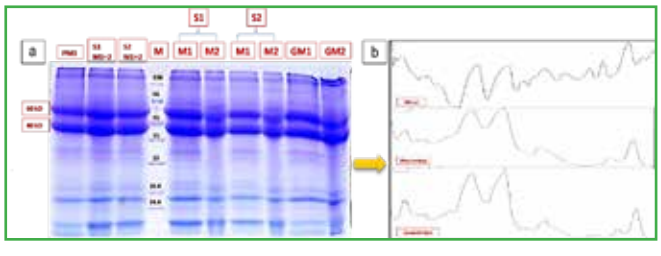


Figure 32: Proteomic analysis of pashmina wool. Prominent bands at approximately 40 kDa and 60 kDa corresponded to keratin proteins (**a**). Densitometric analysis revealed consistent peak patterns across wool samples reflecting higher protein content (**b**).

Investigating the role of purine degradation pathway genes of hemibiotroph fungal pathogens during host-pathogen interaction and their potential to confer disease resistance in maize

Conferring tolerance against banded leaf and sheath blight in maize by genome editing

Rhizoctonia solani causes banded leaf and sheath blight in maize. Many resistance genes in the maize genome have been recorded for conferring tolerance against banded leaf and sheath blight. The *ZmFBL41* gene sequence retrieved from the maize genome database and primer was designed for amplifying in tropical maize genotype DMRH 1308 (**Figure 33**). Further, the exon 1 and exon 2 sequences were amplified through the polymerase chain reaction using maize genomic DNA as a template, and the expected amplicon size (1.5 Kb) was seen in agarose gel electrophoresis. Guide RNA (gRNA) has been designed using CRISPRdirect software. This synthesized oligonucleotide has been cloned in the binary vector pRGEB32-BAR based on restriction-based cloning utilizing the BsaI restriction site.

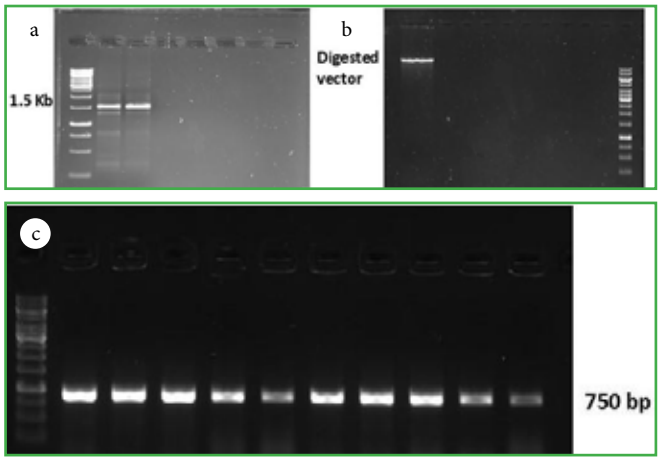


Figure 33: PCR Amplification of maize resistance gene; Lane No. 1: 1 Kb ladder, 2: PCR (-DMSO), 3: PCR (+DMSO) (**a**). Restriction digestion of vector; 1: Digested pRGEB32-BAR; 2: 1 Kb ladder (**b**). Colony PCR of DH5α transformed with cloned gRNA in pRGEB32-BAR; 1: 1 Kb ladder, 2-11: C1-C10 (**c**).

Screening of *Brassica carinata* derived *Brassica juncea* introgression lines under aluminum toxicity stress conditions

Screening *Brassica juncea* introgression lines for aluminum toxicity tolerance

Aluminum (Al) toxicity is one of the important factors impeding crop growth under acidic soil conditions. Nearly about 30.6 Mha of arable land are affected by highly acidic soil conditions, which accounts for 9.3% of the total geographical area of India, while in Jharkhand, the extent of area under slightly acidic soil is 84.9% covering 6.7 Mha.

Figure 34: Facility developed at institute for screening of mustard genotypes under Al toxicity and control conditions (**a**). Phenotypic variation in root morphology under Al toxicity and control conditions in inbred lines and *Brassica juncea* cv (DRMRIJ 31) (**b**).

Improving the level of Al toxicity stress tolerance in Indian mustard genotypes using *B. carinata* (known for its tolerance to abiotic stresses, including Al toxicity) while retaining its original agronomic characteristics shall help in sustainable agriculture. Around 150 inbred lines (ILs) were screened for differential Al

concentration using completely randomized design with four replications under control and treatment. The germination and transfer protocol were standardized for uniform plant growth. The optimum Al concentration for screening was standardized as 200 µM through serial experiments. Results revealed significant genetic variability for root morphological traits (**Figure 34**), highlighting the potential of these ILs for future genetic improvement and tolerance studies.

Nanotechnology-inspired immune-sorting approach of bovine spermatozoa

Validation of *RAB2B, VDAC1, TLR4* and *KDM1* proteins in sex sorted spermatozoa of *Bos indicus*

The aim of this study was to confirm the differential presence of *RAB2B*, *VDAC1*, *TLR4* and *KDM1* proteins in X- and Y-chromosome bearing spermatozoa of *Bos indicus* bulls. Previous liquid chromatography-tandem mass spectrometry based proteomic and RNA-sequencing analysis have found their specificity in the plasma membrane of Y-chromosome bearing bovine spermatozoa. Interesting candidates were enriched for transcriptome profiling *viz*., *RAB2B,* regulates vesicle trafficking during acrosome formation, *VDAC1,* regulates sperm motility through Ca^{2+} transmembrane flow, which impacts male fertility. Genes like *TLR4,* mediates acrosome reaction, oxidative stress markers, and sperm motility, whereas *KDM1,* regulates the differentiation and maintenance of bovine spermatozoa. The western blotting analysis validated the presence of these proteins in the total cell lysate and plasma membrane fractions of both X- and Y-bearing spermatozoa (**Figure 35**). These genes and related molecular phenotypes can be a good candidate for developing nanotechnology inspired sperm sorting.

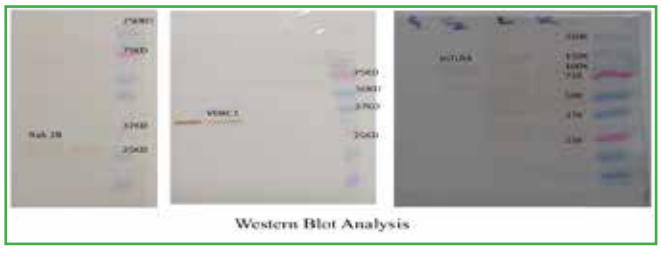


Figure 35: Western blotting revealed the presence of *RAB2B, VDAC1* and *TLR4* in the total cell lysate and plasma membrane fractions of X- and Y-bearing spermatozoa.

Machine learning approach to optimize dairy production management practices for improved performance of artificial insemination with sex-sorted semen

Dairy sector in India encompasses a diverse range of operations, from marginal and small-scale farmers to organized enterprises. The use of sex-sorted semen (SSS) in artificial insemination (AI) has the potential to transform the sector radically. The major factors that influence adoption of SSS include production systems, choice of improver breeds, herd structure and conception rates (CR), other than the cost of SSS. Due to interrelations of these factors, identifying the prime variables is crucial. We adopted a machine learning (ML) approach aimed to establish a decision support system for the application of SSS in Indian dairying (**Figure 36**). The CR of AI with conventional semen (CS) was observed to be 46.15%, in contrast to 34.37% with SSS. The HF crossbreeds outperformed other breeds (44.23%), followed by Sahiwal (40.6%) under SSS. The heifers were superior with 75% CR. The highest CR (45.2%) was recorded in the intensive management system (IMS). The female calves born in the SSS group (89.39%) were significantly higher than the CS group (48.33%) ($p<0.05$). In terms of the average calving score, the CS group fared below the SSS group (2.41 vs. 1.15) ($p<0.05$). The influence of parity on CR was observed to be significant ($p<0.05$). The highest profit was achieved under IMS ($p<0.05$). In conclusion, the IMS benefits the most from SSS through careful choice of breeds and parity of the cattle. This will aid in decision making for use of SSS to further increase the milk production and animal welfare.

Copy number variation of the Y-chromosome specific genes (*HSFY1* and *ZNF280BY*) in different genetic backgrounds of cattle

This study investigated the copy number variation (CNV) of Y chromosome-specific genes in 11 cattle breeds and populations belonging to three genetic backgrounds *viz*., indicine, taurine and their crossbreds, in order to understand their association with bull fertility. The CNV analysis was performed using standard curve based quantitative PCR to measure the absolute copy numbers of Heat-shock transcription factor, Y-linked (*HSFY*) and Zinc finger protein 280B, Y-linked (*ZNF280BY*) genes. Given the established link between *HSFY* and *ZNF280BY* CNVs with male fertility in both humans and cattle, it raises an important question about their role in interplay with different genetic backgrounds. Our investigation into the CNVs of *HSFY* and *ZNF280BY* in bulls shows significant differences among three genetic backgrounds ($p<0.05$). The mean log10 CN values for *HSFY* gene were estimated as 5.0±0.11 in indicine, 3.99±0.16 in taurine and 4.30±0.16 in taurine x indicine genetic backgrounds. The corresponding mean values with respect to *ZNF280BY* gene were 7.07±0.15, 6.97±0.17, 6.72±0.28, respectively. Post-thaw seminal parameters, namely total motility (%), progressive motility (%), rapid, slow and local motility (%), immotile sperm (%), acrosome defect (%), total composite score (%), progressive composite score (%) and viability (%) were analyzed using CASA which revealed significant differences among the three genetic backgrounds and among different breeds and populations ($p<0.05$)

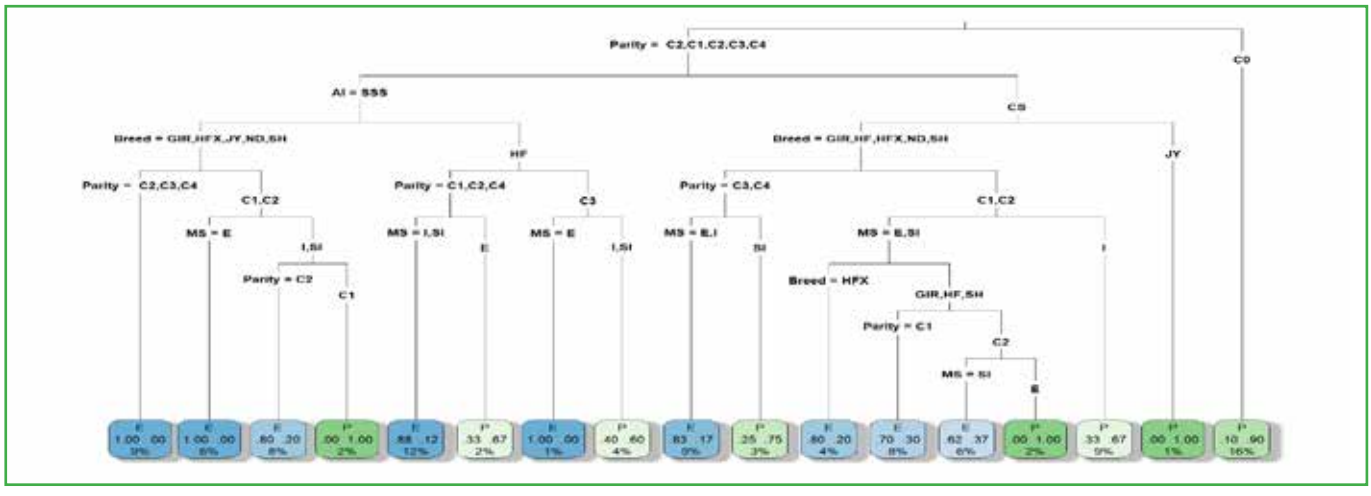


Figure 36: Decision tree classifier trained for decision support system for the application of sexed semen sorting in Indian dairying.

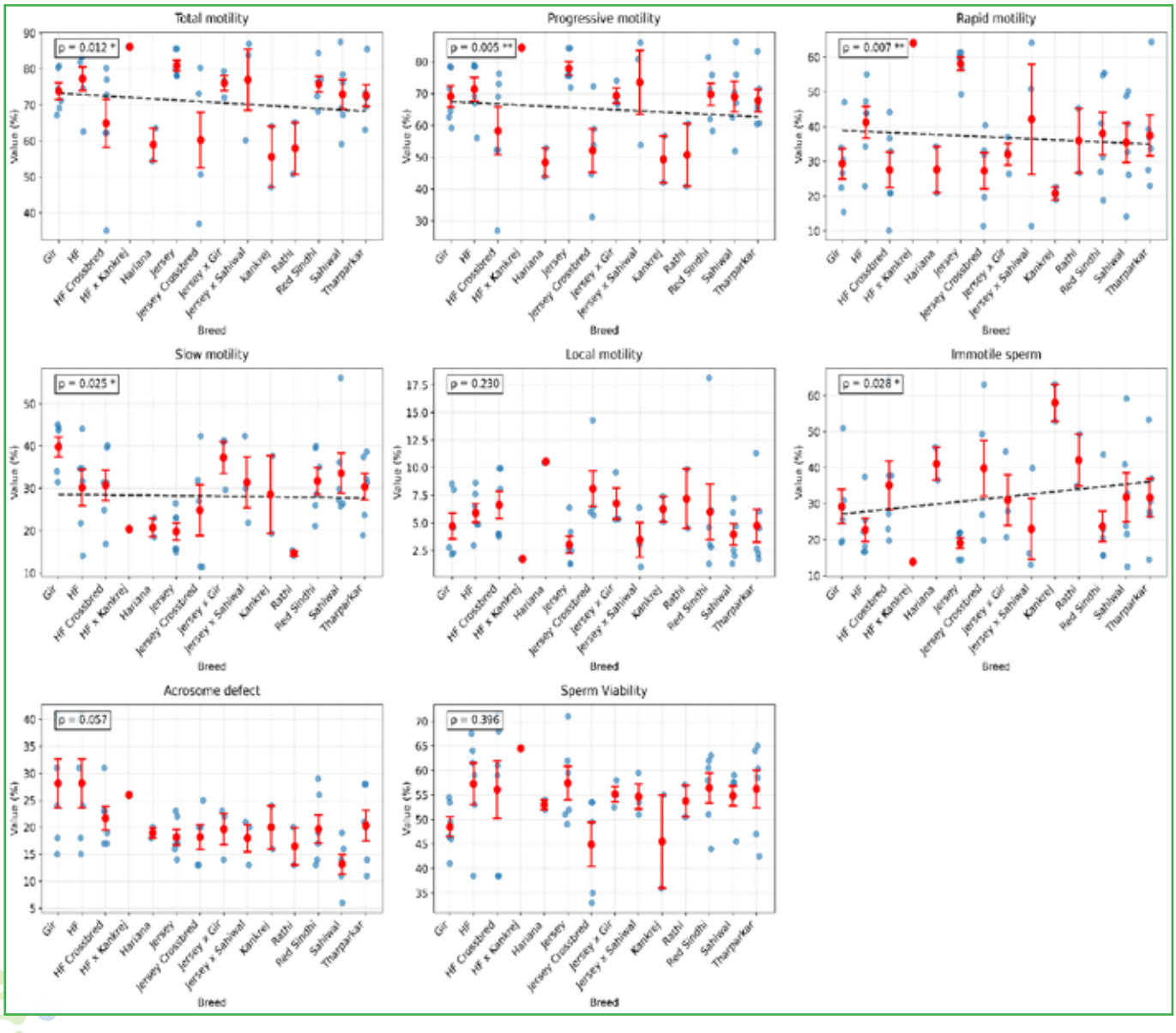


Figure 37: Post-thaw seminal parameters, analyzed using computer assisted semen analyzer (CASA) revealed significant differences among different breeds and populations ($p<0.05$).

Enhancing climate resiliance and ensuring food security with genome edition tools

Standardization of regeneration and transformation protocols in cotton

In planta transformation in cotton

We standardized an *Agrobacterium*-mediated in-planta transformation protocol for the Coker 310 and Coker 312 cotton varieties. Twenty seeds of each genotype were sown in pots, and seven-day-old seedlings were used for transformation. A vertical incision was made at the cotyledonary node to expose the meristematic tissue, ensuring that the apical meristem remained intact and the cotyledonary leaves stayed attached. *Agrobacterium tumefaciens* containing the pCambia1302 plant expression vector was used for transformation. *Agrobacterium tumefaciens* cultures were grown overnight in YEM broth containing 50 mg/L kanamycin and 25 mg/L rifampicin. The bacterial cultures, harvested at an OD_{600} of 0.6, were centrifuged at 4000 rpm for 5 minutes, and the pellet was resuspended in 1 mL of modified vir induction medium (75 mM MES, pH 5.4, 2% glucose, and 100 µM acetosyringone). For inoculation, 20 µL of the bacterial suspension was applied to the exposed meristematic cells. A ring of absorbent cotton was wrapped around the wound below the cotyledonary node and secured with plastic tape to stabilise the cotyledonary leaves. The seedlings were incubated at 28°C under a 10-hour light and 14-hour dark cycle, covered with sterilised perforated plastic cups. The inoculation was repeated daily for four consecutive days without removing the cotton wrapping. On the fourth day, the cotton was carefully removed, and the wounded areas were washed 2-3 times with a 550 mg/L clavam antibiotic solution. After four weeks of inoculation, DNA was isolated from the inoculated plants and checked for PCR amplification using primers specific to the hygromycin B resistance gene present in the backbone of the pCambia1302 plant expression vector. The PCR amplification results from the in-planta transformed plants are depicted in **Figure 38.**

Tissue culture regeneration of cotton

We utilised both Coker 310 and Coker 312 cotton varieties to standardise tissue culture regeneration protocols. Shoots were successfully regenerated from callus tissues using varying hormonal concentrations for different stages, including germination, shoot induction, rooting, callus formation, and shoot regeneration. Rooting of the callus-derived shoots is currently in progress. The details of the hormone concentrations employed at each stage of tissue culture are provided in **Table 4**, and the plant response at each stage is depicted in **Figure 39.**

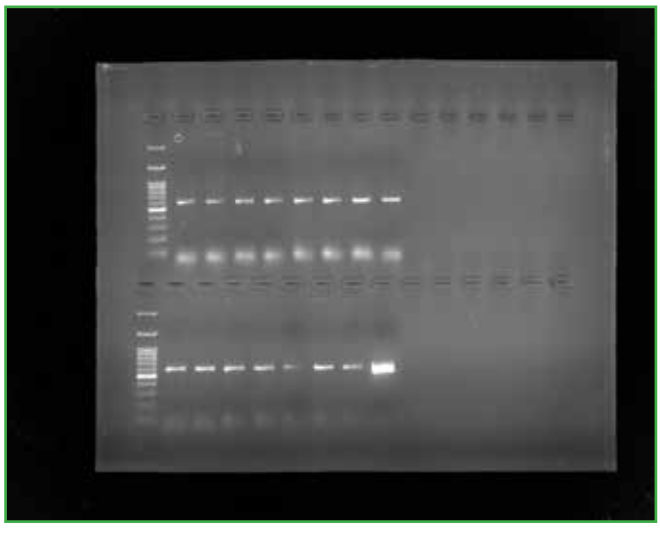


Figure 38: Molecular validation through PCR using hygromycin primers confirms successful transformation of *Agrobacterium tumefaciens* (EHA 105-GUS) in the cotton. Lane 1: Ladder (100 bp); Lanes 2–15: PCR products of the hygromycin resistance gene (amplicon size: 590 bp) from DNA isolated from 15 transformed cotton plants; Lane 16: Positive control.

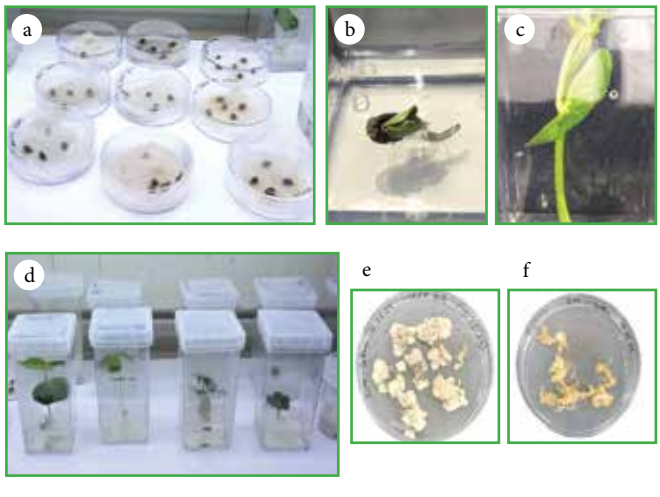


Figure 39: *In-vitro* regeneration protocol for the cotton genotype Coker 312. (**a**) Sterilized cotton seeds placed on germination paper, (**b**) Germinated cotton seeds on the medium, (**c** & **d**) Developed shoots and roots were observed when placed on the MS medium supplemented with growth hormones, (**e**) Callus proliferation of the soyabean on callus induction medium. (**f**) Soyabean shoots are regenerated from the callus on the shoot regeneration medium supplemented with BAP.

Table 4: Media composition and duration required for tissue culture regeneration of cotton.

Stage	Media	No. of Days
Seed Germination	Murashige and Skoog (MS) (1/2 strength i.e., 2.2g/L) + 3% Maltose	1-2 weeks
Shoot Induction Medium	MS (1/2 strength) + 3% Maltose + BAP (6-Benzylaminopurine) (1mg/ml) + 2,4-D (2,4-Dichlorophenoxyacetic acid) (0.5 mg/ml)	2-3 weeks
Rooting Induction Medium	MS (1/2 strength) + 3% Maltose + BAP (0.5 mg/ml) + IBA (Indole-3-butyric acid) (1 mg/ml)	2-3 weeks
Callus Induction Medium	MS (1/2 strength) + 3% Maltose + BAP (0.5 mg/ml) + 1 mg/ml 2,4-D	1-2 months
Callus Proliferation Medium	MS (1/2 strength) + 3% Maltose + BAP (0.5 mg/ml) + 2 mg/ml 2,4-D+ 0.5 mg/ml KIN (Kinetin)	2- 6 months
Shoot Regeneration Medium	MS (1/2 strength) + 3% Maltose + BAP (1 mg/ml) + 0.5 mg/ml 2,4-D	1-3 months
Root Regeneration Medium	MS (1/2 strength) + 3% Maltose + BAP (0.5 mg/ml) + 1 mg/ml IBA	Under process

Standardization of regeneration and transformation protocols in peanut

Transformation in peanut

We standardized the *Agrobacterium*-mediated transformation protocol for the TG37A peanut variety. In our current study, pCAMBIA1301 binary vector for plant transformation, was utilized which contains hygromycin and kanamycin as a selectable marker and the *GUS* reporter gene. The *Agrobacterium* bacterial culture was propagated in Luria Bertani (LB) broth for 24 hrs at 29^{0}C. The hypocotyl was used as an explant which was obtained and sectioned up to 4 mm from three-week-old germinated peanut seedlings. Pre-incised hypocotyls with a 1:8 dilution of the broth culture in sterile distilled water and subsequently cultured on a co-cultivation medium comprising MS, sucrose, 2,4-D (1 mg/mL), kinetin (0.5 mg/mL), and acetosyringone (200 µM) under photoperiod light for 48 hours. After co-cultivation, the explants were transferred to selective media containing MS, 3% sucrose, kanamycin (50 mg/L), and cefotaxime (400 mg/L) for 2 weeks, followed by subculturing on the same medium for an additional 2 weeks. The selected plants were then transferred to the secondary selective media containing MS, sucrose, and hygromycin for 3-4 weeks. Molecular studies were conducted to confirm the successful transformation of the plants. The PCR amplification results from the transformed plants are depicted in **Figure 40.**

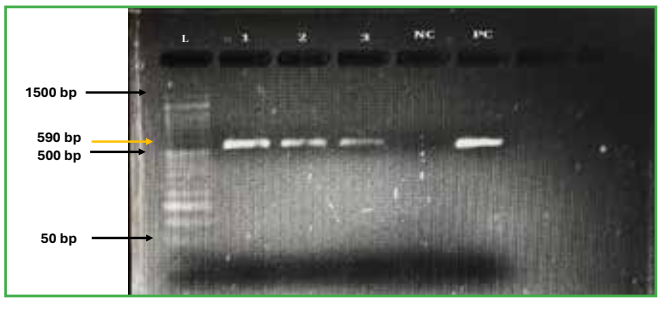


Figure 40: Molecular validation through PCR using hygromycin primers confirms successful transformation of *Agrobacterium tumefaciens* (EHA 105-GUS) in peanut. Lane L: Ladder (100 bp); Lanes 1-3 : PCR products of the hygromycin resistance gene (amplicon size: 590 bp) from DNA isolated from 3 transformed peanut plants; NC: Negative Control, PC: Positive Control.

Tissue culture regeneration of peanut

We utilised the TG37A peanut variety to standardise tissue culture regeneration protocols via direct organogenesis. The seeds sterilization was carried out with 70% ethanol for 10 minutes, followed by 20 minutes in 8% sodium hypochlorite and bavistin (2mg/ml), and then the embryo axes were excised along with half seed from the mature dry seeds. The sterilized seeds were placed on a germination medium. After germination, the explants were placed in a shooting medium and incubated under photoperiod light at 26ºC for one week. Further, it was transferred to a rooting medium and after a week, moved to pots containing a soil-vermicompost mix (1:1) for hardening. The details of the hormone concentrations employed at each stage of tissue culture are provided in **Table 5**, and the plant response at each stage is depicted in **Figure 41.**

Figure 41: *In-vitro* regeneration protocol through direct organogenesis for the genotype TG37A of peanut. (**a**) Embryonic axis along with half seeds placed on germination medium, (**b**) Germinated peanut seeds on the medium, (**c**) Developed peanut shoots on shoot induction medium, (**d**) Shoot proliferation of the peanut on the shoot multiplication medium, (**e**) Root development on the root induction medium (**f**) Hardening stage of the regenerated peanut.

Table 5: Media composition and duration required for tissue culture regeneration of peanut.

Stage	Media	No. of Days
Seed Germination	MS (Full strength i.e., 4.4 g/L) + 3% Sucrose	1-2 weeks
Shoot Induction Medium	MS (Full strength) + 3% Sucrose + BAP (1mg/ml) + 2,4-D (0.5 mg/ml)	2-3 weeks
Shoot aMu-ltiplication Medium	MS (Full strength) + 3% Sucrose + BAP (2 mg/ml) + 2,4-D (0.5 mg/ml)	2-3 weeks
Root Regeneration Medium	MS (Full strength) + 3% Sucrose + BAP (0.5 mg/ml) + 1 mg/ml IBA	3-5 weeks
Hardening	Autoclaved soil: vermicompost mix (1:1)	2-3 weeks

Standardization of regeneration and transformation protocols in soyabean

Transformation in soyabean

We standardized the *Agrobacterium*-mediated transformation protocol for soyabean genotype JS335. In the current study, we used the pCAMBIA1301 vector, an *Agrobacterium* binary vector for plant transformation which includes genes conferring resistance to hygromycin and kanamycin and a GUS gene, which serve as selectable markers. The bacterial culture of *Agrobacterium* was propagated in Luria-Bertani (LB) broth for 24 hours. Half seeds were used as an explant, pre-incised with a sterile scalpel, were infected with a 1:10 (broth culture: sterile distilled water) dilution and further incubated for 30 min. The infected explant was placed on the co-cultivation medium in the dark chambers for 48 hours. Furthermore, the explants were washed with liquid shoot induction medium supplemented with antibiotics for 1 hour. The washed explants were transferred to fresh shoot induction medium (B5 + sucrose + BAP + MES ((2-(N-morpholino) ethanesulfonic acid)) for 10 days, further washing steps with the antibiotic solution was repeated. The selected plants were then transferred to secondary selective media containing MS, sucrose, and hygromycin for 3-4 weeks. The transformation of the plants will be validated through molecular studies. The PCR amplification results from the transformed plants are depicted in **Figure 42.**

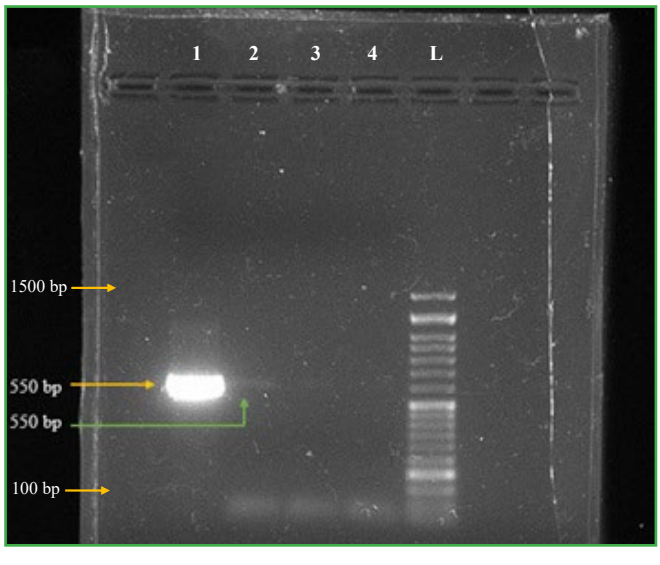


Figure 42: Molecular validation through PCR using hygromycin primers confirms successful transformation of *Agrobacterium tumefaciens* (EHA 105-GUS) in soyabean. Lane 1: Positive control, Lane 2- PCR products of the hygromycin resistance gene (amplicon size: 590 bp) from DNA isolated from transformed soyabean plant, Lane 3-4: Non-transformed soyabean plant, Lane L: Ladder (100 bp)

Tissue culture regeneration of soyabean

We utilised the JS335 soyabean variety to standardise tissue culture regeneration protocols. The seeds sterilization was carried out with 70% ethanol for 10 minutes, followed by 20 minutes in 4% sodium hypochlorite and Bavistin (3mg/ml), and then the embryo axes were excised along with half seed from the mature dry seeds. The sterilized seeds were placed

on a germination medium. After germination, the cotyledonary node was used as an explant, further placed on a shooting medium and incubated under photoperiod light at 26ºC for 1-3 weeks. The regenerated shoots were transferred to a rooting medium and after 3-4 weeks the plantlets were moved to the pots containing an autoclaved soil: vermicompost: cocopeat (1:3:2) for hardening. The details of the hormone concentrations employed at each stage of tissue culture are provided in **Table 6**, and the plant response at each stage is depicted in **Figure 43.**

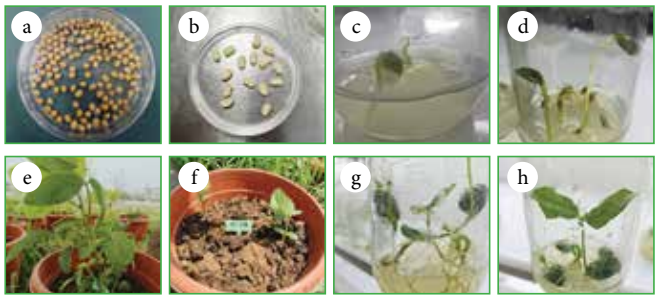


Figure 43: *In-vitro* regeneration protocol for the soyabean. (**a**) Soyabean seeds genotype JS335, (**b**) half seeds of the soyabean, (**c**) germinated soyabean seeds on the medium, (**d**) developed shoots on shoot induction medium, (**e** & **f**) shoot proliferation of the soyabean is observed on the shoot multiplication medium, (**g**) root development of the regenerated soyabean shoots on the root induction medium, (**h**) hardening stage of the regenerated soyabean.

Table 6: Media composition and duration required for tissue culture regeneration of soyabean.

Stage	Media	No. of Days
Seed Germination	MS (Full strength) with vitamin B5 + 3% Sucrose	1 week
Shoot Induction Medium	MS (Full strength) with vitamin B5 + 3% Sucrose + BAP (2 mg/ml) + MES salt (1 mg/ml) + acetosyringone (200 µM)	1-3 weeks
Root Induction Medium	MS (Full strength) + 3% Sucrose + IBA (1 mg/ml) + MES salt (1mg/ml)	3-4 weeks
Hardening	Autoclaved soil: vermicompost mix: cocopeat (1:3:2)	4-5 weeks

Standardization of Regeneration and Transformation Protocols in Urd Bean

Transformation and regeneration of urd bean

Urd bean seeds sterilized was carried out by 70% EtOH for 2 mins, 1% Bavistin for 10- 15 mins and 4% sodium hypochlorite solution, supplemented with one drop of Tween 20. The bacterial culture of *Agrobacterium* was propagated in Luria-Bertani (LB) broth for 24 hours. The broth containing the culture is centrifuges 5000 rpm for 15 mins resulting in pellet which is then resuspended in 1/2-strength liquid Murashige and Skoog (MS) medium, which is supplemented with acetosyringone (200 µM) to enhance the transformation efficiency. The sterilized seeds were pricked with the help of sterile needle, further immersed into the *Agrobacterium* suspension which was incubated for one hour in the dark. The infected seeds are transferred to a co-cultivation medium, which were maintained under dark conditions for 72 hours. The infected seeds are carefully washed with double-distilled water and antibiotics (clavam 400mg/ml) to eliminate the growth of *Agrobacterium*. Further, transferred on the regeneration medium supplemented with growth hormones for the seed growth and development, incubated for 2-3 weeks. The developed regenerated plantlets were transferred on the selective medium containing hygromycin (50mg/ml) for 2-3 weeks. Molecular validation via PCR of the transformed plantlets is under process, this entire protocol is well depicted in **Figure 44**. The details of the hormone concentrations employed at each stage of tissue culture are provided in **Table 7.**

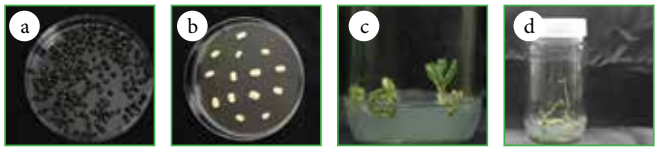


Figure 44: Transformation protocol in the Urdbean: (**a**) urdbean seeds, (**b**) co-cultivation medium of the sterilised urdbean seeds immersed in agrobacterium suspension, (**c**) seeds placed on regeneration medium supplemented with growth hormones showing shoots and roots proliferation, (**e**) transformed plantlets of urdbean growing on the selective medium containing hygromycin.

Table 7: Media composition and duration required for transformation of urd bean.

Stage	Media	No. of Days
Seed Germination	MS (Full strength) + 2% Sucrose	1 week
Co-cultivation medium	MS (Full strength) + 3% Sucrose + 0.05% PVP + BAP (2 mg/ml)	2-3 weeks
Regeneration medium	MS (Full strength) + 3% Sucrose + BAP (1.5 mg/ml) + MES salt (2 mg/ml)	2-3 weeks
Selective medium	MS (Full strength) + 3% Sucrose + BAP (1.5 mg/ml) + Hygromycin (50 mg/ml)	2-3 weeks

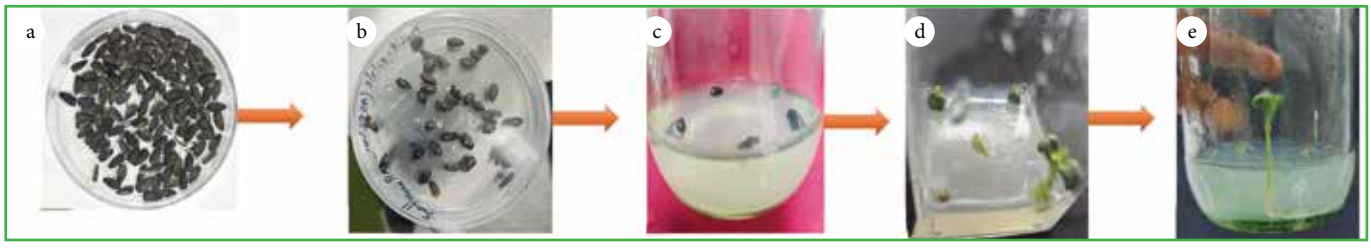


Figure 45: *In-vitro* regeneration protocol for the sunflower. (**a**) Sunflower seeds, (**b**) sterilised sunflower seeds, (**c**) sterilised seeds placed on the germination medium, (**d**) germinated sunflower seeds placed on the shoot induction medium, (**e**) shoot proliferation of the sunflower seeds.

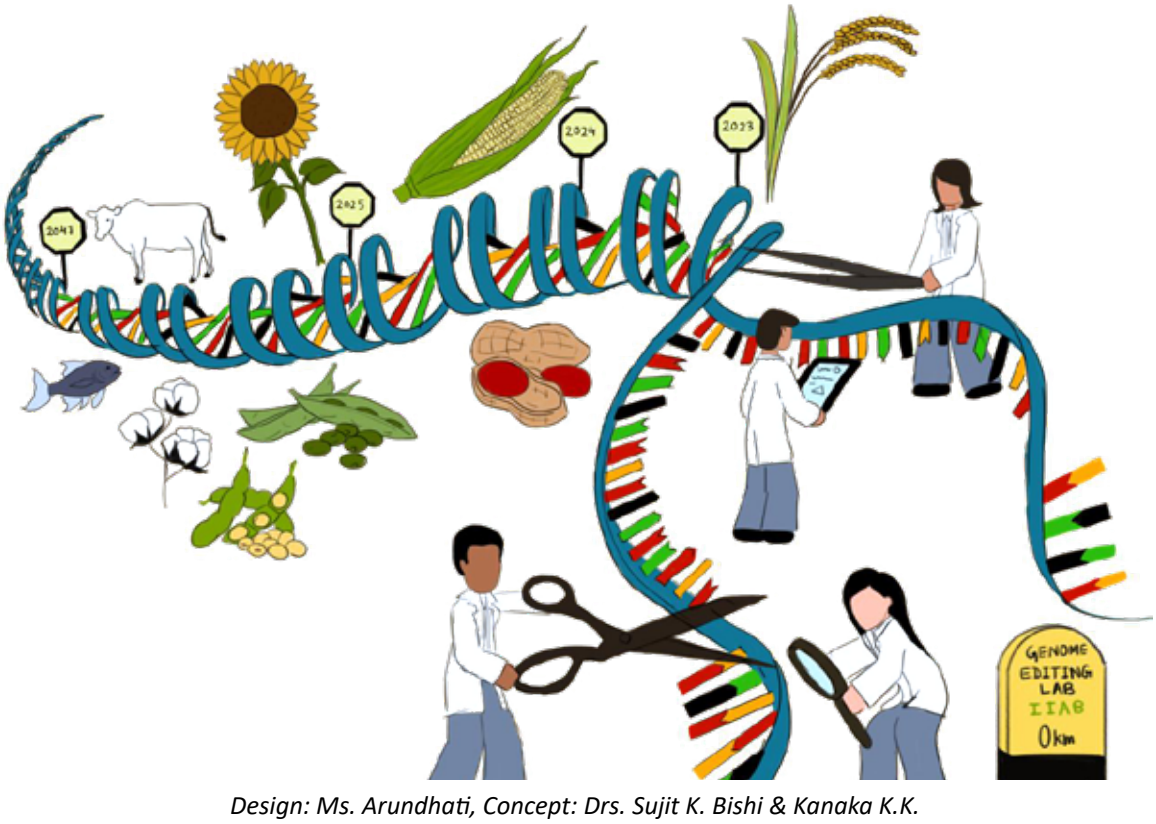
Standardization of regeneration and transformation protocols in sunflower

Tissue culture regeneration of sunflower

Sunflower seeds were sterilized and cultured on Murashige and Skoog (MS) medium supplemented with 4% sucrose. The seeds are incubated for two weeks under controlled environmental conditions to ensure uniform germination and the development of healthy explants. The cotyledonary nodes were used as an explant which were derived from germinated seedlings, further transferred to shoot induction medium for 2-3 weeks. For shoot multiplication, regenerated shoots were sub cultured onto a shoot multiplication medium supplemented with BAP for 3-4 weeks. Further, the root induction of the sunflower is in process, all the procedure can be depicted in **Figure 45**. The details of the hormone concentrations employed at each stage of tissue culture are provided in **Table 8.**

Table 8: Media composition and duration required for tissue culture regeneration of sunflower.

Stage	Media	No. of Days
Seed Germination	MS (Full strength) + 4% Sucrose	2 weeks
Shoot Induction Medium	MS (Full strength) + 4% Sucrose + BAP (1.5 mg/ml) + MES (1 mg/ml)	2-3 weeks
Shoot Multiplication Medium	MS (Full strength) + 4% Sucrose + BAP (1.5 mg/ml) + MES salt (2 mg/ml)	3-4 weeks



Design: Ms. Arundhati, Concept: Drs. Sujit K. Bishi & Kanaka K.K.

Academic Activities

Under the "One ICAR" initiative and in alignment with the New Education Policy (NEP), ICAR has established the IARI Mega University, adopting a hub-and-spoke model. In this framework, the ICAR-Indian Institute of Agricultural Biotechnology (IIAB), Ranchi, serves as the nodal institute for the Ranchi Hub. This hub integrates the collaborative efforts of four ICAR institutes: Indian Institute of Agricultural Biotechnology, National Institute for Secondary Agriculture (NISA), the ICAR-Research Complex for Eastern Region (ICAR-RCER-RS), and Research Station of the National Bureau of Plant Genetic Resources (NBPGR-RS), Bhusur, Ranchi.

The Ranchi hub offers a wide range of academic programs, including B.Tech. in Biotechnology, M.Sc. (Agriculture) degrees in four disciplines: i) Genetics and Plant Breeding (GPB), ii) Molecular Biology and Biotechnology (MBB), iii) Agricultural Chemicals, and iv) Biochemistry and an M.Tech. in Agricultural Processing and Food Engineering (AE). Additionally, Ph.D. programs are available in GPB, MBB, and Biochemistry. Currently, the university hosts a diverse cohort of 110 students from across the country, fostering a vibrant academic and research community.

UG Program

The Ranchi Hub is continuing B. Tech. (Biotechnology) degree program in affiliation with ICAR-IARI. The program started in academic year 2022-23 from the month of January in online mode and from April onwards in offline mode. A total of 28 students were admitted to the first Semester representing different parts of the country. The two semesters of the first year of UG program have been completed successfully. A total of 34 courses including Biotechnology core courses (15), Deficiency/Remedial courses (4), General courses (8), Basic Science course (2) and Agricultural/ Animal Science Courses (10), have been undertaken successfully In academic year 2023-24 and 2024-25, a total of 20 and 21 students, respectively have been enrolled in B. Tech. Biotechnology program.

PG Program

In 2023-24, altogether 16 students (three in MBB, six in GPB, one in Biochemistry, four in Agricultural Chemicals and two in AE) have been enrolled in the PG program. The list of passed out students (11) till August 2024 in mentioned in **Table 9**.

Table 9: List of M.Sc. (Ag) students passed out from ICAR-IIAB till August, 2024.

Master Degree Program			
Sl. No.	**Name of the student**	**Research Topic**	**Major Advisor**
Molecular Biology and Biotechnology (MBB)			
1.	Mr. Palli Tarun Kumar	Understanding the nano-silica induced molecular regulations in chickpea, *Cicerarietinum* L.	Dr. Biplab Sarkar
2.	Ms. Jamshida D.	Identification and characterisation of genes responsible for anthocyanin content in winged bean (*Psophocarpus tetragonolobus* L.)	Dr. Kishor U. Tribhuvan
3.	Ms. Anusha T.	Molecular insights into the fungicidal action of green silvernano particles against the chickpea wilt caused by *Fusarium oxysporum*.	Dr. Biplab Sarkar
4.	Mr. Diwakar Singh	Identification and expression analysis of gene(s) responsible for nodulation in winged bean (*Psophocarpus tetragonolobus* (L.))	Dr. Kishor U. Tribhuvan
5.	Mr. Ankit Patel	Development of *in-vitro* regeneration protocol for strawberry *Fragaria ananassa*	Dr. Kishor U. Tribhuvan

Sl. No.	Name of the student	Research Topic	Major Advisor
		Master Degree Program	
		Genetics and Plant Breeding (GPB)	
6.	Mr. Vallipeta Samantha Reddy	Inheritance and mapping of genomic regions for brown spot resistance in rice (*Oryza sativa* L.)	Dr. Vijai Pal Bhadana
7.	Mr. Aritabha Kole	Identification of genomic regions for kernel row number in maize (*Zea mays* L.)	Dr. Sujay Rakshit
8.	Mr. Anand Maurya	Characterization of M_2 population of winged bean (*Psophocarpustetragonolobus*) through agro-morphological traits and molecular markers.	Dr. Sudhir Kumar
9.	Mr. Kommula Uday	Estimation of genetic diversity for low phosphorus tolerance in paddy (*Oryza sativa* L.) Landraces from *Chotanagpur* plateau region	Dr. Sashi Bhushan Choudhary
10.	Mr. Pratap Ghosh	Identification of the gene for seed coat color in winged bean (*Psophocarpus tetragonolobus* L.)	Dr. Avinash Pandey
		Plant Biochemistry	
11.	Mr. Ayush Singhania	Study on differential accumulation pattern of L-DOPA in faba bean (*Vicia faba* L.) Leaves: biochemical and molecular perspectives	Dr. Sujit K. Bishi

Seat matrix of IARI mega university-Ranchi hub for Academic Year 2023-2024

The coursework for 16 students admitted to Master's programs in three disciplines *viz*., GPB, MBB and Biochemistry has been successfully completed by the hub for the academic session 2023-24. A total of 16 courses for Master's programs were independently taught by the faculty members from the Ranchi Hub, comprising IIAB, NISA, ICAR-RCER-RC, and NBPGR-RS. Currently a total of 69 UG, 35 PG and six Ph.D. students are pursuing the degree programs **Table 10**.

Table 10: Discipline wise list of UG, PG and Ph.D. students of ICAR-IIAB.

Program	Discipline	No. of Admission	Session/Batch
UG (B.Tech.-Biotechnology)	Biotechnology	28	2022-2026
	Biotechnology	20	2023-2027
	Biotechnology	21	2024-2028
PG (M.Sc.-Ag)	Molecular Biology & Biotechnology	5	2022-2024
	Genetics & Plant Breeding	5	2022-2024
	Biochemistry	1	2022-2024
PG (M.Sc.-Ag)	Molecular Biology & Biotechnology	3	2023-2025
	Genetics & Plant Breeding	6	2023-2025
	Biochemistry	1	2023-2025
	Agricultural Chemicals	4	2023-2025
PG (M.Tech.)	Agricultural processing and food engineering	2	2023-2025
PG (M.Sc.-Ag)	Molecular Biology & Biotechnology	5	2024-2026
	Genetics & Plant Breeding	7	2024-2026
	Agricultural Chemicals	4	2024-2026
PG (M.Tech.)	Agricultural processing and food engineering	3	2024-2026
Ph.D.	Molecular Biology & Biotechnology	2	2023-2026
	Genetics & Plant Breeding	3	2023-2026
	Biochemistry	1	2023-2026

Placement of students

The passed-out students have been well placed/ pursuing higher studies in well reputed Institutes, upon qualifying different national competitive exams viz., ICAR-SRF, DBT, CSIR-NET, ICMR, GATE. All the 11 M.Sc. students who passed out in academic year 2024-25, have cleared ICAR- Ph.D. entrance exam, five students qualified CSIR-UGC NET exam out of which four have qualified for JRF, two students have qualified DBT-BET exam.

Regular seminars

The talk series for the students has been started. It is scheduled every Monday from May (academic year 2024-25), in which scientists from different fields were invited to interact with students (**Table 11**).

Table 11: List of weekly seminars given on various topics by scientists from different discipline.

Sl. No.	Speaker	Date	Topic
1	Dr. Kishor U. Tribhuvan	May 03, 2024	Transcription analysis: when and how?
2	Dr. Biplab Sarkar	May 10, 2024	Nanobiotechnology, an innovation tool for next-generation biotechnology
3	Dr. Khela Ram Soren	May 17, 2024	Genotype-independent plant transformation by manipulating developmental regulatory genes
4	Dr. Sanjay K. Gupta	June 07, 2024	Microplastic pollution: A mounting concern of emerging pollutants in aquaculture
5	Dr. Sudhir Kumar	June 14, 2024	Speed breeding in crop plants
6	Dr. Madan Kumar	June 28, 2024	How do plants communicate?
7	Dr. Shambhu K. Lal	July 05, 2024	Basics of molecular cloning
8	Dr. Omkar M. Limbalkar	July 12, 2024	Genome editing for crop improvement: current and future perspectives
9	Drs. Tanmaya K. Sahu and Sujay B. Kademani	July 26, 2024	Working with adobe photoshop and MS publisher
11	Dr. Ramya N.	August 02, 2024	Therapeutic uses of insects and insect products
12	Dr. Avinash Pandey	August 16, 2024	Development and utilization of core collection
14	Dr. Sandip Garai	August 23, 2024	PCA for data analysis

Deeksharambh program

ICAR-IIAB had organized the first Deeksharambh programme for newly admitted UG students of B.Tech. Biotechnology from October 15-28, 2024 and for PG students from October 21-28, 2024 under the chairmanship of Dr. Sujay Rakshit, Director of the institute. Approximately 32 students participated in this special induction program, designed as per the New Education Policy - 2020 and following the guidelines set by the UGC and the graduate school of ICAR-IARI. The comprehensive programme aims to provide freshers with complete information about the new courses, including their scope and objectives. This also covered important details regarding discipline, course structure, and extracurricular activities, along with special talks by notable personalities and scientists from in and around the Institute. Each day started from 6.00 A.M. in the morning with yoga session. The different talks and sessions were held each day- Familiarization with the various wings of the Institute, experience of the legacy of the partner Institutes viz. National Institute of Secondary Agriculture (NISA), RCER-RS, Plandu and NBPGR-RS, Ranchi, visit to R K mission T.B. Sanitorium and interaction with Swami Ji to get a glance of importance of empathy and human values, talk on '*Stress Management*' by Brambhkumari Indu of AOL and Clinical Counsellor Miss Nisha Mishra, '*Holistic education*' by Dr. Debajani Roy, HOD Geography Dept., Ranchi University, Ranchi. Talks on Topics of relevance for today's need and societal issues were also discussed- '*Cybercrimes- a challenge of internet and AI era*' delivered by DSP, Cyber Crime, Ranchi, '*Core Human Values for Societal Transformation*' was delivered by Sh. S.P. Singh, Former District Judge, Ranchi etc. '*Discipline -key to self-development and nation building*' by a senior officer of CRPF, Ranchi, '*Communication enhancement and interpersonal relationship development*' by Dr. Pampa Sen, '*Time management- key to success*' by Dr. Hari Haran, Former HR Head, MTI, SAIL, Ranchi and '*Cleanliness, Health & Hygiene*' by Sh. Pankaj Mall, Director, Astitva Welfare Foundation were some of the interesting sessions which was really enjoyed by the students in which they

Glimpses of Deeksharambh program 2024 organized by ICAR-IIAB Ranchi hub

learn by the light-hearted interaction with the speakers. Students also participated in extra- curricular activities like drawing, extempore, poem recitation and various indoor and outdoor games and also were encouraged by the certificate of participation in the closing ceremony of the two- week programme. This programme not only helped students to gain insight of the objectives they would set for their academic programme but also a sense of belonging to the Institute as their second home far from home.

Other academic activities

Students freshers welcome

Faculty-student interaction and freshers' welcome of the students of IARI Mega University Ranchi Hub was organized on January 12, 2024 **(Figure 46).** The family of ICAR-IIAB, Ranchi, and the sister institutions of the hub including the faculties and staff along with their families welcomed the new entrants with jubilant celebrations.

Figure 46: Students-Faculty interaction during freshers welcome program.

Exposure visits of B. Tech students to Ranchi Veterinary College, BAU, Ranchi

A one-day Exposure visit of B.Tech. (Biotechnology) students to Ranchi Veterinary College, BAU, Ranchi was held on January 30, 2024. The visit aimed to familiarize students with veterinary operations and livestock management. The day began with a session at the veterinary clinical complex, where Drs. Abhishek and Ritu discussed procedures such as sample collection, X-rays, and ultrasonography. The students then toured various farms, including the Goat, Cattle, and Swine farms, where Dr. Ravindra Kumar and Dr. Ansar Ahamad explained housing, feeding, and management practices. The visit, coordinated by Drs. Amit Kumar, Kanaka K.K., and Kartik Sharma, provided valuable practical insights into veterinary practices and livestock management.

Student exposure visit to Jharkhand Milk Federation (JMF) and Medha dairy plant

On March 15, 2024, an exposure visit for B.Tech 1st and 2nd year students to the JMF dairy and feed plant at Hotwar, Ranchi and Medha dairy plant, Ranchi were organized. The students learned about various dairy operations, including milk collection, processing, packaging, distribution, feed pelleting, and other social initiatives. Students gained insights into large-scale milk processing stages and quality assurance techniques, enhancing their practical understanding of dairy plant operations **(Figure 48).**

Figure 48: Exposure visit of students to Medha dairy plant, Ranchi.

Student exposure visit to various ICAR institutes

From March 22–27, 2024, a seven-day exposure visit for M.Sc. and Ph.D. students to ICAR institutes and KVKs in Sikkim and West Bengal was organized **(Figure 49)**. The students explored integrative farming, farmers' producer's organization, and outreach initiatives at ICAR-Central Institute for Subtropical Horticulture Malda, learned about orchid tissue culture and its significance at ICAR-NRC Orchid and gained insights into organic and zero-budget natural farming at ICAR Research Complex NEH, Sikkim. These visits offered valuable interactions with experts, broadening their knowledge and inspiring future endeavors in agriculture.

Figure 49: Exposure visit of M.Sc. and Ph.D. students to ICAR institutes and KVK's in Sikkim and West Bengal.

Agri Biotech Students Organization for Value Education (ABOVE)

Students of IIAB Ranchi hub are engaged in 'Agri Biotech Students Organization for Value Education' (ABOVE) an

initiative for service beyond the mandated activities for the children of laborers. This initiative reflects their commitment to community service and educational outreach, encouraging creativity and learning among underprivileged children **(Figure 50).**

Figure 50: Glimpses of Agri Biotech Students Organization for Value Education (ABOVE).

Institute's sports meet 2024

The IARI Mega University, Ranchi Hub, organized a Sports Meet on November 16-17, 2024. Students actively participated in various indoor games such as chess and carrom, and outdoor sports like cricket, volleyball, and athletics. The event fostered teamwork, discipline and sportsmanship among students, showcasing their talents and enthusiasm. Outstanding performers were awarded for their achievements by Director, ICAR-IIAB **(Figure 51).**

Figure 51: Glimpses of the sports meet held on November 16-17, 2024, showcasing students participating in a variety of indoor and outdoor games and events followed by prize distribution.

Outreach Activities

Tribal Sub-Plan (TSP)

ICAR-IIAB and ASHA foundation celebrate International Women's Day-2024

On March 8, 2024, ICAR-IIAB and the ASHA foundation hosted a grand celebration of International Women's Day at New Bhusur Ground, Namkum, Ranchi. Themed *"Invest in Women: Accelerate Progress,"* the event highlighted the crucial role of women's empowerment in societal development. Dr. Sujay Rakshit, Director, ICAR-IIAB, and other dignitaries emphasized respect and equality, inspiring a diverse audience (over 1,000 participants), including leaders, officials, entrepreneurs, students, and farmers. The event concluded with the distribution of 20 battery-operated sprayer machines to women farmers, reinforcing the belief that empowering women is key to sustainable progress and a brighter future (**Figure 52**).

Figure 52: Distribution of battery operated sprayer machines to progressive women farmers during International Women's Day, 2024.

Strengthening fish farming among tribal communities

ICAR-IIAB organized two events to support and empower tribal fish farmers. On March 21, 2024, a fish feed distribution program was held at Maheshpur, Angara, benefiting 18 tribal farmers (**Figure 53a**). The initiative aimed to enhance local fish farming, a vital livelihood for tribal families. Farmers received high-quality fish feed, essential for improving fish growth and yield, along with guidance on efficient aquaculture practices to boost productivity and income. On August 30, 2024, a training and sensitization program was conducted at ICAR-IIAB, Ranchi, in collaboration with NBFGR, Lucknow **(Figure 53b)**. Attended by 30 tribal farmers from nearby villages, the event focused on skill enhancement through demonstrations of water quality control, fish health management, and other best practices. Farmers were also provided with fish feed and fingerlings to support sustainable fish farming (**Figure 53c**).

Figure 53: Distribution of fish feed to the tribal fish farmers (**a**). Sensitization and capacity development of tribal fish farmers (**b**). Distribution of fish fingerlings and feeds (**c**).

Promotion of sustainable agriculture through short-duration paddy seeds distribution under TSP

ICAR-IIAB, Ranchi, organized two impactful paddy seed distribution events in June and July 2024 to support tribal farmers. On June 28, 2024, under the Tribal Sub Plan Scheme, around 150 tribal farmers from six panchayats in the Namkum block of Ranchi namely Lalkhatanga, Dungri, Chandaghansi, Bandhua, Hurwa, and Lali, received 10 kilograms of Shabhagi Dhan, a high-yielding, climate-resilient paddy variety (**Figure 54**). This initiative aimed to enhance agricultural productivity and food security while improving farmers' livelihoods. On July 03, 2024, in collaboration with ICAR-CISH Regional Station and supported by Pradan NGO Atari, Kolkata, CR-320 variety paddy seeds

were distributed to 1,765 tribal farmers across Purulia, Bankura, and Malda districts in West Bengal. This short-duration, agro-climate-suited variety was introduced alongside training on its cultivation techniques to optimize productivity and resilience. Both programs exemplify ICAR-IIAB's commitment to empowering tribal farmers through sustainable agricultural practices and access to high-quality seeds.

Figure 54: Distribution of Sahbhagi Paddy seeds among tribal farmers.

Organizing animal health camp

On July 02, 2024, an animal health camp was held at Rurungkocha, Namkum, in association with Ranchi Veterinary College faculty and interns, attracting participation from over 150 farmers in the region. The camp extended vaccination services for goats against *peste des petits ruminants* (PPR) and cattle haemorrhagic septicaemia disease, along with essential medicines to improve livestock health (**Figure 55**). The health camp focused on preventing infectious diseases, promoting animal health, and enhancing livestock productivity. Farmers were also provided with valuable knowledge on proper animal health care management, feeding practices, and effective disease prevention measures, reinforcing the camp's objective of fostering sustainable livestock care in the community.

Figure 55: Glimpse of animal health camp in Rurungkocha village, Ranchi, Jharkhand.

Mass tree plantation drive on 96th foundation day of ICAR

On July 16, 2024, ICAR-IIAB in collaboration with the ASHA Foundation, Namkum, celebrated the 96th foundation day of ICAR at Chandaghansi Panchayat Bhavan, with the participation of over 700 villagers. The event started with a huge rally to unite attendees and set a positive tone (**Figure 56a**)**.** A key highlight was the planting of saplings by the dignitaries, symbolizing a commitment to environmental conservation. Speeches emphasized ICAR's role in advancing agriculture and improving farmers' lives. The event also included the distribution of 10,000 Litchi and Mango saplings across six panchayats to promote environmental sustainability (**Figure 56b**)**.** A cultural performance by ICAR-IIAB students and villagers added a festive touch to the plantation drive. The event concluded with gratitude for the community's participation, celebrating collective efforts toward sustainable agricultural growth and community development.

Figure 56: A rally on mass tree plantation drive near Chandaghansi Panchayat Bhavan on the eve of 96th foundation day celebration of "Indian Council of Agricultural Research" **(a).** Distribution of mango and litchi plant saplings to the villagers (**b**).

Namkum girls shine at sub-junior national football championship sponsored by ICAR-IIAB

A team of 35 girls from Namkum, Ranchi, represented in the Sub-Junior Girls National Football Championship held between August 24-31, 2024 in Malda district, West Bengal. Upon rigorous training in collaboration with the ASHA Foundation at New Bhusur Ground, Namkum, the girls showcased remarkable talent and sportsmanship, securing 2nd place in the competition. This initiative aimed to encourage girls' participation in sports, foster teamwork, and boost their confidence **(Figure 56).** It provided these young athletes with a platform to demonstrate their abilities and represent their community on a national stage, inspiring future generations to embrace sports as a path to personal and collective growth.

Figure 56: Girl students participation in sub-junior national football tournament, in Malda district, West Bengal.

Awareness program on lac cultivation

ICAR-IIAB organized an awareness program on lac cultivation for 200 tribal farmers at ICAR-NISA, Namkum, on September 20, 2024. The session aimed to educate farmers on lac cultivation as a profitable agro-based enterprise, emphasizing its potential to provide supplementary income to the marginal farmers.

Figure 57: Awareness program on advanced lac cultivation methods for lac farmers.

The awareness program featured practical demonstrations on establishing lac cultivation, equipping farmers with essential knowledge about the selection of host trees and the management of lac insects. This initiative sought to diversify the income sources of tribal farmers while promoting sustainable and eco-friendly agricultural practices **(Figure 57).**

Scientific duck farming training and distribution program

A khaki campbell duckling training and distribution program was organized under Tribal Sub-Plan on September 24, 2024 at the ICAR-IIAB campus and was attended by over 30 farmers from adjoining villages of Ranchi, Jharkhand **(Figure 58).** The Khaki Campbell ducks are known for their disease resistance and climate resilience. Unlike other duck varieties, Khaki Campbell can lay more than 300 eggs/year and may be reared with less water, adding additional income to the farmers. The ducklings were distributed along with concentrated feed and a mineral mixture. The Director and Joint Directors of ICAR-IIAB, scientists, the Asha self-help group, and progressive tribal duck farmers participated in the program. The interactions with scientists have encouraged the farmers to adopt new techniques in duck farming through feeding practices, minimum water utilization, and breeding techniques. It was also highlighted that duck farming can bring revolutionary changes in the state of Jharkhand.

Figure 58: Scientific duck farming training and distribution of ducklings among tribal farmers.

Foundation stone laying of multipurpose center

On October 4, 2024 ICAR-IIAB hosted the foundation stone laying ceremony for a Multipurpose Center dedicated to training and supporting scheduled caste and scheduled tribe farmers. The event was graced by the Hon'ble Minister for Agriculture and Farmers Welfare, Govt. of India, Sh. Shivraj Singh Chauhan, and attended by over 600 small and marginal farmers. The

multipurpose center is expected to provide training on modern farming techniques, access to agricultural resources, and a platform for farmer welfare initiatives. The program also included the distribution of small agricultural tools to enhance local farmers' productivity and promote advanced farming practices (**Figure 59**).

Figure 59: Distribution of agricultural equipment by Hon'ble Minister of Agriculture and Farmer's Welfare, Govt. of India, Sh. Shivraj Singh Chauhan.

Field day on rice

On October 29, 2024, ICAR-IIAB organized a field day on rice cultivation for 25 tribal farmers at its Ranchi campus. Led by Dr. Vijai Pal Bhadana, Joint Director (Research), the event primarily focused on modern rice farming practices, including improved seed varieties, pest management, and efficient use of water. Through hands-on demonstrations and interactive discussions, farmers were introduced to the latest research and techniques for optimizing rice production under field conditions. The program aimed to equip farmers with the scientific knowledge and tools needed to enhance productivity, ultimately contributing to improved crop yields and sustainable farming practices (**Figure 60**).

Figure 60: Field day on rice cultivation for tribal farmers.

Mustard seed distribution program

On December 6, 2024 ICAR-IIAB, Ranchi, organized a mustard seed distribution event, benefiting 300 tribal farmers from neighboring villages. Farmers received RH-761 and NRCHB-101 mustard seed varieties, selected for their high yield potential and strong disease resistance **(Figure 61).** A comprehensive guidelines on mustard cultivation were provided, covering soil preparation, planting techniques, and pest management. This initiative aimed to boost mustard production, an important cash crop for the region, while enhancing agricultural income and promoting crop diversification among tribal farmers. By equipping farmers with quality seeds and cultivation knowledge, the program sought to support sustainable and profitable farming practices.

Figure 61: Distribution of mustard seeds to the tribal farmers.

Vegetable kit distribution program

On December 12, 2024 ICAR-IIAB distributed vegetable kits to 150 tribal farmers in the villages of Lali, Chandagansi, and Jhingi (**Figure 62**). The kits contained seeds for pea, tomato, carrot, radish, coriander, and chili, selected for their suitability for kitchen gardening. The initiative aimed to encourage home-based vegetable farming, ensuring improved nutrition and an additional income source for the farmers. Along with the kits, farmers were trained in establishing and maintaining kitchen gardens, focusing on water management and organic farming practices. This program empowers tribal farmers to grow their own vegetables, reducing reliance on external markets and promoting self-sufficiency.

Figure 62: Distribution of vegetable kits to the tribal farmers.

Table 8: List of activities under Tribal Sub-Plan (TSP) in 2024.

Sl. No.	Program	Venue	No. of Beneficiaries
1	International Women's Day Celebration	New Bhusur Ground, Namkum, Ranchi	1000
2	Fish Feed Distribution Program	Maheshpur, Angara, Ranchi	18
3	Large-scale promotion and distribution of short-duration paddy seeds	ICAR-IIAB, Ranchi	150
4	Animal Health Camp	Rurungkocha, Namkum	150
5	CR-320 Paddy Distribution Program	Purulia, Bankura, Malda of West Bengal	1765
6	Mass Tree Planting Ceremony on 96th foundation day of ICAR	Lali, Namkum, Ranchi	700
7	Sub-Junior Girls National Football Championship	Malda, West Bengal	35
8	Sensitization and Capacity Development of Tribal Fish Farmers	ICAR-IIAB, Ranchi	30
9	Awareness Program on Lac Cultivation	NISA, Namkum	200
10	Scientific Duck Farming Training and Distribution Program	ICAR-IIAB, Ranchi	30
11	Foundation Stone Laying of Multipurpose Center	ICAR-IIAB, Ranchi	600
12	Field Day on Rice	ICAR-IIAB, Ranchi	25
13	Mustard Seed Distribution Program	ICAR-IIAB, Ranchi	300
14	Vegetable Kit Distribution Program	ICAR-IIAB, Ranchi	100

Distribution of CR Dhan 320 to scheduled caste farmers

Under SCSP, 78 quintals of CR Dhan 320 (FS) were procured and provided to approximately 920 farmers of Purulia district under Chota Nagpur (CNP) region, adjacent district Bankura connecting CNP region to the plains, and Malda and Balurghat districts of West Bengal in partnership with ICAR-CISH RRS Malda, ATARI Kolkata, WRID Department, Govt. of WB, and NGOs **(Figure 63).**

Figure 63: Distribution of CR Dhan 320 to the scheduled caste farmers.

Partnership of ICAR-IIAB with seven different organization for implementation of SCSP proposals

During the period April to December 2024, the institute has partnered with seven organizations for implementation of SCSP benefitting score of farmers. They include i) WBUAFS, Kolkata, West Bengal, ii) WBCADC, KVK Sonamukhi, Bankura, West Bengal, iii) Visva Bharati, Sriniketan, West bengal, iv) KVK (ICAR-RCER), Ramgarh, Jharkhand, v) BCKV Mohanpur, West Bengal, vi) KVK Kaimur, Bihar and vii) UBKV, Coochbehar, West Bengal.

Organizing Kisan Gosthi

A Kisan Gosthi was organized on October 06, 2024 which witnessed participation of more than 500 farmers from the Jharkhand state. The farmers were oriented on agronomic practices, animal husbandry, fisheries, agriculture waste management, etc. **(Figure 65)**. The Kisan Gosthi was organized on the occasion of foundation stone laying ceremony of multipurpose center for training and facilitation of SC/ST farmers under SCSP and TSP Schemes, by Hon'ble Minister for Agriculture and Farmers Welfare, Government of India, Sh. Shivraj Singh Chauhan and Sh. Sanjay Seth, Hon'ble Member of Parliament (Ranchi Loksabha).

Figure 65: Kisan Goshti organized by ICAR-IIAB.

North-Eastern Himalayan Component (NEH)

Under the NEH component, ICAR-IIAB has initiated biotechnological research on important commodities in the NEH region. Recognizing the potential of orchid farming in Sikkim, a project was initiated on "Promotion of Orchids in Sikkim for Enhanced Livelihood Security" in collaboration with the ICAR-NRC for Orchids in Pakyong, Sikkim in 2023 **(Figure 66).** As part of this initiative, seventeen "Naturally Ventilated Polyhouses" were distributed to farmers alongside, tissue-culture hardened plants to more than 100 farmers. The other inputs such as organic nutrient formulations were also distributed to support the orchid growth. Furthermore, another collaborative project titled "Development of a high-density SNP genotyping assay for Yak and its validation" was undertaken in partnership with the ICAR-NRC on Yak in Arunachal Pradesh.

Figure 66: Promotion of Orchid cultivation in Sikkim.

Mera Gaon Mera Gaurav (MGMG)

In 2024, under the Government of India's "Mera Gaon Mera Gaurav program", two multidisciplinary teams of scientists from ICAR-IIAB were formed. These teams identified sixteen villages across Ranchi district of Jharkhand, engaging approximately 600 farmers. Scientists frequently visited adopted villages to engage with farmers and understood their challenges. General sensitization activities were organized on aspects of improved crop production techniques, integrated pest and nutrient management, soil health management, post-harvest handling and value addition to agricultural products. Scientist also encouraged the farmers to diversify into allied activities such as horticulture, beekeeping, poultry farming, and fisheries to increase their income. Additionally, a special campaign was conducted to promote the *Swachhta Abhiyan*, focusing on cleanliness and sanitation drives in Lalkhatanga and Garkhantanga panchayats, with the active participation of the local community. During the village visits, scientists stressed the significance of growing off-season vegetables under low-cost poly-house conditions. As part of the program, demonstration, and sensitization activities were organized to address livestock health, including deworming of pigs, vaccination, and artificial insemination in goats. A special initiative was undertaken to train farmers in the preparation of feed pellets using locally available ingredients, empowering them to produce cost-effective and nutritionally balanced feed for livestock. During the visit, scientists sensitized the farmers about the impact of climate change on agriculture and the importance of adopting resilient practices.

Figure 67: Input distribution duting a visit under MGMG program.

Other Institutional Activities

Institute Technology Management Unit (ITMU)

In 2024, the Intellectual Property and Technology Management Unit (ITMU) of ICAR-IIAB has made significant strides in fostering innovation and intellectual property (IP) protection. One patent entitled, "*Natural gum-based nanocomposite hydrogel having antibacterial and wound healing effects and a method of preparation thereof (Patent no.: 497567)*" was granted on January 2024 in collaboration with ICAR-NISA, Ranchi. Another submitted patent entitled, "*Alcoholic nano-silver having anti-viral and anti-biofilm efficacy and method of preparation thereof (Patent application number MP/EI/69397/2021-Del)*" is under examination phase. In addition to patents, ITMU has successfully registered two trademarks, i.e., the ICAR-IIAB institute logo and the DHURWA (Dynamic Hub for Research, Welfare, and Agri-preneurship) logo. The institute also received ICAR certification on "*Green nano-copper and copper-silver nanocomposite formulation, for controlling major fungal and bacterial pathogens in rice (Oryza sativa) and chickpea (Cicer arietinum L.)*", as a promising green nano-technology initiative.

Dynamic Hub for Research, Welfare and Agripreneurship
DHURWA
ICAR-IIAB

Figure 68: Logo of DHURWA registered as trademark.

To promote awareness and capacity-building on intellectual property rights (IPR), ITMU organized several seminars and guest lectures for students, technical staff, scientists, and farmers. One of the notable speakers Dr. Shyamala Kandadai, Associate Professor and Dean of Faculty at the National University of Study and Research in Law (NUSRL), Ranchi, Jharkhand delivered a lecture, entitled "IP and the SDGs: Building Our Common Future with Innovation and Creativity", sharing insights on various types of IP and their role in sustainable development. Professor M.R. Sreenivasa Murthy, IPR Chair Professor at NUSRL, Ranchi, discussed advancements in IP protection (**Figure 69**) and Dr. Praveen Malik, CEO of Agrinnovate India Limited, New Delhi engaged with scientists and students in an interactive session regarding future innovations. Additionally, a three-day workshop was conducted for tribal farmers emphasizing grassroots innovation and focused on smart farming **(Figure 70).** Furthermore, ITMU is working to add plant varieties for registration, and technology transfer as well as enhancing the different IP portfolios of the institute.

Figure 69: Lecture by Prof. M. R. Sreenivasa Murthy on advancements in IP protection.

Figure 70: A workshop organized for awareness among tribal farmers.

Agri-Business Incubation Center (ABI)

The Agri-Business Incubation (ABI) center at the ICAR-IIAB, Ranchi, has been established to provide essential physical, technical, business, and networking support to emerging agri-businesses and entrepreneurs. The center conducted the following program during 2024.

Awareness and sensitization program

The ABI organized a series of awareness cum sensitization programs (March 20-22 and June 05, 2024) to educate students, farmers, and stakeholders about the ABI center. In Rajaporam, farmers and stakeholders learned about ABI's objectives, support services, and funding opportunities, including interactive question-and-answer sessions and a field visit demonstrating sustainable farming practices. At Farm B of ICAR-IIAB in Ranchi, local farmers were introduced to enhanced farming techniques and crop diversification benefits. Additionally, students from Jharkhand Rai University's Faculty of Agriculture received an overview of ABI's support for agricultural entrepreneurship, with a focus on encouraging students to pursue agricultural ventures **(Figure 71).**

Figure 71: A lecture on Agri-Business Incubation (ABI) center's objectives, support services, and funding opportunities to farmers by Dr. Sujay B. Kademani, In-charge, ABI center, ICAR-IIAB.

Graduation ceremony

ICAR-IIAB hosted a graduation ceremony for Mr. Vikash K. Choudhary of Garima, Integrated Agro Farm Pvt. Ltd., an incubator who completed his incubation at ABI on March 28, 2024 **(Figure 72).** The event, led by Dr. Sujay Rakshit, Director of ICAR-IIAB, featured the presentation of Vikash's graduation certificate. Dr. Rakshit highlighted the extensive support services offered by ABI, including mentorship and resources for agricultural innovation. The ceremony included dynamic discussions on agri-business opportunities, showcasing ABI's dedication to fostering agricultural entrepreneurship and motivating students to embark on their ventures.

Figure 72: Graduation ceremony of Vikash K. Choudhary of Garima Integrated Agro Farm Pvt. Ltd., an incubator who completed his incubation from ABI center, ICAR-IIAB.

Sensitization program on BIRAC-BIG grant

ICAR-IIAB, in collaboration with a-IDEA, ICAR-NAARM organized a sensitization program at ICAR-NISA on May 15, 2024 to shed light on the BIRAC-Biotechnology Ignition Grant (BIG) **(Figure 73).** The event attracted several participants, including aspiring entrepreneurs, students, and scientists from various nearby colleges and institutions. The program focused on exploring funding opportunities and support available for agri-business and biotechnology ventures through the BIRAC-BIG grant. Attendees gained valuable insights into how they can leverage these grants to boost their agricultural innovations and entrepreneurial projects.

Figure 73: Sensitization program on the BIRAC-Biotechnology Ignition Grant (BIG) to different stakeholders.

Important Institutional Meetings

Quinquennial Review Team (QRT) Meeting

On February 23-24, 2024, and May 27, 2024 the QRT team conducted a critical review of ICAR-IIAB, Ranchi's work over the past five years (2017-18 to 2021-22) **(Figure 74),** adhering to the existing ICAR guidelines. The review was led by Prof. Sudhir K. Sopory, Emeritus Senior Scientist from ICGEB, New Delhi. The team included distinguished members namely Dr. Kuldeep Singh (Ex. Director of ICAR-NBPGR, New Delhi), Dr. R.K. Singh (Ex. Director of ICAR-IVRI, Izatnagar), Dr. W.S. Lakra (Ex. Director of ICAR-CIFE, Mumbai), Prof. R. Rama Kumar (TISS, Mumbai Campus) and Dr. Arvind Kapoor (Advisor at Acsen Agriscience Pvt. Ltd., Gurgaon). The final report has been prepared accordingly on May 27, 2024.

Figure 74: Quinquennial Review Team reviewing ICAR-IIAB, Ranchi's work over the past five years (2017-18 to 2021-22).

Research Advisory Committee (RAC) Meeting

The 11th RAC meeting of the ICAR- IIAB, Ranchi was held on February 20-21, 2024 in both physical and virtual mode under the chairmanship of Dr. Baldev Singh Dhillon (Former Vice Chancellor, PAU, Ludhiana) to review the progress of ongoing research programs. Hon'ble Members, Dr. Probodh Borah (Head, Department of Animal Biotechnology, College of Veterinary Science, AAU, Khanapara), Prof. K.C. Bansal (Former Director, ICAR-NBPGR, New Delhi), Prof. Dr. Indrani Karunasagar (Director Projects & DST-TEC, NITTE University, Mangalore and Former Associate Director Research, KVAFSU), Dr. K.S. Subramanian (Director Research Tamil Nadu Agricultural University, Coimbatore), Dr. Bijendra Pal (Director Research, Bioseed Research India, Hyderabad), Dr. D.K. Yadava, ADG (Seed), Dr. Vidya Gupta (Former CSIR Emeritus Scientist, NCL Springfields, Pune), and Dr. Sujay Rakshit, Director and scientific staff of the institute attended the meeting. Dr. Vijai Pal Bhadana, Joint Director (Research) and Dr. Kishore K. Krishnani, Joint Director (Academics) presented the research and academic activities of the institute to the RAC committee respectively during the last one year **(Figure 75**). The Action Taken Report (ATR) on the recommendations of the last meeting of the RAC was presented by Dr. Madan Kumar, Member Secretary, RAC. In the meeting, all the members acknowledged the challenges of manpower and infrastructure requirements of the institute, however, stressed on the need to intensify the research activities to meet the mandate of the Institute. The RAC expressed its satisfaction on the ATR and emphasized the need for the institute to focus on basic research in plants, animals, and fisheries using advanced technologies, synergizing efforts with the private sector, and developing impactful products.

Figure 75: Scientists interacting with RAC members.

Institute Research Council (IRC) Meeting

The Institute Research Council (IRC) was held on April 25-26, 2024 under the chairmanship of the Director to review the progress of on-going research projects in the institute and review the newly presented projects for approval/modification. Dr. Madhurendu K. Gupta, DRI cum Dean PGs and University Professor, and Chairman, Dept. of Veterinary Pathology, Ranchi Veterinary College, BAU, Ranchi, served as the external expert. The meeting commenced with a welcome address by the IRC member secretary, followed by the opening remarks by the Director (**Figure 76**). Presentations for new project proposals were made by the Project Investigators (PIs) from the different Schools of ICAR-IIAB on April 25, 2024 and the on-going project on April 26, 2024. All together nine on-going sub-research projects and 13 new sub-research projects were presented in the IRC meeting. The chairman and the expert of the IRC expressed their satisfaction with the progress of the on-going research projects and encouraged scientists to continue working towards their goals. The IRC committee also appreciated

new research project proposals presented by new scientists. The chairman and external expert urged the young scientists to identify the current problems and take up focused work according to societal needs. They encouraged the scientists to seek external funding for their research work and were advised to explore corporate social responsibility (CSR) funds from private entities/PSUs. Chairman also highlighted the need for working in collaboration and integrating soil, microbe, plant, animal, and human health.

Figure 76: Institute Research Council meeting reviewing ongoing projects and new institutional project proposals.

Major Events

Mega Kisan Mela at Kharsawa

A Mega Kisan Mela was organized on January 1-2, 2024 by ATARI, Patna in collaboration with ICAR-IIAB, Ranchi at Kharsawa. The stall of ICAR-IIAB, Ranchi was visited by Sh. C. P. Radhakrishnan, Governor of Jharkhand along with Hon'ble Sh. Arjun Munda, Union Minister for Agriculture and Farmers Welfare **(Figure 77).** Dr. Trilochan Mahapatra, Chairman, PPV and FR also visited and appreciated the efforts of the institute. Many farmers and enthusiastic students also visited the stall.

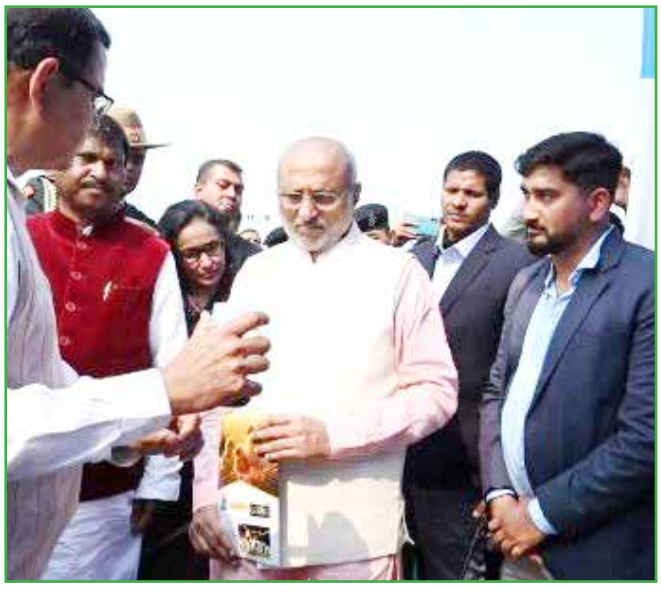


Figure 77: ICAR-I IAB's stall visited by the Governor of Jharkhand Govt. during Mega Kisan Mela organized at Kharsawa.

Farmers meet in KVK Kalyan

One day farmers' meet on "Encouraging Innovation to Adopt Climate Resilient Agriculture' was organized on January 21, 2024, by KVK, Kalyan, West Bengal, in collaboration with ICAR-ATARI, Kolkata, ICAR-IIAB, Ranchi ICAR-IIHR, Bengaluru and ICAR-CIFRI, Barrackpore. Hon'ble DG, ICAR, Dr. Himanshu Pathak, and Swami Shivapradananda, Secretary, Ramakrishna Mission Vidyapith, Purulia inaugurated the program (**Figure 78**). Fish fingerlings sponsored by ICAR-IIAB, Ranchi under the SCSP project were released in ponds by Hon'ble DG.

Republic Day and Independence Day Celebration

The Republic Day as well as Independence Day were celebrated in the institute with scintillating performances from the students and faculty (**Figure 79**). During Republic Day celebration, the best research paper and best review paper were awarded to Drs. Shambhu K. Lal and Sujit K. Bishi respectively for the year 2023.

Figure 78: Farmers meet in KVK Kalyan followed by input distribution.

Figure 79: Celebration of Republic Day and Independence Day.

Visit of DG, ICAR to ICAR-IIAB, Ranchi

On February 3, 2024, Dr. Himansu Pathak, Hon'ble DG of ICAR and Secretary of DARE, Government of

India, reviewed the activities of ICAR-IIAB, Ranchi, and engaged in discussions with students. The meeting was attended by several esteemed ICAR dignitaries **(Figure 80)**, including Dr. S.K. Singh, DDG (Horticulture), ICAR; Dr. Dheer Singh, Director of ICAR-NDRI, Karnal; Dr. Gyanendra Singh, Director of ICAR-IIWBR, Karnal; Dr. Sujay Rakshit, Director of ICAR-IIAB, Ranchi; Dr. Bikas Das, Director of ICAR-NRC Litchi, Muzaffarpur; Dr. Pradeep Dey, Director of ICAR-ATARI (Zone-V), Kolkata; and Dr. Vishal Nath, OSD at ICAR-IARI, Jharkhand.

Figure 80: Glimpses of the visit of DG and esteemed ICAR dignitaries to ICAR-IIAB.

International Women's Day Celebration

On March 8, 2024, ICAR-IIAB and the ASHA Foundation celebrated International Women's Day at New Bhusur Ground, Namkum, Ranchi, with the theme "*Invest in Women: Accelerate Progress*." The event, attended by over 1,000 participants, highlighted women's empowerment and honored women change-makers from the Namkum block for their impactful contributions (**Figure 81**).

Figure 81: Input distribution during international women's cay celebration.

Institute participation in Krishi Mela's

ICAR-IIAB showcased an exhibition stall at Dairy Mela and Agricultural Exhibition program during March 9-11, 2024 held at Khuntkatti Ground, Chaibasa, Jharkhand. During the program Hon'ble Minister for Agriculture and Farmers Welfare, Govt., of India Sh. Arjun Munda visited the exhibition stall and appreciated the progress of the institute (**Figure 82**).

Figure 82: Visit of Hon'ble Union Minister for Agriculture and Farmers Welfare to ICAR-IIAB stalls at Dairy Mela.

ICAR-IIAB, Ranchi participated and displayed stall to farmers and visitors in Pusa Krishi Vigyan Mela organized by ICAR-IARI, New Delhi at Simdega, Jharkhand on March 10-12, 2024. The mela was attended by various dignitaries from both ICAR and non-ICAR institute. Hon'ble Minister for Agriculture and Farmers Welfare, Government of India Sh. Arjun Munda visited the exhibition stall of the ICAR-IIAB (**Figure 83**).

Figure 83: Participation of ICAR-IIAB in Pusa Krishi Vigyan Mela.

Workshop on Entrepreneurship Development

On June 3, 2024, the ICAR-IIAB hosted a workshop on entrepreneurship development for IARI Mega University Ranchi hub students. Planned by Dr. Sujay Rakshit, Director of IIAB, and coordinated by Dr. Kishore K. Krishnani, Joint Director (Academics), the program featured expert sessions on innovative ventures in agriculture. Highlights included discussions on pearl farming by Dr. Sweta Pradhan, practical insights into pearl culture by Mr. Ashok Manwani, mushroom cultivation by Mr. Avinash Kumar, poultry hatchery management by Mr. Vikash Kumar Choudhary,

vegetable cultivation by Mr. Baijnath Mahto, and lac cultivation by Mr. Shaktidar Koiri. The workshop concluded with encouragement from Dr. Krishnani to transform knowledge into entrepreneurial success, fostering job creators in agriculture (**Figure 84)**.

Figure 84: Workshop on entrepreneurship development program.

World Environment Day

ICAR-IIAB, marked "World Environment Day" on June 05, 2024 with the theme "*Land Restoration, Desertification and Drought Resilience*". Sh. Devesh Mittal, Deputy General Manager (B&O), SBI, Ranchi, attended the program as the chief guest (**Figure 85**). The program was inaugurated with massive tree plantation drive by the guests, staffs and students at Farm A of the institute, symbolizing the commitment to green and clean campus.

Figure 85: Celebration of World Environment Day through massive tree plantation drive.

Visit of DDG (Crop Science), ICAR to ICAR-IIAB, Ranchi

Dr. Tilak Raj Sharma, Deputy Director General (Crop Science), ICAR visited ICAR-IIAB, Ranchi on July 28, 2024. Dr. Sharma, inspected various facilities being created at the institute and reviewed the ongoing research (**Figure 86)**, and development activities of the institute. Dr. Sharma appreciated the efforts being made at the institute under the leadership of Dr. Sujay Rakhsit, Director, ICAR-IIAB.

Figure 86: Review of ongoing research projects of ICAR-IIAB by DDG (Crop Science) followed by addressing faculty and students and plantation.

Visit of girls students under DST's Vigyan Jyoti program

An exposure visit was hosted by ICAR-IIAB for the 12th standard girl students under DST Vigyan Jyoti Knowledge Partner Schools, including Jawahar Navodaya Vidyalaya, Gumla, Kendriya Vidyalaya, Gumla, and Kasturba Gandhi Balika Vidyalaya on September 4, 2024. The students and their accompanying teachers were welcomed by Dr. Sujay Rakshit, Director and Dr. Vijai Pal Bhadana, Joint Director (Research). The visit was coordinated by Drs. Ganesh N. Aderao and Omkar M. Limbalkar. During the visit, the girl students were introduced to various career opportunities available in agriculture, veterinary sciences, and fishery sciences. They were introduced to the institute's laboratories and explained about ongoing research activities **(Figure 87)**.

Figure 87: Exposure visit of girl students under the DST Vigyan Jyoti knowledge partner program.

हिंदी दिवस एवं हिंदी पखवाडा

संस्थान में सितम्बर 13, 2024 को हिंदी दिवस समारोह आयोजन के साथ दिनांक 13 से 30 सितम्बर 2024 की अवधि में हिंदी पखवाड़े का आयोजन किया गया। इस उपलक्ष्य पर संस्थान निदेशक डॉ सुजय रक्षित, संयुक्त निदेशक (अनुसन्धान) डॉ विजयपाल भडाना, संयुक्त निदेशक (शैक्षणिक) डॉ किशोर कुमार कृष्णानी, संस्थान के सभी वैज्ञानिकगण, अधिकारीगण एवम् सभी छात्र छात्राएं उपस्थित

रहे (चित्र 88)। निदेशक महोदय डॉ रक्षित ने अपने अभिवादन में सभी को हिंदी दिवस की शुभकामनायें दी एवम् हिंदी भाषा की महत्ता पर प्रकाश डाला। उन्होंने बताया की हिंदी कैसे हमारे विभिन्नता पूर्ण देश को एकता के सूत्र में बांधती है। उन्होंने संस्थान का अधिकतर कार्य हिंदी भाषा में करने के लिए आह्वान किया। संयुक्त निदेशक (अनुसन्धान) डॉ भडाना ने इस अवसर पर हमारी मातृभाषा हिंदी के प्रचार प्रसार पर जोर दिया।

चित्र 88: संस्थान में हिंदी पखवाडा अवधि में विभिन्न प्रतियोगिताओ का आयोजन।

संयुक्त निदेशक (शैक्षणिक) डॉ कृष्णानी ने भी इस हिंदी दिवस से जुड़े अपने अनुभव साझा किये। आयोजन समारोह का संचालन डॉ साक्षी कैथ द्वारा किया गया। संस्थान के विद्यार्थियों द्वारा इस अवसर पर भाषण एवम् कविता पाठ का अनुसरण किया गया। राजभाषा प्रभारी डॉ कार्तिक शर्मा ने हिंदी पखवाड़े के दौरान होने वाली विभिन्न प्रतियोगिताओ के विषय में विस्तार से चर्चा की। हिंदी पखवाडा अवधि में संस्थान में विभिन्न प्रतियोगिताओ का आयोजन सफलतापूर्वक किया गया जिसमे संस्थान के सभी अधिकारीयों उत्साहपूर्वक सम्मिलित हुए। विभिन्न प्रतियोगिताओ में हिंदी निबंध, हिंदी शब्दानुवाद, हिंदी श्रुतलेख, कविता, वाद विवाद एवम् सुलेख प्रतियोगिता सम्मिलित थी। हिंदी पखवाड़े के समापन पश्चात सभी विजेताओ को पुरूस्कार देकर सम्मानित किया गया। सम्पूर्ण पखवाड़े का प्रबंधन डॉ कार्तिक शर्मा, डॉ साक्षी कैथ एवम् डॉ सौमाजित सरकार द्वारा किया गया।

Internal Complaints Committee (ICC) Workshop

ICAR-IIAB organized ICC workshops on September 30 and December 9, 2024, emphasizing awareness of making the workplace safe for all. The chief guest Dr. Kiran, Former GM (HR) CCL, addressed the gathering to raise awareness about workplace harassment and rendering a safe, inclusive environment. Attended by over 80 participants, the sessions highlighted the ICC's role, legal framework, and strategies for addressing grievances, concluding with an action plan for enhanced workplace safety **(Figure 89).**

Figure 89: Internal complaints committee workshop.

Vigilance Week Celebration

ICAR-IIAB, Ranchi, celebrated Vigilance Awareness Week 2024 from October 28 to November 3, with the theme "*सत्यनिष्ठा की संस्कृति से राष्ट्र की समृद्धि* (*Culture of Integrity for Nation's Prosperity*)". The week featured an oath-taking ceremony, awareness programs, and a panel discussion chaired by Director Dr. Sujay Rakshit, emphasizing integrity for personal and national growth. Vigilance officer Dr. Sujit K. Bishi commended the efforts to foster a culture of vigilance and integrity within the institute **(Figure 90).**

Figure 90: Integrity pledge during vigilence week celebration.

Institute-Industry meet

An Institute-Industry meet was organized by the institutes on November 11, 2024 with the stakeholders from the dairy, feed, and poultry industries viz., Dr. Abhijeet Mitra (Animal Husbandry Commissioner, Govt. of India), Dr. Shyam Zawar (National Mentor, MoFAH&D, GoI), Dr. TC Gupta, (Group Head, Productivity Enhancement, JMF), Dr. Sachin Joshi (Chief Thematic Program Executive BAIF, Pune), Shri Manish (Puresh Daily), Sh. Kanwal Kapoor (Osam Dairy), Shri Vikash K. Choudhary (Director, Divyansh Agro, Ranchi), Sh. D.K. Tiwari, (State Head, BISLD, BAIF, Jharkhand), Dr. Subhash V. (AVP and Head, Cattle Genetics Pvt. Ltd.), Sh. Anirvid Sarkar (Director, Agrivet Consultancy Pvt. Ltd. Kolkata), Dr. Debabrat Sharma (Jharkhand Women's Self-Supporting Poultry Co-Operative Federation Ltd.)

and Dr. Sayantani Sihi Arora, (Chief Scientific Officer, Agrivet Consultancy Pvt. Ltd. Kolkata).

Figure 91: Glimpse of Institute-Industry Meet.

The institute-industry meet was aimed to reorient the research activities, exploring the collaborative/ sponsored research at the interface of plant-animal-fish-microbe targeting the livestock sector, and exploring the possibilities for supporting the academic program through internship/ job placements, and fellowships. The meet was chaired by Dr. Sujay Rakshit, Director, co-chaired by Dr. Vijai Pal Bhadana, Joint Director (Research) and coordinated by Drs. Soumen Naskar, Ganesh N. Aderao, Nikhil K.C., Amit Kumar, and Sakshi Kaith **(Figure 91).**

World Soil Day Celebration

To highlight the soil's importance in maintaining a healthy ecosystem and human well-being among the farmers and students, "World Soil Day" was celebrated by ICAR-IIAB, on December 05, 2024 with the theme "*Soil and Water: A Source of life*". The participants were explained the need to conserve the soil and water for sustainable agriculture followed by practical exposure to soil sampling, crop residue recycling, vermicompost preparation, and scientific cultivation of different crops on the farm **(Figure 92).**

Figure 92: Celebration of World Soil Day at ICAR-IIAB.

Training and Capacity Building

Trainings organized

Sl. No.	Name	Number of Participants	Organizer	Date	Place
1.	Animal health camp cum awareness program on "Entrepreneurship development in livestock sector"	50	ICAR-IIAB and Ranchi Veterinary College	July 02-04, 2024	Rurungkocha Village, Namkum, Ranchi
2.	Hands-on workshop on "Biovia discovery studio"	15	ICAR-IIAB and Altem Technologies Pvt. Ltd., Bengaluru	September 07-08, 2024	ICAR-IIAB campus
3.	Training on "Scientific duck rearing and duckling distribution program" under Tribal Sub-Plan	32	ICAR-IIAB	September 24, 2024	ICAR-IIAB campus
4.	Scientific feeding and management of goats	20	ICAR-IIAB	December 07-09, 2024	ICAR-IIAB campus

Trainings/Workshop/Mela attended

Sl. No.	Name of Scientist	Title of workshop/ training	Duration	Organizers
1	Drs. Sujay Rakshit, Vijai Pal Bhadana, Biplab Sarkar, Avinash Pandey, Soumen Naskar, Sujay B. Kademani, Amit Kumar and Sudhir Kumar	Mega Kisan Mela	January 01-02, 2024	National Seeds Corporation and Ministry of Agriculture and Farmers Welfare, Jharkhad
2	Dr. Soumajit Sarkar	Professional attachment training on *"in ovo* and *in vitro* evaluation of neutralization potential of nano-biomaterials against highly pathogenic avian influenza (H5N1) virus"	January 08 to April 07, 2024	ICAR-National Institute of High-Security Animal Diseases, Bhopal, Madhya Pradesh
3	Drs. Sujay Rakshit, Vijai Pal Bhadana, Biplab Sarkar, Avinash Pandey, Soumen Naskar, Sujay B. Kademani, Amit Kumar and Sudhir Kumar	Regional agriculture fair for eastern region	February 03-05, 2024	ICAR- National Institute for Secondary Agriculture, Ranchi, Jharkhand
4	Dr. Amit Kumar	Short course on "Technological innovation in assisted reproductive technologies for the improvement of the caprine germplasm"	February 05-14, 2024	ICAR-Central Institute for Research on Goats, Makhdoom, Uttar Pradesh

Sl. No.	Name of Scientist	Title of workshop/ training	Duration	Organizers
5	Dr. Biplab Sarkar	Participated in SRIJAN-2: A workshop	February 13-15, 2024	ITMC, New Delhi and National Academy of Agricultural Sciences, New Delhi
6	Drs. Sujay Rakshit, Amit Kumar and Sudhir Kumar	Indian Agricultural Research Institute, PUSA mela	March 01, 2024	Simdega, Jharkhand
7	Dr. Sujay B. Kademani	Training on "Innovations in digital extension"	March 11-15, 2024	ICAR- National Academy of Agricultural Research Management, Hyderabad, Telangana
8	Dr. Kartik Sharma	Training on "Reclamation and management of salt affected soil"	March 26-28, 2024	ICAR- Central Soil Salinity Research Institute, Karnal, Haryana
9	Drs. Suryakant Manik and Sujay B. Kademani	Pedagogy development program on "Enhancing pedagogical competencies for agricultural education"	April 01-05, 2024	National Academy of Agricultural Sciences, New Delhi
10	Drs. Kartik Sharma and Kanaka K.K.	Pedagogy development program on "Enhancing pedagogical competencies for agricultural education"	April 30 to May 04, 2024	National Academy of Agricultural Sciences, New Delhi
11	Dr. Sakshi Kaith	Hand on training course in proteomics	July 01-05, 2024	Center for Molecular and Cellular Platforms, Bengaluru, Karnataka
12	Dr. Sujay B. Kademani	Capacity building program on "Building successful incubation ecosystems"	July 03-05, 2024	ICAR- National Academy of Agricultural Research Management, Hyderabad, Telangana
13	Dr. Ramya N.	Cloning and Characterization of eye colour gene, Tryptophan 2, 3-dioxygenase in Potato tuber moth, *Phthorimaea operculella* (Professional attachment training)	August 05 to November 04, 2024	ICAR-NBAIR, Bengaluru
14	Drs. Biplab Sarkar, Sujit K. Bishi and Suryakant Manik	Hands-on Workshop on "Biovia discovery studio"	September 07-08, 2024	ICAR-IIAB and Altem Technologies Pvt. Ltd., Bengaluru, Karnataka
15	Dr. Sujit K. Bishi	Yoga break at work places (online)	October 15, 2024	Dept. of Personnel and Training, Govt. of India, New Delhi
16	Dr. Soumajit Sarkar	Workshop attended on "AMR pathogens and their mitigation from a one health point of view"	December 02-07, 2024	ICAR- Central Institute of Fisheries Technology, Kochin, Kerala
17	Dr. Kartik Sharma	Biennial workshop of AICRP on "Integrated farming systems"	December 02-05, 2024	Punjab Agricultural University, Ludhiana, Punjab

Conferences/Symposia Attended

Sl. No.	Name of Scientist	Title	Duration	Place
1.	Dr. Kishore K. Krishnani	National conference on "Microbial bioprospecting for environmental conservation and restoration"	February 05-06, 2024	Department of microbiology, ADT's Shardabai Pawar mahila arts, commerce and science college, Pune, Maharashtra
2.	Dr. Kanaka K.K.	National Conference on "Animal production systems and its role in sustainable use of AnGR"	February 15-16, 2024	Society for Conservation of Domestic Animal Biodiversity in collaboration with Dept. of AGB, NTR College of Veterinary Sciences, Gannavaram, Andhra Pradesh
3.	Dr. Sanjay K. Gupta	National Conference on climate crisis and biodiversity mitigation for sustainable development and livelihood	February 22-23, 2024	Fakir Mohan University, Balasore, Odisha
4.	Dr. Sanjay K. Gupta	Indian Fisheries and Aquaculture Forum	February 23-25, 2024	ICAR-CIFRI, Barrackpore, Kolkata, India
5.	Dr. Kishore K. Krishnani	International micro-organism Day on "Microbial bioremediation of contaminants of environmental and emerging concern"	September 21, 2024	Ranchi University
6.	Drs. Biplab Sarkar, Sudhir Kumar and Avinash Pandey	International conference on "Ecotoxicology and environmental sciences"	October 21-22, 2024	Amity University, Ranchi and Institute of Ecotoxicology and Environmental Sciences, Kolkata
7.	Dr. Ganesh N. Aderao	International conference on "Trace elements in man and animals"	November 08-12, 2024	Pennsylvania State University, USA and Ramaiah Group of Institutions, India
8.	Dr. Soumen Naskar	National conference on "New vistas in harnessing genetic resources for sustainable animal"	November 21-22, 2024	Indian Society for Animal Genetic Breeding in collaboration with Bihar Veterinary College, Patna
9.	Drs. Sujay B. Kademani and Kartik Sharma	Global Soils Conference-2024	November 20-22, 2024	Indian Society of Soil Sciences, New Delhi
10.	Dr. Sanjay K. Gupta	National seminar on "Advances in environment management for sustainable fisheries and livestock production"	November 18-19, 2024	College of Fisheries, Kishanganj, Bihar

Sl. No.	Name of Scientist	Title	Duration	Place
11.	Dr. Kishore K. Krishnani	International conference on "Advances in biotechnology and bioinformatics and the Convention of the Biotech Research Society on unseen hazards and remediation strategies of microplastics-contaminants of emerging concern"	November 26-28, 2024	Dr. D. Y. Patil Vidyapeeth, Pune, Maharashtra
12.	Dr. Suryakant Manik	Indian phytopathological society eastern zonal meet and national conference on "Holistic approaches for biotic and abiotic stress management in crops for sustainable agriculture"	November 28-29, 2024	Central Rainfed Upland Rice Research Station, ICAR-National Rice Research Institute, Cuttack, Jharkhand
13.	Dr. Amit Kumar	Annual convention of ISSAR and national symposium on "Challenges in enhancing reproductive efficiency of livestock: An Indian perspective"	November 29 to December 01, 2024	Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana, Punjab
14.	Drs. Sudhir Kumar and Avinash Pandey	International Conference on " Emerging Trends in Translational Bioinformatics	December, 05-07, 2024	Birla Institute of Technology, Mesra, Ranchi India
15.	Drs. Avinash Pandey, Kishor U. Tribhuvan, Madan Kumar Sanjay K. Gupta, Sudhir Kumar and Sujit K. Bishi	National conference on "Farmers orientation towards climate change and upgradation to sustainable agriculture"	December 23-24, 2024	GAPS, CREA, PKVSS, S and T SIRI Green Agri Professional Society Sambodhi Retreat, Govindpur, Dhanbad, Jharkhand
16.	Dr. Kishore K. Krishnani	International Conference of International Academy of Physical Sciences on "Occurrence and remediation of contaminants of emerging concern with major emphasis on microplastics and nanomaterials"	December 21, 2024	Pt. Ravishankar Shukla University, Raipur, Chhattisgarh

Linkages and Collaborations

ICAR-IIAB inked MoUs to facilitate collaborative efforts in research and academic activities with following organizations:

1. ICAR- National Academy of Agricultural Research Management, Hyderabad, Telangana
2. Guru Govind Singh Educational Society's Technical Campus (GGSESTC), Chas Bokaro, Jharkhand
3. Dau Shri Vasudev Chandrakar Kamdhenu Vishwavidyalaya (CGKV), Durg, Chhattisgarh
4. Dr. Rajendra Prasad Central Agricultural University (RPCAU), Pusa, Bihar
5. Uttar Banga Krishi Viswavidyalaya (UBKV), West Bengal
6. National University of Study and Research in Law, Ranchi, Jharkhand
7. National Institute of Advanced Manufacturing Technology (NIAMT), Ranchi, Jharkhand
8. The Dean, Rajiv Gandhi Institute of Veterinary Education and Research (RIVR), Puducherry
9. Dr. Shyama Prasad Mukherjee University (DSPMU), Ranchi, Jharkhand (**Renewed**)

Rajiv Gandhi Institute of Veterinary Education and Research (RIVR), Puducherry

ICAR-NAARM, Hyderabad, Telangana

Guru Govind Singh Educational Society's Technical Campus (GGSESTC), Chas, Bokaro

National Institute of Advanced Manufacturing Technology (NIAMT), Ranchi

Dr. Shyama Prasad Mukherjee University (DSPMU), Ranchi

Dau Shri Vasudev Chandrakar Kamdhenu Vishwavidyalaya (CGKV), Durg

National University of Study and Research in Law, Ranchi

Uttar banga Krishi Viswavidyalaya (UBKV), West Bengal

Dr. Rajendra Prasad Central Agricultural University (RPCAU), Pusa, Bihar

Figure 93a: Signing of MoU by ICAR-IIAB with NIAMT, Ranchi, Jharkhand.

Figure 93b: Signing of MoU by ICAR-IIAB with Guru Gobind Singh Educational Society's Technical Campus, Bokaro.

Awards and Recognitions

Sl. No.	Award Details	Event/Organization	Date	Awardee
1.	Dr. S.K. Vasal Award for excellence in Hybrid Crop Research 2024	Trust for Advancement of Agricultural Sciences (TAAS), New Delhi	December 20, 2024	Dr. Sujay Rakshit
2.	BHU centennial award for outstanding contribution in the field of environmental biotechnology	Banaras Hindu University, Varanasi	November 26, 2024	Dr. Kishore K. Krishnani
3.	Young Scientist award	Mosaic India and S.M. Sehgal foundation, New Delhi	October 24, 2024	Dr. Jayanta Layek
4.	Young Investigator Award	Pennsylvania State University and Ramaiah Group of Institutions, India	November 11, 2024	Dr. Ganesh N. Aderao
5.	Dr. V.G. Jhingran gold medal for best Indian fisheries scientist	National seminar on *'Advances in environment management for sustainable fisheries & livestock production*' held at College of Fisheries (BASU), Kishanganj, Bihar	November 19, 2024	Dr. Sanjay K. Gupta
6.	Young Scientist award	Dr. B. Vasantharaj David foundation excellence awards -2024.	November 17, 2024	Dr. Ramya N.
7.	Best Oral presentation award	13th IFAF – Fostering Indian fisheries and aquaculture for attaining sustainable development goals held at Kolkata, India.	February 25, 2024	Dr. Sanjay K. Gupta
8.	Best Research contribution award	7th International conference on aquaculture and marine biology organized by conference Mind.	March 22-23, 2024	Dr. Sanjay K. Gupta
9.	Best Poster award	39th Annual convention and national symposium of ISSAR on "Challenges in enhancing reproductive efficiency of livestock: An Indian perspective"	December 01, 2024	Dr. Amit Kumar

Dr. Sujay Rakshit received Dr. S.K. Vasal Award for excellence in Hybrid Crop Research.

Dr. Kishore K. Krishnani received BHU centennial award for outstanding contribution in the field of environmental biotechnology.

Recognitions

1. Dr. Soumajit Sarkar has been certified by the ICAR-National Institute of High-Security Animal Diseases, Bhopal, for his experience working in Biosafety Level 3 laboratory during February to April, 2024.

2. Dr. Amit Kumar delivered an invited talk on reproductive management in animals on September 09, 2024 at KVK, Torpa, Khunti, Jharkhand.

3. Dr. Ganesh N. Aderao delivered an expert lecture on "Climate Resilient Dairy" at the CII-Food and Agriculture Center of Excellence (FACE) on September 10, 2024, in Patna.

4. Dr. Tanmaya K. Sahu delivered two invited lectures during the workshop on "Emerging Frontiers in Stress Biology" held at Banasthali Vidyapith, Rajasthan, from October 18-20, 2024.

5. Dr. Ganesh N. Aderao delivered expert lectures to dairy farmers during regional dairy farmers meets organized by Patanjali feeds division in Bokaro on October 18, 2024, and Jamshedpur on October 20, 2024.

6. Dr. Jayanta Layek delivered lead lecture on the topic "*Designing integrated organic farming system for sustainable hill agriculture*" in the National Conference on "Hill Agro-Ecosystem: Challenges and Opportunities for Achieving Sustainable Development Goals" organized by ICAR-RC-NEHR, Nagaland Center and IAHF, Nagaland during November 29-30, 2024.

7. Dr. Sujit K. Bishi delivered a lead lecture on "*Development and Genotypic Regulation of L-DOPA Accumulation in Faba Bean: Insights into Metabolic Shifts and Gene Expression Dynamics*" in 2nd National Conference on Farmers Orientation Towards Climate Change and Upgradation to Sustainability, FOCUS-2024 during December 23-24, 2024, in Dhanbad, Jharkhand.

8. Dr. Madan Kumar delivered a keynote lecture on "*Morphological evaluation of grain Amaranthus germplasm for seed shattering tolerance*" in 2nd National Conference on Farmers Orientation Towards Climate Change and Upgradation to Sustainability, FOCUS-2024 during December 23-24, 2024, in Dhanbad, Jharkhand.

9. Dr. Shambhu K. Lal delivered a keynote lecture on "*Optimization of an efficient and reproducible regeneration system in tropical maize (Zea mays L.) based on seed-derived nodal explants*" in 2nd National Conference on Farmers Orientation Towards Climate Change and Upgradation to Sustainability, FOCUS-2024 during December 23-24, 2024, in Dhanbad, Jharkhand.

Development of tools

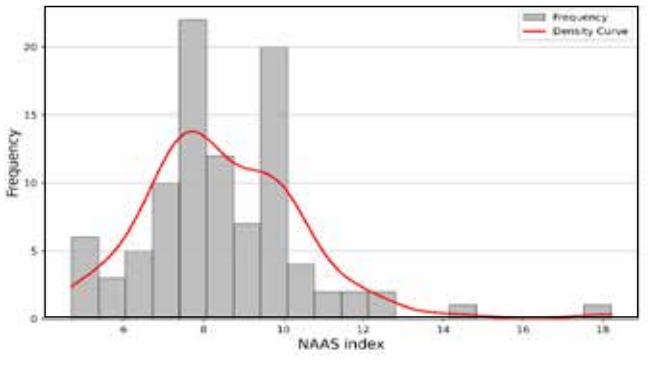
1. Dr. Kanaka K.K. developed and standardized pipelines for various population and quantitative genetics metrics, has been published on GitHub (https://github.com/kkokay07/pq-genetics).

2. Dr. Kanaka K.K. developed and standardized a cloud-based pipelines for teaching purposes, published on GitHub (https:/github.com/kkokay07/GenomicClass_on_Cloud).

Dr. Jayanta Layek received Young Scientist award by Mosaic India and S.M. Sehgal foundation, New Delhi.

Dr. Sanjay K. Gupta received Dr. V.G. Jhingran gold medal for best Indian fisheries scientist.

Publications



NAAS index scores of research and review papers published by ICAR-IIAB faculty during 2024.

Research articles

Abrar, F.P.N., Maiti, S., Jha, S.K., Garai, S., Bhakat, M., Dixit, A.K., Roy, S.K., Kademani, S.B., Ranjan, A., Kujur, S., Quader, S.W., Madhulata. C., Gosh, B. and Barman, B. 2024. Farmers' satisfaction with climate-resilient agriculture technologies in the coastal low-lying region of Kerala. *Agricultural Mechanization in Asia, Africa and Latin America*, 55(09), p.1870. **(NAAS 6.40)**

Akram, M., Iquebal, M.A., Baptala, K.G., Jaiswal, S., Gopalakrishnan Kesharivarmen, S., Kamaal, N., Bohra, A., Soren, K.R., Sachan, D.K., Husain, R. and Kumar, D. 2024. Genome assembly and annotation of *Spilosoma obliqua* multicapsid nucleopolyhedrovirus from Bihar hairy catrpillar, an agriculturally important insect pest. *Journal of Phytopathology*, 172(3), p.13308. **(NAAS 7.40)**

Arora, A., Bhamare, D., Das, A.K., Dixit, S., Venadan, S., Yathish, K.R., Kumar, R., Paul, D., Sekhar, J.C., Neelam, S. and Nandi, S. 2024. Development of high-amylose maize (*Zea mays* L.) genotypes adapted to Indian conditions through molecular breeding. *Crop and Pasture Science*, 75(3). **(NAAS 7.80)**

Arora, A., Das, A.K., Dixit, S., Yathish, K.R., Singh, S.B., Sekhar, J.C., Ravikesavan, R., Sahi, J.P., Kumar, I.S., Mahadevu, P. and Swain, D. 2024. Genetic diversity analysis and heterotic grouping of Indian white maize inbred lines using combining ability and SNP markers. *Crop Science*, 64(2), pp.726-737. **(NAAS 8.00)**

Arora, A., Das, A.K., Kumar, R., Sharma, S., Kaur, N., Dixit, S., Kaur, Y., Saxena, D.C. and Rakshit, S. 2024. Development of high-yielding white maize hybrids with better chapatti-making quality compared to traditionally used local landraces. *Frontiers in Nutrition*, 11, p.1330662. **(NAAS 10.00)**

Bhadra, S., Krishnani, K.K., Sharma, A., Sahoo, U. and Majeedkutty, B.R.A. 2024. *Curcuma longa* and *Allium sativum* as health promoters in genetically improved farmed Tilapia (GIFT)-A green drug approach in hi-tech aquaculture using biofloc. *Aquaculture*, 582, p.740516. **(NAAS 9.90)**

Bhagat, R., Walia, S.S., Dheri, G.S., Singh, G. and Sharma, K. 2024. Pear (*Pyrus communis*)-based agroecosystem improves soil nutrient dynamics, microbial biomass, enzymatic activity, farm productivity and profitability. *Scientia Horticulturae*, 336, p.113398. **(NAAS 9.90)**

Chakraborty, P., Krishnani, K.K., Mulchandani, A., Paniprasad, K., Sarkar, D.J., Sawant, P.B., Kumar, N., Sarkar, B., Mallik, A., Pal, P. and Nagendrasai, K. 2024. Speciation-specific chromium bioaccumulation and detoxification in fish using hydrogel microencapsulated biogenic nanosilver and zeolite synergizing with biomarkers. *Environmental Geochemistry and Health*, 46(8), p.298. **(NAAS 9.20)**

Choudhary, A., Devadasan, M.J., Sukhija, N., Kanaka, K.K., Kumar, D.R., Vineeth, M.R., Surya, T., Verma, A., Niranjan, S.K. and Sivalingam, J. 2024. Genome-wide identification of SNPs and their annotation in Indian Gir cattle. *Cytology and Genetics*, 58(4), p.312. **(NAAS 6.50)**

Choudhary, A., Sukhija, N., Kanaka, K.K., Jaglan, K., Devadasan, M.J., Kumar, D.R., Vineeth, M.R., Tamil, S., Niranjan, S.K., Verma, A. and Sivalingam, J. 2024. Genetic blueprinting of novel and performance traits-related SNPs in Indian Gir cattle using latest reference assembly: ddRAD analysis of Gir cattle for SNP discovery. *Indian Journal of Dairy Science*, 77(1). **(NAAS 6.20)**

Chowdhury, A.R., Kumar, R., Mahanty, A., Mukherjee, K., Kumar, S., Tribhuvan, K.U., Sheel, R., Lenka, S., Singh, B.K., Chattopadhyay, C. and Sharma, T.R. 2024. Inhibitory role of copper and silver nanocomposite on important bacterial and fungal pathogens in rice (*Oryza sativa*). *Scientific Reports*, 14(1), p.1779. **(NAAS 9.80)**

Datta, D., Manna, M., Parmar, H., Karippadakam, S., Rashid, A., Mehta, S., Lal, S.K., Venkatapuram,

A.K., Singh, J., Reddy, M.K. and Patnaik, S. 2024. Investigating the *Phi* use efficiency of a NADP utilizing phosphite dehydrogenase in rice. *Journal of Plant Biology*, 67(3), pp.231-240. **(NAAS 8.20)**

Devi, A.D., Dass, A., Dhar, S., Layek, J., Singh, A., Kaur, R., Singh, T., and Nithin, K.K. 2024. Productivity and profitability enhancement in rice through precision nitrogen supply in the north-eastern region of India. *Journal of Soil and Water Conservation*, 23(2), pp.188–195. **(NAAS 8.20)**

Foysal, M.J., Kawser, A.R., Paul, S.I., Chaklader, M.R., Gupta, S.K., Tay, A., Neilan, B.A., Gagnon, M.M., Fotedar, R., Rahman, M.M. and Timms, V.J. 2024. Prevalence of opportunistic pathogens and anti-microbial resistance in urban aquaculture ponds. *Journal of Hazardous Materials*, 474, p.134661. **(NAAS 18.20)**

Garai, S., Paul, R.K. and Paul, A.K. 2024. Spillover effects of Covid-19 induced lockdown on onion prices in India. *Journal of Scientific Research and Reports*, 30(3), pp.21-31. **(NAAS 5.17)**

Garai, S., Paul, R.K., Yeasin, M. and Paul, A.K. 2024. CEEMDAN-based hybrid machine learning models for time series forecasting using MARS algorithm and PSO-optimization. *Neural Processing Letters*, 56(2), p.92. **(NAAS 8.60)**

Gautam, A., Kumar, N., Saxena, A.C., Sharma, A.K., Govil, K., Patel, S.K., Channabasappa, N.K., Singh, P. and Yadav, J.S. 2024. Evaluation of specific markers for diagnosis of prostatic affections in unneutered dogs-a cross-sectional study. *Annals of Forest Research*, 67(2), pp.31-50. **(NAAS 7.70)**

Ghasal, P.C., Choudhary, J. Raghvendra, K.J., Meena, A.L., Narwal, E. and Shivay, Y.S. 2024. Sustainability and ecosystem services under organic farming. *Journal of Agricultural Physics*, 24, pp.187-200. **(NAAS 4.78)**

Goli, R.C., Mahar, K., Chishi, K.G., Choudhary, S., Rathi, P., Sree, C.C., Haritha, P., Sukhija, N. and Kanaka, K.K. 2024. Runs of Homozygosity assessment using reduced representation sequencing highlight the evidence of random mating in emu (*Dromaius novaehollandiae*), *Genome*. *(In Press)*. **(NAAS 8.30)**

Goli, R.C., Mahar, K., Manohar, P.S., Chishi, K.G., Prabhu, I.G., Choudhary, S., Rathi, P., Chinnareddyvari, C.S., Haritha, P., Metta, M. and Shetkar, M. 2024. Insights from homozygous signatures of *Cervus nippon* revealed genetic architecture for components of fitness. *Mammalian Genome*, 35(4), pp.657-672. **(NAAS 8.70)**

Gupta, A., Gupta, S.K. and Mishra, P.K. 2024. Investigating *Semecarpus anacardium* leaves extract towards augmenting growth and haematological indices in *Labeo rohita* fingerlings. *Flora and Fauna*, 30(2), pp. 206-216. **(NAAS 6.04)**

Gupta, S.K., Gupta, A., Choudhary, J.S., Foysal, M.J., Gupta, R., Sarkar, B. and Krishnani, K.K. 2024. Dietary chia (*Salvia hispanica* L.) seeds oil supplementation augments growth performance and gut microbial composition in *Labeo rohita* fingerlings. *Scientific Reports*, 15(1), pp. 1-18. **(NAAS 9.80)**

Gupta, S.K., Gupta, R., Gupta, A., Foysal, M.J. and Krishnani, K.K. 2024. Chia (*Salvia hispanica*) seed oil modulates the haemato-immunological re-sponse, antioxidative status and cytokine gene expression of tropical freshwater teleost, *Labeo rohita. Biology.* (*InPress*). **(NAAS 9.80)**

Gurumurthy, S., Ashu, A., Kruthika, S., Solanke, A.P., Basavaraja, T., Soren, K.R., Rane, J., Pathak, H. and Prasad, P.V. 2024. An innovative natural speed breeding technique for accelerated chickpea (*Cicer arietinum* L.) generation turnover. *Plant Methods*, 20(1), p.177. **(NAAS 10.70)**

Gurumurthy, S., Mamatha, B.C., Basu, P.S., Rudresh, K., Basavaraja, T., Bheemanahalli, R., Pal, M., Jha, P., Soren, K.R., Nidagundi, J.M. and Reddy, S. 2024. Identification of photothermo-insensitive with climate-smart early-maturing chickpea genotypes. *Plant Genetic Resources*, 22(3), pp.149-157. **(NAAS 7.20)**

Harika, N., Verma, A.K., Krishnani, K.K., Hittinahalli, C.M., Reddy, R. and Pai, M. 2024. Supplementation of potassium in aquaculture wastewater and its effect on growth performance of basil (*Ocimum basilicumin* L) and pangasius (*Pangasianodon hypophthalmus*) in NFT-based aquaponics. *Scientia Horticulturae*, 323, p.112521. **(NAAS 9.90)**

Jacob, J. and Krishnani, K.K. 2024. Dehalococcoides-assisted reductive dechlorination of xenobiotics and recalcitrant compounds. *Current Science*, 127(10). **(NAAS 7.10)**

Jena, S., Sanyal, R., Jawed, D.M., Sengupta, K., Pradhan, B., Sinha, S.K., Sarkar, B., Kumar, S., Lenka, S.K., Naskar, S. and Bhadana, V.P. 2024. Spatio-temporal expression of polyphenol oxidase unveils the dynamics of L-DOPA accumulation in faba bean

(*Vicia faba* L.). *Physiology and Molecular Biology of Plants*, pp.1-12. **(NAAS 9.40)**

Jesna, P., Das, B.K., Sarkar, D.J., Krishnani, K.K., Chadha, N.K. and Hemaprasanth, K. 2024. Effect of nanoformulated cypermethrin, a parasiticide in *Labeo rohita* fingerlings: impact on biochemical, haematological, and stress response. *Environmental Science and Pollution Research*, 31(55), pp.63863-63875. **(NAAS 6.00)**

Jha, G.K., Kumar, P., Kademani, S.B., Abrar, P.F. and Ranjan, A. 2024. Nutrient intake disparities among public distribution system beneficiaries in the Bundelkhand region. *Current Science*, 127(2), p.214. **(NAAS 7.10)**

Kademani, S., Nain, M.S., Singh, R. and Roy, S.K. 2024. Analysis and profiling of agri-entrepreneurship promoting institutions. *Indian Journal of Extension Education*, 60(1), pp.35-40. **(NAAS 5.02)**

Kademani, S., Nain, M.S., Singh, R., Kumar, S., Parsad, R., Sharma, D.K., Roy, S.K., Karjigi, K.D., Prabhakar, I., Mahapatra, A. and Patil, M. 2024. Unveiling challenges and strategizing solutions for sustainable agri-entrepreneurship development. *Frontiers in Sustainable Food Systems*, 8, p.1447371. **(NAAS 9.70)**

Krishnani, K.K., Kailasam, M., Brahmane, M.P., Das, B.K., Sukhdhane, K., Panigrahi, A., Bera, A. and Ezhil, P. 2024. Unveiling the effect of stocking density and salinity on mucus-associated greenwater qualities, physiology, and growth performance of euryhaline milkfish *Chanos Chanos*. *Agricultural Research*, pp.1-13. **(NAAS 7.40)**

Kumar, A., Das, S.P., Pandey, A., Singh, S.P., Kaur, S., Jaiswal, S., Philanim, W.S., Touthang, L., Verma, V.K., Singh, B.K. and Mishra, V.K. 2024. Genetic diversity and population structure analysis in Job's tears (*Coix lacryma-jobi* L.) collections from northeastern Himalayan region. *Genetic Resources and Crop Evolution*, pp.1-23. **(NAAS 7.60)**

Kumar, A., Touthang, L., Das, S.P., Krishnappa, R., Pandey, A., Prasad, A., Singh, S.P., Kaur, S., Aochen, C., Verma, V.K. and Umakanta, N. 2024. Dissecting genetic variation for agro-morphological traits of elevated temperature under CO_2-temperature gradient chamber and validation of markers linked to heat tolerance of rice (*Oryza sativa* L.) cultivars of north-eastern Himalayan region. *Euphytica*, 220(12), p.186. **(NAAS 7.60)**

Kumar, B., Choudhary, M., Kumar, P., Kumar, S., Sravani, D., Vinodhana, N.K., Kumar, G.S., Gami, R., Vyas, M., Jat, B.S. and Dagla, M.C. 2024. GGE biplot analysis and selection indices for yield and stability assessment of maize (*Zea mays* L.) genotypes under drought and irrigated conditions. *Indian Journal of Genetics and Plant Breeding*, 84(02), pp.209-215. **(NAAS 7.00)**

Kumar, K., Durgesh, K., Anjoy, P., Srivastava, H., Tribhuvan, K.U., Sevanthi, A.M., Singh, A., Prabha, R., Sharma, S., Joshi, R. and Jain, P.K. 2024. transcriptional reprogramming and allelic variation in pleiotropic QTL regulates days to flowering and growth habit in pigeon pea. *Plant, Cell & Environment.* **(NAAS 12.3)**

Kumar, K., Jha, S.K., Kumar, V., Sagar, P., Tripathi, S., Rathore, M., Singh, A.K., Soren, K.R. and Dixit, G.P. 2024. Identification and characterization of *NHX* gene family for their role under salt stress in *Vigna mungo*. *Physiologia Plantarum*, 176(5), p.e14563. **(NAAS 11.40)**

Kumar, R., Das, A.K., Kaur, Y., Kumar, S., Shukla, S., Chikkappa, G.K., Chaudhary, D.P. and Rakshit, S. 2024. Strategic genetic amelioration of quality protein maize (QPM) germplasm and its utilization in hybrid breeding. *Plant Genetic Resources*, 22(6), pp.359-367. **(NAAS 7.20)**

Kumar, R., Kumar, S., Chikkappa, G.K., Das, A.K., Dhonde, S., Kaur, Y., Kumar, S., Shukla, S. and Rakshit, S. 2024. Unveiling genotype×environment dynamics for grain yield in QPM hybrids through AMMI, GGE Biplot, and MTSI approach. *Indian Journal of Genetics and Plant Breeding*, 84(03), pp.449-460. **(NAAS 7.00)**

Kumar, R., Rao, K.K., Mondal, S., Choudhary, J.S., Kumar, S., Jat, S.L., Mishra, J.S., Singh, A.K., Upadhyay, P.K., Das, A. and Singh, V.K. 2024. A comprehensive analysis of resource conservation strategies: Impacts on productivity, energetics, and environmental footprints in rice-based systems of the Eastern Indo-Gangetic Plains. *Current Research in Environmental Sustainability*, 8, p.100271. **(NAAS 9.70)**

Lokesha, E., Jadhav, S.E., Aderao, G.N., Chaudhary, P., Gupta, S.K., Dutta, N. and Singh, G. 2024. High dietary zinc promotes its optimal absorption through modulation of key transporter genes, *SOD1*, and *HSP70* expression in heat-stressed rats. *Biological Trace Element Research*, pp.1-14. **(NAAS 9.40)**

Lyngdoh, M.E., Chettri, J., Kharchandy, V.F., Sheel, R., Choudhury, A.R., Sarkar, B., Pattanayak, A., Deori, S., Abedin, S.N. and Kadirvel, G. 2024. Synthesis of green zinc-oxide nanoparticles and its dose-dependent beneficial effect on spermatozoa during preservation: sperm functional integrity, fertility and antimicrobial activity. *Frontiers in Bioengineering and Biotechnology*, 12, p.1326143. **(NAAS 10.30)**

Magudeeswari, P., Balakrishnan, D., Surapaneni, M., Krishnam Raju, A., Rao, Y.V., Pranay, G., Valarmathi, P., Bhadana, V.P., Neelamraju, S. and Sundaram, R.M. 2024. Exploring stable low soil phosphorous stress tolerance in rice using novel allele recombination from *Oryza rufipogon*. *Plant Breeding*, 1(1). pp.19. **(NAAS 7.50)**

Mahar, K., Goli, R.C., Chishi, K.G., Ganguly, I., Dixit, S.P., Singh, S., Choudhary, S., Rathi, P., Chinnareddyvari, C.S., Diwakar, V. and Metta, M. 2024. Runs of homozygosity decipher genetic diversity in cattle breed dwelling in the colder regions of the world. *Cytogenetic and Genome Research*, 164(4), pp.154-164. **(NAAS 7.70)**

Mani, P., Priyadarsini, S., K. Channabasappa, N., Sahoo, P.R., Singh, R., Saxena, M., Upmanyu, V., Agrawal, R.K., Singh, P., Saini, M. and Kumar, A. 2024. Role of *narL* gene in the pathogenesis of *Salmonella typhimurium*. *Journal of Basic Microbiology*, 64(5), p.2300456. **(NAAS 9.50)**

Manjuprakash, Gowda, G.V., and Sujay, B.K. 2024. Determinants of farmer suicide syndrome: a comprehensive analysis. *Gujarat Journal of Extension Education*, 37(1), pp.76-81. **(NAAS 5.30)**

Narwal, E., Choudhary, J., Kumar, M., Amarowicz, R., Kumar, S., Radha, Chandran, D., Dhumal, S., Singh, S., Senapathy, M. and Rajalingam, S. 2024. Botanicals as promising antimicrobial agents for enhancing oral health: a comprehensive review. *Critical Reviews in Microbiology*, pp.1-24. **(NAAS 12.00)**

Nguyen, T.T.T., Foysal, M.J., Gupta, S.K., Tay, A., Fotedar, R. and Gagnon, M.M. 2024. Effects of carbon source addition in rearing water on sediment characteristics, growth and health of cultured marron (*Cherax cainii*). *Scientific Reports*, 14(1), p.1349. **(NAAS 9.80)**

Padala, V.K., Venkatesh, Y.N., Rajna, S., Ramya, N. and Chander, S. 2024. Incidence of pest and natural enemies in direct seeded rice and transplanted rice. *National Academy Science Letters*, pp.1-4. **(NAAS 7.20)**

Pahal, S., Srivastava, H., Saxena, S., Tribhuvan, K.U., Kaila, T., Sharma, S., Grewal, S., Singh, N.K. and Gaikwad, K. 2024. Comparative transcriptome analysis of two contrasting genotypes provides new insights into the drought response mechanism in pigeon pea (*Cajanus cajan* L. Millsp.). *Genes & Genomics*, 46(1), pp.65-94. **(NAAS 7.60)**

Pai, M., Verma, A.K., Krishnani, K.K., Varghese, T., Hittinahalli, C.M. and Verma, M.K. 2024. Stocking density optimization and its impact on growth and physiological responses of Nile tilapia (*Oreochromis niloticus*) reared in hybrid biofloc-RAS culture system. *Aquaculture*, 588, pp.740920. **(NAAS 9.90)**

Pandey, A., Lap, B., Aochen, C., Kumar, A., Tyagi, W. and Rai, M. 2024. Assessment of genetic variability in Job's tears (*Coix lacryma-jobi* L.) Germplasm from Indian NEH region using morpho-physiological traits and SSR markers. *Plant Molecular Biology Reporter*, pp.1-11. **(NAAS 7.60)**

Pandey, A., Pathan, M.A., Ananthan, P.S., Sudhagar, A., Krishnani, K.K., Sreedharan, K., Kumar, P., Thirunavukkarasar, R. and Harikrishna, V. 2024. Stocking for sustainable aqua-venture: optimal growth, yield and economic analysis of *Penaeus vannamei* culture in inland saline water (ISW) of India. *Environment, Development and Sustainability*, 26(3), pp.6913-6942. **(NAAS 10.70)**

Pandey, A., Pathan, M.A., Sudhagar, S.A., Krishnani, K.K., Sreedharan, K., Prakash, S. and Jana, P. 2024. Influence of crowding density mediated stress on haematological, biochemical indices and molecular changes of *Penaeus vannamei* reared in inland saline water (ISW) sourced earthen ponds. *Aquaculture International*, pp.1-16. **(NAAS 8.20)**

Pandey, N., Rajavat, A.S., Vaishnav, R., Singh, A.N., Kumar, S., Mishra, V., Kumar, M. and Shrivastava, N. 2024. Mining of rice rhizobacteria to control false smut and improve plant growth in rice (*Oryza sativa* L.). *European Journal of Plant Pathology*, pp.1-14. **(NAAS 7.70)**

Pandey, N., Vaishnav, R., Rajavat, A.S., Singh, A.N., Kumar, S., Tripathi, R.M., Kumar, M. and Shrivastava, N. 2024. Exploring the potential of *Bacillus* for crop productivity and sustainable solution for combating rice false smut disease. *Frontiers in Microbiology*, 15, p.1405090. **(NAAS 10.00)**

Panzade, K.P., Tribhuvan, K.U., Pawar, D.V., Jasrotia, R.S., Gaikwad, K., Dalal, M., Kumar, R.R., Singh, M.P., Awasthi, O.P. and Padaria, J.C. 2024. Discovering

the regulators of heat stress tolerance in *Ziziphus nummularia* (Burm. f) wight and walk.-arn. *Physiology and Molecular Biology of Plants*, 30(3), pp.497-511. **(NAAS 9.40)**

Paramanik, B., Mahanta, S., Das, B., Patra, P.S., Choudhury, A., Ghatak, P., Layek, J., Dutta, G., Saikia, N. and Biswakarma, N. 2024. Enhancing rice productivity through holistic nutrient management: integrating vermicompost and azolla for improved agronomic performance and sustainability. *Journal of Plant Nutrition*, pp.1-15. **(NAAS 7.60)**

Pathak, M.S., Sukhdhane, K., Krishnani, K.K. and Chanu, T.I. 2024. Exploring the toxicity of chromium on aquatic ecosystems: a comprehensive assessment of growth, physiological responses, genotoxicity, and histological alterations in *Etroplus suratensis* juveniles. *Aquaculture International*, 32(7), pp.9987-10008. **(NAAS 8.20)**

Patra, S., Chakraborty, D., Verma, V.K., Pande, R., Sangma, R.H.C., Chakraborty, M., Layek, J. and Hazarika, S. 2024. Influence of shifting thermal regimes on tomato fruit borer, *Helicoverpa armigera* (Hubner) in the Eastern Himalaya: implications for pest management strategies. *International Journal of Biometeorology*, 68(11), pp.2241-2251. **(NASS 9.00)**

Priyadarsini, S., Mani, P., Singh, R., Nikhil, K.C., Sahoo, P.R., Kesavan, M., Saxena, M., Sahoo, M., Saini, M. and Kumar, A. 2024. Deletion of both anaerobic regulator genes *fnr* and *narL* compromises the colonization of *Salmonella typhimurium* in mice model. *World Journal of Microbiology and Biotechnology*, 40(12), pp.1-14. **(NAAS 10.00)**

Ramya, N., Padala, V.K., Sagar, D., Rupali, J.S., Kumar, H., Reshma, R., Yadav, P. and Subramanian, S. 2024. Decoding the copulation and courtship patterns of an invasive pest, *Spodoptera frugiperda* from India. *Current Science*, 126(9). **(NAAS 7.10)**

Rangappa, K., Choudhury, B.U., Kumar, A., Das, S.P., Ayam, G., Hazarika, S., Moirangthem, P., Layek, J., Nandha, A., Debnath, S. and Mishra, V.K. 2024. Comparative stress physiological analysis of indigenous rice cultivars of Eastern Himalayan Region under elevated temperature of changing climate. *Plant Physiology Reports*, pp.1-17. **(NAAS 7.50)**

Rangappa, K., Das, A., Layek, J., Basavaraj, S., Debnath, S., Bhupenchandra, I., Devi, A.G., Mohapatra, K.P., Choudhury, B.U. and Mishra, V.K. 2024. Conservation tillage and residue management practices in rice improves stress tolerance of succeeding vegetable pea by regulating physiological traits in Eastern Himalayas. *Scientia Horticulturae*, 327, p.112842. **(NAAS 9.90)**

Sahu, S., Rao, A.R., Sahu, T.K., Pandey, J., Varshney, S., Kumar, A. and Gaikwad, K. 2024. Predictive role of cluster bean (*Cyamopsis tetragonoloba*) derived miRNAs in human and cattle health. *Genes*, 15(4), p.448. **(NAAS 8.80)**

Sahu, T.K., Verma, S.K., Gayacharan, Singh, N.P., Joshi, D.C., Wankhede, D.P., Singh, M., Bhardwaj, R., Singh, B., Parida, S.K. and Chattopadhyay, D. 2024. Transcriptome-wide association mapping provides insights into the genetic basis and candidate genes governing flowering, maturity and seed weight in rice bean (*Vigna umbellata*). *BMC Plant Biology*, 24(1), p.379. **(NAAS 10.30)**

Shinde, S.V., Sukhdhane, K.S., Krishnani, K.K., Rani, B.A., Pathak, M.S., Chanu, T.I. and Munilkumar, S. 2024. Inclusion of organic and inorganic extractive species improves growth, survival and physiological responses of GIFT fish reared in freshwater integrated multi-trophic aquaculture system. *Aquaculture*, 580, p.740346. **(NAAS 9.90)**

Shinde, S.V., Sukhdhane, K.S., Sawant, S.S., Krishnani, K.K., Munilkumar, S., Majeedkutty, Rani B.A., Chanu, T.I. and Pathak, M.S. 2024. Amelioration of water quality and physiological performance of GIFT fish through the incorporation of lemna minor and *Lamellidens marginalis* for ecological bioremediation in freshwater integrated multi-trophic aquaculture system. *Aquaculture International*, pp.1-21. **(NAAS 8.20)**

Sivalingam, J., Niranjan, S.K., Yadav, D.K., Singh, S.P., Sukhija, N., Kanaka, K.K., Singh, P.K. and Singh, A.P. 2024. Phenotypic and genetic characterization of unexplored, potential cattle population of Madhya Pradesh. *Tropical Animal Health and Production*, 56(2), p.102. **(NAAS 7.70)**

Sukhija, N., Goli, R.C., Sukhija, M., Rathi, P., Jaglan, K., Dash, A., Nandhini, P.B. and Kanaka, K.K. 2024. Evolutionary stamps for adaptation traced in *Cervus nippon* genome using reduced representation sequencing. *Conservation Genetics Resources*, 16(1), pp.135-146. **(NAAS 6.90)**

Sunil, N., Sivaraj, N., Bhadru, D., Vinodhana, K., Kachhapur, R.M., Sravani, D., Madhu, B., Ramesh, P., Dhandapani, A. and Rakshit, S. 2024. DIVA-GIS and MaxEnt based diversity indices help in

understanding trait and geographic diversity in maize in India. *Maydica*, 67(1). **(NAAS 6.40)**

Tribhuvan, K.U., Mishra, T., Dilip, S., Pandey, A., Kumar, S., Mahato, J.L., Raiger, H.L., Pattanayak, A. and Singh, B.K. 2024. Genic-SSR-based genetic diversity and population structure analysis in a global germplasm collection highlights the African origin of winged bean (*Psophocarpus tetragonolobus* L.). *Genetic Resources and Crop Evolution*, 71(1), pp.309-329. **(NAAS 7.60)**

Tribhuvan, K.U., Mishra, T., Kaur, S., Pandey, A., Choudhary, S.B., Bhadana, V.P., Rakshit, S. and Singh, B.K. 2024. Identification and characterization of novel drought-responsive lncRNAs in stone apple (*Aegle marmelos* L.) through whole-transcriptome analysis. *Current Plant Biology*, 38, p.100336. **(NAAS 11.40)**

Tribhuvan, K.U., Shivakumaraswamy, M., Mishra, T., Kaur, S., Sarkar, B., Pattanayak, A. and Singh, B.K. 2024. Identification, genomic localization, and functional validation of salt-stress-related lncRNAs in Indian Mustard (*Brassica juncea* L.). *BMC genomics*, 25(1), p.1121. **(NAAS 9.50)**

Tripathi, S., Bharadwaj, C., Hembram, M., Kumar, N., Konda, A.K., Mondal, B., Gupta, N.C., Dixit, G.P. and Soren, K.R. 2024. Delving into the BURP super family: A Comprehensive QTL-assisted study on *RD22* genes and its role in salinity stress tolerance in chickpea. *Biochemical Genetics*, pp.1-25. **(NAAS 8.10)**

Venadan, S., Das, A.K., Yathish, K.R., Chaudhary, D.P., Arora, A. and Rakshit, S. 2024. Variability for kernel starch components in Indian maize germplasm and identification of polymorphic molecular marker for selected waxy maize genotypes. *Cereal Research Communications*, 52(3), pp.1093-1105. **(NAAS 7.60)**

Verma, V.K., Pandey, A., Thirugnanavel, A., Rymbai, H., Dutta, N., Kumar, A., Bhutia, T.L., Jha, A.K. and Mishra, V.K. 2024. Ecology, genetic diversity, and population structure among commercial varieties and local landraces of *Capsicum* spp. grown in northeastern states of India. *Frontiers in Plant Science*, 15, p.1379637. **(NAAS 10.10)**

Waghmare, S.D., Prakash, S., Krishnani, K.K., Sharma, A., Yadav, V.K. and Qureshi, N. 2024. Tilapia-sugarcane integrated farming system for sustainable development of climate-resilient agri-aquaculture. *Journal of Experimental Zoology India*, 27(1). **(NAAS 7.90)**

Waghmare, S.D., Prakash, S., Sharma, A., Krishnani, K.K., Yadav, V.K. and Qureshi, N.W. 2024. Evaluating economic viability and environmental externalities of integrated tilapia-sugarcane farming in Maharashtra. *Agricultural Water Management*, 302, p.108967. **(NAAS 11.90)**

Yadav, A.K., Singh, C.K., Wankhede, D.P., Kalia, R.K., Pradhan, S., Ujjainwal, S., Sahu, T.K., Nathawat, N.S., Kakani, R.K., Rani, R. and Kumar, R. 2024. Combined genome-wide association study and expression analysis unravels candidate genes associated with seed weight in moth bean (*Vigna aconitifolia* (Jacq.) Marechal). *Journal of Plant Growth Regulation*, pp.1-14. **(NAAS 9.90)**

Yadav, S.R., Chavan, B.R., Chadha, N.K., Bodake, P.S., Krishnani, K.K., Sawant, P.B. and Bhosle, R. 2024. Influence of different stocking densities of pearlspot (*Etroplus suratensis*) on plankton diversity indices of biofilm-based rearing system. *Journal of Environmental Biology*, 45(5), pp.551-557. **(NAAS 6.60)**

Murasing, D. K., Umar, S. I. U., Naskar, S., and Sharma, M. (2024). Isolation of plasma membrane proteins from bovine spermatozoa using ultracentrifugation. *International Journal of Advanced Biochemistry Research*, 8(8S):1139-1143. **(NAAS 5.70)**

Umar, S. I. U., Prasad, S., Naskar, S., Chowdhury, P., Rana, A., and Das, P. J. (2024). Development and optimization of an efficient RNA isolation protocol from bovine (Bos indicus) spermatozoa. *Biochemistry and Biophysics Reports*, *40*, 101862. **(NAAS 8.30)**

Review papers

Bhagat, R., Walia, S.S., Sharma, K., Singh, R., Singh, G. and Hossain, A. 2024. The integrated farming system is an environmentally friendly and cost-effective approach to the sustainability of agri-food systems in the modern era of the changing climate: A comprehensive review. *Food and Energy Security*, 13(1), p.534. **(NAAS 10.00)**

Ghare, M., Vishwakarma, K., Tripathi, S., Dixit, G.P. and Soren, K.R. 2024. Unveiling the benefits of resistant starch in legumes: overview of current and future prospective. *Starch-Stärke*, p.2300212. **(NAAS 8.60)**

Giri, S.S., Kim, H.J., Jung, W.J., Lee, S.B., Joo, S.J., Gupta, S.K. and Park, S.C. 2024. Probiotics in addressing heavy metal toxicities in fish farming: Current progress and perspective. *Ecotoxicology and*

Environmental Safety, 282, p.116755. **(NAAS 12.20)**

Goli, R.C., Chishi, K.G., Ganguly, I., Singh, S., Dixit, S.P., Rathi, P., Diwakar, V., Limbalkar, O.M., Sukhija, N. and Kanaka, K.K. 2024. Global and local ancestry and its importance: a review. *Current Genomics*, 25(4), pp.237-260. **(NAAS 7.80)**

Goli, R.C., Sukhija, N., Rathi, P., Chishi, K.G., Koloi, S., Malik, A.A., Purohit, P.B., Shetkar, M. and Kanaka, K.K. 2024. Unraveling the genetic tapestry of Indian chicken: A comprehensive study of molecular variations and diversity. *Ecological Genetics and Genomics*, p.100220. **(NAAS 6.90)**

Idapuganti, R.G., Das, A., Sungoh, H., Layek, J., Mandal, S., Verma, B.C., Lal, R., Rangappa, K., Babu, S. and Hazarika, S. 2024. Can biochar conserve soil moisture and improve soil properties for sustainable intensification of acid soils in the Eastern Indian Himalayas? *Land Degradation & Development*, 35(3), pp.1192-1208. **(NAAS 9.60)**

Jaiswal, S., Singh, L.B., Kumar, K., Vijayan, J., Shettigar, N., Jha, S.K. and Soren, K.R. 2024. Anti-CRISPR proteins: a weapon of phage-bacterial arm race for genome editing. *The Nucleus*, 67(1), pp.47-59. **(NAAS 8.10)**

Kanaka, K.K., Singh, S., Ganguly, I., Dash, A., Sukhja, N., Nandhini, P.B. and Dixit, S.P. 2024. Epigenetic mechanisms and their significance in livestock species. *Journal of Livestock Biodiversity*, 11(2). **(NAAS 5.10)**

Kumar, R., Patel, S.K., Verma, A., Joshi, G.S., Bisen, H.K., Asrani, R.K., Rana, J., Niranjan, A.K. and Pandey, M.K. 2024. *Saussurea costus* (falc.) lipsch: A promising ally against cancer. *Pharmacological Research-Natural Products*, 5, p.100123.

Lal, S.K., Gaggar, P., Kumar, S., Mallikarjuna, M.G., Vishwakarma, C., Rakshit, S., Pandey, A., Achary, V.M.M. and Mehta, S. 2024. Recent advancements in nitrogen use efficiency in crop plants achieved by genomics and targeted genetic engineering approaches. *Plant Molecular Biology Reporter*, pp.1-15. **(NAAS 7.60)**

Mohanty, P., Singh, P.K., Lenka, B., Adhya, T.K., Verma, S.K., Ayreen, Z., Patro, S., Sarkar, B., Mohapatra, R.K. and Mishra, S. 2024. Biofabricated nanomaterials in sustainable agriculture: insights, challenges and prospects. *Biofabrication*, 16(4), pp.1-16. **(NAAS 14.20)**

Nikhil, K.C., Sarkar, S., Patel, S.K., Aderao, G.N., Kanaka, K.K., Agrawal, A., Niranjan, A.K. and Emran, T.B. 2024. Battling Kyasanur forest disease: the race for robust and long-lasting Kyasanur forest disease vaccine. *IJS Global Health*, 7(6), p.00496.

Rathod, A.K., Somagond, Y.M., Lokesha, E., Kumar, A., Kanaka, K.K., Nikhil, K.C., Jadhav, S.E., and Aderao, G.N. 2024. Role of micronutrients in production and reproduction of farm animals under climate change scenario. *Tropical Animal Health and Production*. (*InPress*). **(NAAS 7.70)**

Rayanoothala, P.S., Manil, S., Acharya, L.K., Garai, S. and Sunani, S.K. 2024. From obscurity to urgency: the rising tide of false smut disease in Indian rice cultivation, *Food and Scientific Reports*, 5(11), pp. 1-5.

Saha, S., Pandey, P., Kumar, A., Babu, S., Layek, J., Chaudhury, S. and Das, A. 2024. Agro-ecosystem services in hill agriculture- A North East Indian perspective. *Journal of Agricultural Physics*, 24(2), pp.135-155. **(NAAS 4.70)**

Abstracts

Murasing DK, Ul Umar SI, Naskar S, Sharma M, Prasad S. 2024. Characterization of RAB2B and VDAC1 Proteins in X- and Y-Chromosome-Bearing Spermatozoa of Bos indicus: Implications for Spermatogenesis and Fertilization. In: National Conference on Advances in Biotechnology for Animal Welfare and Production (August 01, 2024), org. by/at Uttarakhand Council for Biotechnology, Pantnagar in association with Indian Society of Animal Production and Management (ISAPM).

Mishra V.K., Kanaka K.K., Umar S.I.U., Naskar S. Dynamic trends in livestock and poultry production of Jharkhand: A comprehensive meta-analysis of livestock census and production data. *In:* Compendium, National Symposium on "Animal production systems and its role in sustainable use of AnGR" and XXI Annual Convention of Society for Conservation of Domestic Animal Biodiversity" (SOCDAB-2024) (Feb. 15-16, 2024), Gannavaram, Andhra Pradesh. p. 77-78.

Umar SIU, Prasad S, Garai S, Rakshit S, Naskar S. 2024. Machine Learning Approach to Optimize Dairy Production Management Practices vis-à-vis Artificial Insemination with Conventional and Sex Sorted Semen. In Compendium, XVIII Annual Convention of ISAGB and National Conference ISAGBCON 2024 on New Vistas in Harnessing Genetic Resources for Sustainable Animal Production, Patna. p. 239.

Kumar, A., Kanaka, K.K., Naskar, S., Aderao, G.N., Nikhil, K.C., Sarkar, S., Kaith, S., and Kamal, R. 2024. Evaluation of the reliability of an electronic estrus detector for estrus detection in Black Bengal goats (*Capra hircus*). In *39th Annual Convention and National Symposium of ISSAR: Challenges in Enhancing Reproductive Efficiency of Livestock: An Indian Perspective* (November 29–December 1, 2024). College of Veterinary Science, Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana (ISSARCON 2024). pp: 353

Aderao, G. N., Jadhav, S. E., Pattanaik, A. K., Lakesha, E., Choudhary, P., Dutta, N. and Singh, G. (2024). Higher dietary selenium levels improve antioxidant and immune response and trace mineral metabolism in goats under heat stress condition. In Sustainable Animal Nutrition for Global Health and Production: Innovations and Directions -ANACON 2024, 23 rd -25 th January, 2024, MVC, Chennai, 25 th January 2024, RN_056.

Choudhary, P., Jadhav, S. E., Lakesha, E. Aderao, G. N., Muwel, N., Choubey, P. K., Thamizan, P., Pattanaik, A. K. and Dutta, N. 2024. Effect of dietary Zinc levels and endotoxin on in vitro rumen fermentation and microbial mineral composition. In Sustainable Animal Nutrition for Global Health and Production: Innovations and Directions - ANACON 2024, 23 rd -25 th January, 2024, MVC, Chennai, 25 th January 2024, RN_055.

Kumar, S., Pandey, A.,Tribhuvan, K.U. and Lal, S.K. 2024. Study of genetic variability in horsegram for yield and nutritional traits. In: Abstract book of International Conference on "Ecotoxicology & Environmental Sciences", Ranchi. ICEES-24/CP-083(AP). p: 107.

Books

Aderao, G. N., Layek, J., Kanaka, K.K., Nikhil, K.C., Sharma, K., Kumar, A., Naskar, S., Bhadana, V.P. and Rakshit, S. 2024. Scientific feeding and management of goats. ICAR-Indian Institute of Agricultural Biotechnology, Ranchi, India.

Roy, S.K., Kademani, S.B., Karmakar, S., Ranjan, A., Abrar, F.P.N. and Ananda, K.R. 2024. Integrating traditional knowledge in modern agricultural extension. Weser Books, Aussere Weberstr, Germany.

Tribhuvan, K.U., Sarkar, B., Pandey, A., Soren, K.R., Kaith, S. and Narwal, E. 2024. Laboratory manual for MBB504: Techniques in Molecular Biology I. ICAR-Indian Institute of Agricultural Biotechnology, Ranchi, India.

Book chapters

Aderao, G.N., Somagond, Y.M., Anjali, Upadhyay, V.R., Kumar, A., Pandey, M., Sejian, V. 2024. Climate change and livestock production: Impact of abiotic stressors and its amelioration, in climate-resilient agriculture, in Rao, S.C., Avinashilingam, V.N.A., and Yashavanth, B.S., (eds.). Research and technological advances for resilient agriculture. ICAR-National Academy of Agricultural Research Management, Hyderabad, pp.165–204.

Bhagat, R., Walia, S.S. and Sharma, K. 2024. Microbial fertilizers for plant nutrition under organic and natural farming, in Rai, A.K., Chandra, P., Basak, N., Sundha, P. and Yadav, R.K. (eds.). Plant-microbial interactions for sustainable agriculture. Newcastle upon Tyne: Cambridge Scholars Publishing, pp. 108–134.

Choudhary, J., Narwal, E., Kumar, S., and Singh, S., 2024. Significance of plant growth promoting rhizobacteria in sustainable agriculture under extreme environment, in Rai, A.K., Chandra, P., Basak, N., Sundha, P. and Yadav, R.K., (eds.). rhizospheric interactions for abiotic stress mitigation. Cambridge Scholars Publishing, pp. 9–58.

Dasmandal, T., Kumari, S., Sahu, T.K., Balakrishnan, M., Supriya, P. and Mangrauthia, S.K. 2024. Intervention of bioinformatics and computational biology, in Rao, S.C., Avinashilingam, V.N.A., and Yashavanth, B.S., (eds.). Climate-resilient agriculture research and technological advances for resilient agriculture. ICAR-National Academy of Agricultural Research Management, Hyderabad, pp. 155–178.

Erato, F., Verma, D.K., and Gupta, S.K., 2024. The current status of aquaculture and fisheries: challenges and opportunities, in Verma, D.K., Gupta, S.K., Aga, A.F. and Sarker, S. (eds.). Aquaculture prospects, opportunities & challenges. NIPA, New Delhi, India, pp. 27–36.

Erato, F., Verma, D.K., Gupta, S.K. and Singh, S.K., 2024. Future perspective of eDNA in aquaculture and method, its challenge to small farmers, in Verma, D.K., Gupta, S.K., Aga, A.F. and Sarker, S. (eds.). Aquaculture technological advancements. NIPA, New Delhi, pp. 53–64.

Garai, S., Vinayaka, Barman, S., Udgata, A.R., Paul, N.C., Jaiswal, R., Ramasubramanian, V., Dhandapani, A., and Yashavanth, B.S., 2024. Statistical Modelling Aspects of Climate-Resilient Agriculture, in Rao, C.S., Avinashilingam, N.S., and Yashavanth, B.S.

(eds.). Research and technological advances for resilient agriculture. ICAR-National Academy of Agricultural Research Management, Hyderabad, pp. 179–204.

Gayatri, B.K., Manjuprakash and Kademani, S.B. 2024. Progress in winged bean research on national and international fronts, in Kaur, S., Singh, B.K., Singh, N., and Mishra, V.K. (eds.). Winged bean: prospects and potential in mainstream agriculture. New Delhi: Today & Tomorrow's Printers and Publishers, pp. 157-172.

Gupta, A., Gupta, R., Giri, A.K., Sarkar, B. and Gupta, S.K. 2024. Transforming fisheries and aquaculture management with advancing underwater video techniques, in Durgesh K.V., Gupta, S.K., Aga, A.F. and Sarker, S. (eds). The digital revolution in fisheries and aquaculture. NPH, New Delhi, India, pp. 285–298.

Gupta, S.K., Gupta, A., Gupta, R. and Kumar, S. 2024. Metagenomics profiling of soil from coal mining area: an approach to the coal void aquatic ecosystem of Jharkhand, in Das, B.K., Meena, D.K., Das, A.K., Koushlesh, S.K.M., Shaya Devi Sahoo, A.K., Sajina, A.M., Jesna, P.K. and Thakur, V.R. (eds.). Souvenir. ICAR-Research Complex for NEH Region, Umiam, p. 131.

Kumar, A., Philanim, W.S., Verma, V.K., Pandey, A., Krishnappa, R., and Mishra, V.K., 2023. Buckwheat Improvement: A movement beyond the cereal maze, in Kumar, A., Singh, B.K., Verma, V.K., Krishnappa, R., and Mishra, V.K., (eds.). Buckwheat: A potential crop for nutritional security in Eastern Himalayas. ICAR-Research Complex for NEH Region, Umiam, pp. 1–16.

Layek, J., Saikia, R., Sharma, K., Das, A., Bhadana, V.P., Biswakarma, N., Pandey, A., Bishi, S., Kumar, M., and Naskar, B. 2024. Organic farming: Scope and potential in North Eastern hill region of India, in Naik, M.R., Ramanjaneyulu, A.V., Hudedamani U. and Rao, CS. (eds.). Recent advances in organic farming research. ICAR-National Academy of Agricultural Research Management, pp. 45-62.

Mahawar, H., Choudhary, J. and Narwal, E. 2024. Microbial diversity under organic fertilizer management systems and identification of best fertilizer practice, in Mohanty, S.R., Kollah, B. (eds.). Greenhouse gas regulating microorganisms in soil ecosystems. Springer, Cham.

Manik, S., Mohan, H.M., Patel, A., Rashmi, E.R., Mythra, R., and Sharma, S.K., 2024. Current Scenario of Impact of Climate Changes on Plant Diseases and Their Management Strategies, in Climate-Resilient Agriculture, in Rao, S.C., Avinashilingam, V.N.A., and Yashavanth, B.S., (eds.). Research and technological advances for resilient agriculture. ICAR-National Academy of Agricultural Research Management, Hyderabad, pp. 85–108.

Narwal, E., Choudhary, J., Meena, A.L., Sharma, K., Manik, S., Sujay, B.K., Priya, H., Jaiswal, A. and Mahawar, H. 2024. Nodulation patterns and nitrogen fixing potential of winged bean, in Kaur, S., Singh, B.K., Singh, N. and Mishra, V.K. (eds.). Winged bean: prospects and potential in mainstream agriculture. New Delhi: Today and Tomorrow's Printers and Publishers, pp. 67-85.

Narwal, E., Garg, A.P., Choudhary, J. and Naresh, R.K. 2024. Mycorrhizal symbiosis: A journey from soil to commercial application, in Gupta, A., Jain, S., and Verma, N. (eds.). Industrial applications of soil microbes: Bentham Science Publishers, pp. 17–33.

Philanim, W.S., Kumar, A., Aochen, C., Pandey, A., Singh, A.R., and Umakanta, N., 2023. Origin, Distribution and Genetic Resources of Buckwheat, in Kumar, A., Singh, B.K., Verma, V.K., Krishnappa, R., and Mishra, V.K., (eds.). Buckwheat: A potential crop for nutritional security in Eastern Himalayas. ICAR Research Complex for NEH Region, Umiam, pp. 17–25.

Reddy, A.D., Akhila, D.S., Ramya, P., Rajeshwari, V., Kavitha, G.M., and Gupta, S.K., 2024. Understanding the role of gut microbiome in response to dietary supplement of prebiotics with reference to aquaculture, in Thatoi, H., Pradhan, S.K., and Kumar, U. (eds.). Applications of Metagenomics. Academic Press, Elsevier, pp. 103–127.

Sahoo, K.C., Divija, S.D., Ramya, N., Snehasish, R., Arunkumara, C.G., Mogili Ramaiah, Samal, I., and Jhansi Lakshmi, V., 2023. Emerging insect pests in agriculture-management practices, in climate-resilient agriculture, in Rao, S.C., Avinashilingam, V.N.A., and Yashavanth, B.S., (eds.). Research and technological advances for resilient agriculture. ICAR-National Academy of Agricultural Research Management, Hyderabad, pp. 645–666.

Sahu, T.K., and Rao, A.R. 2024. Computer-aided vaccine design', in Thatoi, H., Mohapatra, S., Das, S.K., and Pradhan, S.K., (eds.). Applied biotechnology and bioinformatics. Wiley, pp. 17–33.

Sarkar, S., Kuniyal, A., Prerna, M., and Fular, A., 2024. Emerging Challenges in Animal Disease

Management, in Climate-Resilient Agriculture, in Rao, S.C., Avinashilingam, V.N.A., and Yashavanth, B.S., (eds.). Research and technological advances for resilient agriculture. ICAR-National Academy of Agricultural Research Management, Hyderabad, pp. 241–245.

Tribhuvan, K.U., Mishra, T., Raj, A., Shivakumaraswamy, M., and Singh, B.K., 2024. Discovery and annotation of long non-coding RNAs (lncRNAs) from transcriptome data, in Joshi H. (ed.). Advances in biotechnology and bioscience. New Delhi:Akinik Publication, pp. 89–112.

Lead papers

Sahoo, A., Bhatt, R.S., Sarkar, S., and Aderao, G.N., 2024. Significance of stall feeding of sheep and goats as an alternative system to traditional grazing. In Performance, Health and Welfare of Small Ruminants under Changing Climate Scenario. ISSGPUCON, pp. 239–251.

Popular articles

Gullnaj K., Lal, S.K., Kumar, K., Kumari, S., Kumar, S., Molla, K.A. and Mondal, A. 2024. Enhancing nitrogen use efficiency in crops for sustainable agriculture, *Agritech Today*. 2(6).

Gullnaj K., Lal, S.K., Kumar, S., Mehta, S., and Kumar, M. 2024. Advances in genetic strategies for reducing phytic acid content in maize: from traditional mutants to CRISPR/Cas9 innovations. *Agritech Today*. 2(7).

Gullnaj K., Lal, S.K., Kumar, S., Mehta, S., Kumar, M., Kumari, S. and Kumari, P. 2024. Engineering maize for drought and salinity tolerance traits through genome editing approaches. *Agritech Today*. 2(6).

Kumar, A. and Singh, A.K. 2024. Revolutionizing goat breeding: Harnessing the potential of artificial insemination in goats. *Vet Alumnus*. 46(1). pp.66-69.

Kumar, S., Pandey, A., Tribhuvan, K.U. and Lal, S.K. 2024. Genetic improvement of agronomic important traits for organic agriculture. *Agritech Today*, 2(3).

Kumari, N., Pandey, A., Tribhuvan, K.U., Lal, S.K. and Kumar, S. 2024. Root and tuber crops for livelihood and nutritional security of farmers. *Agritech Today*, 2(1).

Kumari, S., Gullnaj K., Lal, S.K., Kumar, S., Naskar, S., Kumar, M. and Panditi, V. 2024. Nutritional significance of legume crops. *Agritech Today*. 2(6).

Manik, S., Bishi, S.K., Kademani, S.B. and Soren K.R. 2024. Rugda mushroom: Exploring nutri-medicinal and culinary importance and challenges in commercial cultivation. *Biotica Research Toda,* 6(7).

Mishra, T., Pandey, A., Limbalkar, O.M. and Tribhuvan, K.U. 2024. Evaluation of edible oil for quality and adulteration. *Agritech Today*, 1(10).

Mishra, T., Pandey, A., Limbalkar, O.M. and Tribhuvan, K.U. 2024. Apical root cutting in potato for high-quality seedlings. *Agritech Today*, 1(11).

Padala V.K. and Ramya, N. 2023. Bionomics and management of water lily aphid *Rhopalosiphum nymphaeae* L. in makhana *Euryale ferox* Salisb. Agriculture and food: e-Nesletter. 5(4). pp.1-2.

Rathinam, R.B., Sahu, T.K., Paul, N.C., Bag, K., Kumari, S., Kumar, R. and Tamilarasan, K. 2024. Bio teaming: Unlocking team synergy and lessons from nature for human team building. *Food and Scientific Reports*, 5(7). pp.30-35.

Tirkey, N., Kumar, S., Pandey, A. and Tribhuvan, K.U. 2024. RNAseq: A widely used technique for genome-wide expression analysis. *Agritech Today*, 2(2).

Tribhuvan, K.U., Kumar, S. and Pandey, A. 2024. Participatory plant breeding and seed villages. *Agritech Today*, 2(3).

Tribhuvan, K.U., Kumar, S. and Pandey, A. 2024. Plant molecular farming: Production platforms, applications and challenges. *Agritech Today*, 2(3).

Extension folders

Bishi, S.K., Layek, J., Kumar, M., Pan, R.S., Jawed, D., Singhania, A., Satpati, S., Sravani, C. and Ajith, D. 2024. Production technology of faba bean: A potential legume of Jharkhand.

Layek, J., Bishi, S.K., Sharma, K., Kumar, M., Satpati, A., Layek, J. and Devi, S. 2024. Intercropping for enhancing productivity and soil health in Chota Nagpur plateau.

कुमार, म., बिशी, स.क., लायेक, ज., गुप्ता, स.क., कदेमनी, स., निखिल, के.सी., नरवाल, ए. और कुमार, म., 2024. राजगिराः सेहत और पोषण का खजाना, कृषि विज्ञान पत्रिका, 15(2), पृष्ठ 45–50.

अमित कुमार, गणेश ना. आडेराव, कनका के .के., सौम्यजित सरकार एवम सोमैन नस्कर. 2024. कृत्रिम गर्भाधानः एक सहायक प्रजनन प्रोद्योगिकी.

अमित कुमार, गणेश ना. आडेराव, कनका के .के., सौम्यजित सरकार एवम सोमैन नस्कर. 2024. बकरियों का प्रजनन प्रबंधनः उत्पादकता की देखभाल.

अमित कुमार, गणेश ना. आडेराव, कनका के.के., सौम्यजित सरकार एवम सोमैन नस्कर. 2024. गाय–भैंस को निश्चित समय पर गर्मी में लाने के उपाय.

गिरी, ए.के., गुप्ता, डी.के., सिन्हा, पि.के., कृष्णाप्रकाश, निरंजनकुमार, शेनन.एन. संगमा, संजय कुमार गुप्ता एवं डी. बरुआ. 2024. कार्प मछली पालन के लिए बेहतर प्रबंधन पद्धतिया.

मदन कुमार, सुजीत कुमार बिशी, जयंत लायेक, संजय कुमार गुप्ता, सुजय कदेमनी, निखिल के.सी., एकता नरवाल और मोनिका कुमार. 2024. राजगिराः सेहत और पोषण का खजाना.

संजय कुमार गुप्ता, विप्लव सरकार, सौमेन नस्कर, अमित कुमार. 2024. कार्प नर्सरी तालाब का संचालन एवं प्रबंधन.

संजय कुमार गुप्ता, विप्लव सरकार, सौमेन नस्कर, मदन कुमार. 2024. केजकल्चरः मत्स्यपालन की क्रान्ति.

सौम्यजित सरकार, गणेश एन. आडेराव, सुजय बी.के., अमित कुमार, निखिल के.सी., सोमैन नस्कर. 2024. खाकी कैंपबेल बत्तखों का पोषण और देखभाल.

सौम्यजित सरकार, निखिल के.सी., गणेश एन. आडेराव, सुजय बी.के., अमित कुमार, सोमैन नस्कर. 2024. खाकी कैंपबेल बत्तखों के स्वास्थ्य की देखभाल, उपाय और प्रबंधन.

सौम्यजित सरकार, सुजय बी.के., अमित कुमार, गणेश एन. आडेराव, कनका के.के., सोमैन नस्कर. 2024. ग्रामीण पशुपालन को बढ़ावा देने हेतु झारखंड में खाकी कैंपबेल बत्तख पालन.

Newsletters

Kanaka, K.K., Kumar, A., Bishi, S.K. and Layek, J. 2024. IIAB Newsletter-July to Dec 2023. ICAR-Indian Institute of Agricultural Biotechnology, Ranchi, India. 2(1).

Kumar, A., Kanaka, K.K., Bishi, S.K. and Layek, J. 2024. ICAR-IIAB Newsletter-Jan to June, 2024. ICAR-Indian Institute of Agricultural Biotechnology, Ranchi, India. 3(1).

Annual Report

Kanaka, K.K., Kumar, A., Layek, J., Bishi, S.K. and Rakshit, S. 2024. ICAR-IIAB Annual Report - 2023. ICAR-Indian Institute of Agricultural Biotechnology, Ranchi, India.

Ongoing Research Projects

Sl. No.	Project Title	Principal Investigator
Institute funded		
1.	Understanding the biochemical and molecular regulation of L-DOPA and tannins biosynthesis in faba bean (*Vicia faba* L.)	Dr. Sujit K. Bishi
2.	Understanding the morpho-physiological and molecular mechanism of seed shattering in grain amaranth (*Amaranthus* spp.)	Dr. Madan Kumar
3.	Bioprospecting the plant microbe interactions in the coal mine area for enhanced nutrient.	Dr. Ekta Narwal
4.	Decipher the role of tetrathionate respiration on the colonization and virulence of *Salmonella typhimurium*	Dr. Nikhil K.C.
5.	Effect on different land use systems and management practices on microbial dynamics, soil health and carbon sequestration in acidic soil	Dr. Jayanta Layek
6.	Identification of suitable mustard cultivars and standardization of management practices for enhancing phosphorous use efficiency in rice-fallow	Dr. Kartik
8.	Quantifying gaps for sustaining agricultural production and assessing perception of biotechnology	Dr. Sujay B. Kademani
9.	Improvement of rice yield under low light intensity conditions	Dr. Avinash Pandey
10.	Molecular breeding for the development of rice varieties with inbuilt resistance/ tolerance to drought, low soil phosphorous, and blast	Dr. Vijai Pal Bhadana
11.	Molecular mapping and transcript analysis of seed protein content, digestibility and aluminium toxicity in chickpea (*Cicer arietinum* L.)	Dr. Khela Ram Soren
12.	Creation of variability, genome analysis and identification of genotypes/ QTL for trait of importance in winged bean	Dr. Kishor U. Tribhuvan
13.	Establishment of information resource and prediction servers for the genes related to yield traits, biotic stress, and abiotic stress in agriculturally important crops.	Dr. Tanmaya K. Sahu
14.	Genomic exploration of lesser-known chicken population of Jharkhand	Dr. Kanaka K.K.
15.	Evaluating the nano-inspired degradation of aquatic pollutants with special reference to jute retting and Lac dye waste-water	Dr. Biplab Sarkar
16.	Deciphering the role of the microbiome, including extremophiles in water bodies and surrounding phylloplane in coal mining areas in the perspective of intensive aquaculture, including cage aquaculture system	Dr. Sanjay K. Gupta
17.	Formulation and evaluation of nano-inspired mineral mixture for improving productivity and gut health in livestock and poultry	Dr. Ganesh N. Aderao

Sl. No.	Project Title	Principal Investigator
18.	Study of meat, milk, and fish to detect foodborne bacterial and viral diseases and their anti-microbial resistance profile under one health platform in the Ranchi district of Jharkhand	Dr. Soumajit Sarkar
19.	Exploring the influence of temperature and water activity on the growth, sporulation and Aflatoxin production of Aspergillus spp. and bioprospecting of associated genes	Dr. Suryakant Manik
20.	Exploring cell surface biomarkers of cattle spermatozoa for sex-specific segregation through proteomic and genomic approach	Dr. Soumen Naskar
21.	Investigating the role of purine degrading pathway genes of hemi-biotroph fungal pathogens during host-pathogen interaction and their potential to confer disease resistance in maize	Dr. Shambhu K. Lal
22.	Effect of Ice recrystallization inhibitors on Cryopreservation of Black Bengal buck semen	Dr. Amit Kumar
33.	Identification of genes or genomic regions conferring tolerance to aluminum toxicity and moisture deficit stress conditions in Indian mustard	Dr. Omkar M. Limbalkar
Externally Funded		
1.	Development of Climate Resilient Farming System Models in Jharkhand for food and nutritional security and enhancing Soil Health Funding Agency: **Rashtriya Krishi Vikas Yojana, Govt. of India**	Dr. Jayanta Layek
2.	Pilot project for Crop Diversification Funding Agency: **Department of Agriculture and Farmers Welfare, Govt. of India**	Dr. Jayanta Layek
3.	Gene editing and engineering of mediator subunit med15 to modulate grain size/weight trait in rice Funding Agency: **Department of Biotechnology, Govt. of India**	Dr. Vijai Pal Bhadana (CCPI)
4.	Deciphering and deploying low phosphorus tolerance and nitrogen use efficiency in rice using targeted genomics approach Funding Agency: **National Agriculture Science Fund**	Dr. Avinash Pandey (CCPI)
5.	Identification and characterization of fungal effectors and host factors in rice- false smut patho-system Funding Agency: **National Agriculture Science Fund**	Dr. Kishor U. Tribhuvan (CCPI)
6.	Design and development of novel magnetic nanoparticles and its employment for sex-sorting of bovine spermatozoa Funding Agency: **Anusandhan National Research Foundation**	Dr. Soumen Naskar
7.	Developing transgene-free high-yielding and climate-resilient tropical maize genotypes Funding Agency: **Department of Biotechnology, Govt. of India**	Dr. Shambhu K. Lal (CCPI)

Budget Allocation, Utilization and Revenue generation (in lakh rupees)

Head	RE 2023-24	Total Expenditure 2023-2024	Total Expenditure 2023-2024 in Percentage	BE 2024-25	**Total Expenditure up to 31-12-2023**	**Total Expenditure up to 31-12-2023 in Percentage**
GIA General, Other than NEH TSP & SCSP	672	672	100	570	293.97	43.75
GIA Capital, Other than NEH TSP & SCSP	3223	3223	100	1057	1481.74	45.97
GIA General, NEH	49	49	100	70	26.25	53.57
GIA Capital, NEH	30	30	100	0	22.5	75
GIA General, TSP	35	35	100	55	17.47	49.92
GIA Capital, TSP	92	92	100	90	63.44	68.96
GIA General, SCSP	236	236	100	250	100	42.41
GIA Capital, SCSP	220	220	100	500	90	40.91
Total	4557	4557	100	2592	2095.47	45.98

GIA-General (Non-scheme) 1270: Rs. 214.38 lakh (100% utilization with no expenditure up to 31-12-2023)

Head	FY 2023-24	FY 2024-25 (up to 31-12-2024)
Revenue Generation	28.86	32.87

Developmental Works

Laboratory Development

Lab facilities

ICAR-IIAB is equipped with state-of-the-art laboratory facilities designed to support cutting-edge research in agricultural biotechnology. The institute boasts well-equipped molecular biology and genetics labs, where scientists and researchers engage in the study of plant genetics, genomics and molecular mechanisms. Advanced facilities such as HPLC, CASA, Zeta analyzer and FTIR are integral components of these facilities.


Cell Counter


Inverted Microscope


CASA


Deep freezer


Rotary Evaporator


Zeta analyser


Haematology analyser


Ultra centrifuge


RT-PCR


Computational Facility


Shaker Incubator


Water purification system


Oestrus detector


2D- Electrophoresis


Laminar flow


Semen Filling Machine

Addition of Instrumentation facilities during 2024

Farm Development


Bund making


Land levelling using laser technology

Farm pond digging

Silpauline lined pond

Sprinkler irrigation

Orchad development

Rain water harvesting pond

Head unit for micro-irrigation

Biofloc tank facilities

Small ruminant farm with travis facility

Infrastructure Development

Administrative building

Boys hostel

Type-V quarters (six in number)

Girls hostel

Director's residence

Internal roads along with street lights

Gymnasium

Recreational facility

Paver block laying and avenue plantation

Overhead water tank

Playground

Annapurna mess

750 kW Generator

Important Committees

Quinquennial Review Team (QRT)

CHAIRMAN	Prof. Sudhir K. Sapory Emeritus Senior Scientist, ICGEB, New Delhi
MEMBERS	Dr. Kuldeep Singh, Former Director ICAR-NBPGR, New Delhi
	Dr. R.K. Singh, Former Director ICAR-IVRI, Izatnagar
	Dr. W.S. Lakra, Former Director ICAR-CIFE, Mumbai
	Prof. R. Ramakumar TISS, Mumbai
	Dr. Arvind Kapoor, Advisor Acsen Agriscience Pvt. Ltd., Gurgaon

Research Advisory Committee (RAC)

CHAIRMAN	Dr. S.K. Datta, Former DDG (Crop Science), ICAR, New Delhi
MEMBERS	Dr. R. Srinivasan, Former Director ICAR-NRCPB, New Delhi
	Dr. S.M. Deb, Former Director ICAR-NRC on Yak, Dirang, Arunachal Pradesh
	Dr. A.K. Pal, Former Jt. Director ICAR-CIFE, Mumbai
	Dr. Sujay Rakshit, Director ICAR-IIAB, Ranchi

Institute Management Committee (IMC)

CHAIRMAN	Dr. Sujay Rakshit, Director ICAR-IIAB, Ranchi
MEMBERS	Dr. VP Bhadana, Joint Director (Research)
	Dr. D.K. Yadav, ADG (seed) ICAR, New Delhi
	Dr. Soumen Ghoshal, PS ICAR-NISA, Ranchi
	Dr. S.B. Choudhary, Head ICAR-NBPGR, R.S. Ranchi
	Shri. Ravindra Tudu, External member
	Shri. Dhanraj Singh, External member

Nodal Officers and Responsibilities

Sl.No.	Nodal Officer	Responsibilities
1	Dr. Avinash Pandey	NEH, PME
2	Dr. Biplab Sarkar	ITMU
3	Dr. Kartik Sharma	Rajbhasha Implementation
4	Dr. Khela Ram Soren	TSP, HRD, Library
5	Dr. Madan Kumar	RAC member Secretary
6	Dr. Sanjay K. Gupta	Media Prabhari
7	Dr. Shambhu K. Lal	Swachha Bharat Abhiyan
8	Dr. Soumen Naskar	SCSP, ICAR-MIS, ERP
9	Dr. Sudhir Kumar	AEBAS, MGMG, RTI
10	Dr. Sujay B. Kademani	ABI
11	Dr. Sujit K. Bishi	ARMS, PME (upto September 09, 2024), Vigilance
12	Dr. Tanmaya K. Sahu	KRISHI Portal, NIC
13	Sh. Firoz Khan	GeM
14	Sh. Krishn K. Sharma	e-office, e-HRMS 2.0
15	Sh. Shashi R. Singh	SPARROW

Distinguished Visitors

Visit of Hon'ble Minister for Agriculture and Farmers Welfare, Govt. of India, Sh. Shivraj Singh Chauhan during foundation stone laying of multipurpose center on October 04, 2024

Visit of Hon'ble Chief Minister, Govt. of Jharkhand, Sh. Hemant Soren on August 07, 2024

Visit of Dr. Himansu Pathak, Hon'ble DG of ICAR and Secretary of DARE, Govt. of India

Visit of Dr. Sanjay Kumar, Chairman, ASRB and Sh. D.N. Lal, Deputy Inspector General of CRPF graced the occasion of Teachers Day, 2024

Visit of Dr. Tilak Raj Sharma, DDG (Crop Science), ICAR on July 28, 2024

Visit of Sh. Chandra Shekhar, IAS, Secretary, Department of Revenue, Registration and Land Reforms, Govt. of Jharkhand on November 18, 2024

Visit of Dr. Debjani Roy, Head, Geography Departmet, Ranchi University visited on October 18, 2024

Visit of Mr. Devesh Mittal, Deputy General Manager, State Bank of India on October 16, 2024

Visit of Dr. Praveen Malik, CEO, Agrinnovate and former Animal Husbandry Commissioner of India on Month date, 2024

Visit of Sh. Kafeel Ahmed, Deputy Commandant, CRPF, Ranchi on October 21, 2024

Staff Positions / Appointments / Promotions and Transfers

Staff Position

Scientific

Sl. No.	Category	Sanctioned	Filled	2024
1	RMP (Director + Joint Director)	1+7	1+2	1+2
2	Principal Scientist	10	02	02
3	Senior Scientist	0	8	8
4	Scientist	0	15	15
5	Total	18	28	28

Administrative

Sl. No.	Category	Sanctioned	Filled	2024
1	CAO (SG)	1	1	1
2	Comptroller	1	0	0
3	Sr. F&AO	1	0	0
4	CF & AO	0	1	1
5	Sr. A.O.	1	0	0
6	A.O.	2	1	1
7	A.A.O.	4	3	3
8	PS	3	0	0
9	PA	2	0	0
10	Asst.	9	5	5
11	UDC	7	0	0
12	LDC	8	0	0
13	Official Language Staff	0	0	0
	Total	39	11	11

Technical

Sl. No.	Category	Sanctioned	Filled	2024
1	T-1	10	5	5
2	T-3	10	0	0
3	T-6	2	0	0
	Total	22	5	5

Transfer

Sh. Babul K. Sinha
CAO (SG)
Relieved on 28.06.2024

New Joining

Dr. Tanmaya K. Sahu
joined as a Scientist, Bioinformatics on 01.02.2024

Sh. Krishn K. Sharma
Joined as Administrative officer on 20.03.2024

Sh. Abhay Kumar
Joined as Technician (T1) on 01.05.2024

Sh. Shashi Ranjan Singh
Permanently absorbed as Assistant Administrative Officer on 28.05.2024

Sh. Deepak Kumar
Joined as Technician (T1) on 06.06.2024

Sh. Firoz Khan
Joined as CAO (SG) on 14.06.2024

Sh. Ajay Kumar
Joined as Technician (T1) on 26.04.2024

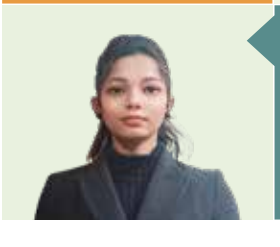
Sh. Kamal Kishor
Joined as Technician (T1) on 10.07.2024

Sh. Pankaj Kumar
Joined as Technician (T1) on 29.08.2024

Sh. Rishikesh K. Sinha
Joined as Assistant on 03.09.2024

Ms. Amisha Prabhat
Joined as Assistant on 01.10.2024

Sh. Ashish K. Jha
Joined as Assistant on 04.09.2024



Ms. Sonam Kumari
joined as Assistant on 06.11.2024

Sh. Rahul Kumar
Joined as Assistant on 04.11.2024

IIAB in Media

Stay in touch

IIAB_Ranchi iiab_ranchi_official ICAR-Indian Institute of Agricultural Biotechnology, Ranchi

ICAR-IIABRanchi ICAR- Indian Institute of Agricultural Biotechnology, Ranchi

Concept: Dr. Sujay B. Kademani

भा.कृ.अनु.प. - भारतीय कृषि जैवप्रौद्योगिकी संस्थान
ICAR - Indian Institute of Agricultural Biotechnology

गढखटंगा, राँची - 834 003 (झारखण्ड)
Garhkhatanga, Ranchi - 834 003 (Jharkhand)

Published by

Director, ICAR - Indian Institute of Agricultural Biotechnology, Ranchi