वार्षिक प्रतिवेदन

ANNUAL REPORT 2022

भा.कृ.अनु.प. भारतीय कृषि जैवप्रौद्योगिकी संस्थान
ICAR- Indian Institute of Agricultural Biotechnology
गढ़खटंगा, रांची- 834003 (झारखण्ड)
Garhkhatanga, Ranchi - 834003 (Jharkhand)

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प्रस्तावना

कृषि और इसके सम्बंधित क्षेत्र भारत की आधी से अधिक आबादी के लिए आजीविका का मुख्य आधार हैं और देश के सामाजिक-आर्थिक ताने-बाने में महत्वपूर्ण योगदान देते हैं। भले ही देश ने कृषि के सभी क्षेत्रों में अभूतपूर्व प्रगति देखी है, लेकिन बहुपक्षीय चुनौतियों, जैसे जलवायु परिवर्तन और संबंधित जैविक/अजैविक तनाव कारकों, सिकुड़ती कृषि योग्य भूमि और प्राकृतिक संसाधनों को देखते हुए, भविष्य में विकास को बनाए रखना एक चुनौतीपूर्ण कार्य होगा। इन चुनौतियों के बावजूद, भारत को अपनी समृद्ध जैव विविधता और उपलब्ध विशाल मानव संसाधन के मामले में बहुत लाभ है।

भा.कृ.अनु.प.–भारतीय कृषि जैवप्रौद्योगिकी संस्थान (ICAR-IIAB), एक उत्कृष्ट संस्था है जो पौधों, जानवरों, मछलियों और सूक्ष्म जीवों को शामिल करते हुए बुनियादी और ट्रांसलेशनल बॉयोटेक्नोलॉजिकल रिसर्च करके समग्र रूप से ज्ञान और नवाचार से प्रेरित कृषि के विकास को बढ़ावा देने के लिए प्रतिबद्ध है। साथ ही, स्नातक, स्नातकोत्तर, डॉक्टरेट और पोस्ट-डॉक्टरेट स्तर पर शिक्षा प्रदान करके जैवप्रौद्योगिकी के अग्रणी क्षेत्रों में कुशल मानव संसाधन विकसित करके, संस्थान को कृषि अनुसंधान और शिक्षा के इस क्षेत्र में बहुत महत्वपूर्ण भूमिका निभानी है।

आईसीएआर-आईआईएबी, रांची में अनुसंधान और शिक्षा के लिए आवश्यक अत्याधुनिक बुनियादी ढांचे का निर्माण किया जा रहा है। क्षेत्र अनुसंधान के लिए फसल अनुसंधान एवं प्रशिक्षण केंद्र, पशुधन अनुसंधान एवं प्रशिक्षण केंद्र और मत्स्य अनुसंधान एवं प्रशिक्षण केंद्र जैसी सुविधाएं और छात्रों के लिए एक छात्रावास और भोजनालय बनकर तैयार हैं साथ ही कई अन्य सुविधाएं जो की निर्माणाधीन है जल्द ही तैयार हो जायेंगी।

संस्थान में उपलब्ध विशेषज्ञता एवं अनुसंधान सुविधाओं के अनुसार, अनुसन्धान कार्य, धान के अलावा संभावित फसलों जैसे की पंखी बीन, बाकला, रामदाना आदि में जीनोमिक संसाधनों का विकास करके मूल्यवान लक्षणों के अंतर्निहित जीन और जीनोमिक क्षेत्रों की पहचान पर केंद्रित है। धान में सूखे के प्रति सहिष्णुता, फास्फोरस उपयोग दक्षता और झुलसा प्रतिरोध क्षमता बढ़ाने के लिए पहले से पता एवं प्रभावी क्यूटीएल/जीनों को मारकर्स की सहायता से ट्रान्सफर करने के प्रयास चल रहे हैं। लिंग-विशिष्ट शुक्राणु पृथक्करण के लिए मवेशियों के शुक्राणु के कोशिका सतह आधारित बायोमार्कर के विकास के लिए भी प्रयास किए जा रहे हैं। जूट रेटिंग अपशिष्ट जल के नैनो-प्रेरित अपघटन और भूमि में अम्लता कम करने के लिए कैल्शियम ऑक्साइड नैनोकणों के उपयोग के प्रारंभिक परिणाम उत्साहजनक हैं। अनुसंधान और वाणिज्यिक अनुप्रयोग के लिए नए सूक्ष्मजीव और जीन प्राप्त करने की संभावना के लिए कोयला खाद्यानों के जलाशयों की सूक्ष्मजीवीय विविधता एवं रूपरेखा के आकलन के लिए मेटाजीनोमिक का उपयोग किया जा रहा है।

कुल नौ में से आठ परास्नातक छात्रों (आणविक जीव विज्ञान और जैव प्रौद्योगिकी में चार, आनुवंशिकी और पादप प्रजनन में चार एवं जैव रसायन में एक) ने इस अवधि के दौरान अपनी डिग्री पूरी की। अधिकांश छात्रों ने सीएसआईआर-यूजीसी, डीबीटी जेआरएफ/नेट, आईसीएआर-एसआरएफ जैसी परीक्षाओं में उच्च स्थान प्राप्त करके प्रतिष्ठित संस्थानों में पीएच.डी. में प्रवेश पाया।

मैं संस्थान में कार्यरत सभी वैज्ञानिकों, प्रशासनिक और वित्त कर्मचारियों, छात्रों, अनुसंधान अध्येताओं और संविदा कर्मचारियों को उनके संस्थान की विभिन्न गतिविधियों में योगदान के लिए धन्यवाद देता हूँ। मैं रिपोर्ट को समय पर प्रकाशित करने के लिए वार्षिक प्रतिवेदन संपादकीय टीम की सराहना करता हूँ।

मैं डॉ. हिमांशु पाठक, सचिव, कृषि अनुसंधान और शिक्षा विभाग, कृषि और किसान कल्याण मंत्रालय, भारत सरकार एवं महानिदेशक, भारतीय कृषि अनुसंधान परिषद् को उनके प्रेरक मार्गदर्शन और संस्थान को भरपूर सहयोग देने के लिए हार्दिक आभार व्यक्त करता हूँ। मैं डॉ. टी. आर. शर्मा, डीडीजी (फसल विज्ञान), आईसीएआर और डॉ. डी. के. यादव, एडीजी (बीज), आईसीएआर को उनके निरंतर समर्थन और प्रोत्साहन के लिए धन्यवाद ज्ञापन करता हूँ। अंत में, 8 दिसंबर, 2022 तक संस्थान का नेतृत्व करने के लिए डॉ. अरुणव पट्टनायक, पूर्व निदेशक–आईआईएबी को मेरा हार्दिक धन्यवाद।

(सुजय रक्षित)
निदेशक

रांची
मार्च, २०२३

PREFACE

Agriculture and its allied sectors are the mainstay of livelihood for more than half of Indian population and contribute significantly to the socio-economic fabric of the country. Even though country has witnessed unprecedented progress in all the sectors of agricultural production systems, in view of multilateral challenges, viz., climate change and associated biotic/abiotic stress factors, shrinking arable land and natural resources, sustaining growth in future will be a daunting task. Despite these challenges, India has huge advantage in terms of its rich biodiversity and vast human resource pool. ICAR-Indian Institute of Agricultural Biotechnology (ICAR-IIAB), an institution of excellence is committed to steer knowledge and innovation driven agricultural growth in holistic manner by undertaking basic and translational biotechnological research encompassing plants, animals, fish and microbes. Also, by developing skilled human resources in the frontier areas of biotechnology through imparting education at undergraduate, post graduate, doctoral and post-doctoral level, the institute is to play very crucial role in this sector of agricultural research and education.

Sate of the art infrastructure required for research and education are being created at ICAR-IIAB, Ranchi. Facilities such as Crop Research and Training Centre, Livestock Research and Training Centre and Fisheries Research and Training Centre, for field research and one hostel and mess for students are ready and several other facilities are coming up. As per availability of expertise and with modest facilities at the institute, research is focused on developing genomic resources and identification of genes/genomic regions underlying the traits of value in potential crops such as winged bean, faba bean, grain amaranth besides rice. Efforts are underway for improving drought tolerance, phosphorus use efficiency and blast resistance in rice by pyramiding known effective QTLs/genes. Efforts are also being made for development of cell surface biomarkers of cattle spermatozoa for sex-specific sperm segregation. Initial results in both nano-inspired degradation of Jute retting waste-water and use of Calcium Oxide Nanoparticles as soil acid neutralizing agent are encouraging. Metagenomic approach is being used for profiling of microbial diversity of coal void reservoir for possibility of getting novel genes and microbes for research and commercial application.

Eight of the nine M.Sc. Students (four in Molecular Biology and Biotechnology; four in Genetics and Plant Breeding; one in Biochemistry) have completed their degree during the period and majority of students have qualified CSIR-UGC, DBT JRF/NET examinations and achieved high ranks in ICAR SRF and Ph.D. entrance examinations.

I would like to extend my sincere thanks to all scientific, administrative and finance staff, students, research fellows and contractual supporting staff of ICAR-IIAB for their contributions in various institute activities. I express my appreciation to the annual report editorial team for timely bringing out the report.

I express my sincere gratitude to Dr. Himanshu Pathak, Secretary, DARE and Director General, ICAR for his inspiring guidance and all out support to the 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 support and encouragements. Last but not least, my heartfelt thanks to Dr. A. Pattanayak, former Director-IIAB for leading the institute till December 8, 2022.

Ranchi
March, 2023

(Sujay Rakshit)
Director, ICAR-IIAB

अधिदेश

- कृषि जैवप्रौद्योगिकी में मूल एवं नीतिगत अनुसंधान
- कृषि जैवप्रौद्योगिकी में शैक्षणिक उत्कृष्टता हेतु गुणवत्तायुक्त मानव संसाधन विकास एवं नीति समर्थन

MANDATE

- Basic and strategic research in agricultural biotechnology
- Development of quality human resources for academic excellence in agricultural biotechnology and policy support

CADRE STRENGTH

CATEGORY OF STAFF	SANCTIONED	FILLED	VACANT
RMP	08	01	07
Scientific	10	11	-
Technical	01	00	01
Administrative	39	03	36
Skilled Supporting	-	-	-
Total	58	15	44

◆

सारांश/ EXECUTIVE SUMMARY

- कुल 40,886 यूनिजिन्स को बेल में असेंबल किया गया और 15,444 SSR, 69 ट्रांसक्रिप्शन फैक्टर (TF) परिवारों से 2,167 TFs, 27 ट्रांसक्रिप्शन रेगुलेटर (TR) परिवारों से 415 TRs, 12 संरक्षित miRNA परिवारों से 26 परिपक्व miRNAs, और 16,811 संभावित lncRNAs की पहचान की गयी। इसके अलावा, 4 lncRNAs को 6 miRNAs के लिए eTMs के रूप में पाया गया।
- कुल 4,107 ईएसटी-एसएसआर की खोज की गई, जिनमें से 166 को सात देशों से प्राप्त पंखीबीन के 79 जनन्द्रव्य परिग्रहणों के संग्रह में जाँचा गया। विभिन्न क्लस्टरिंग विधियों के अनुसार अधिकांश अफ्रीकी परिग्रहण समूह में शामिल हो गये, और बाकी बचे हुए जनन्द्रव्य काल्पनिक भौगोलिक आबादी में फैले हुए पाए गए, जो कि अप्रत्यक्ष रूप से पंखीबीन के अफ्रीकी मूल का होने का समर्थन करता है।
- 98 पंखीबीन जनन्द्रव्य प्राप्तियों की जांच के उपरांत एक जनन्द्रव्य जो प्रकाश-अवधि के लिए असंवेदनशील पाया गया।
- बीडी एफएसीएस कैंटो फ्लो साइटोमीटर के साथ फ्लो साइटोमेट्री के बाद प्रोपीडियम आयोडाइड स्टेनिंग का उपयोग करके पंखीबीन के पहले से ज्ञात 1.22 Gbp के जीनोम आकार के बदले 710.94 Mbp पाया गया।
- निषेचन के 5, 10, 16, और 30 दिनों के अंतराल पर पंखीबीन के बीजों और फलियों में नौ प्रमुख एलर्जेनिसिटी-संबंधित जीनों के अभिव्यक्ति पैटर्न का विश्लेषण करने पर पाया गया कि अधिकांश जीन बीज और फली दोनों में निषेचन के 10 दिनों के बाद ही अधिकतम रूप से व्यक्त होते हैं।
- पंखीबीन के 147 उत्परिवर्तीयों की पहली पीढ़ी (M1) का एग्रो मॉर्फोलॉजिकल लक्षणों के लिए मूल्यांकन करने पर फूल आने के समय (45-50 दिनों), प्रति फली बीजों की संख्या (1 से 20), फलियों के आकार,

- A total of 40,886 unigenes were assembled in bael and used to discover 15,444 perfect SSRs, 2,167 transcription factors (TFs) from 69 TF families, 415 transcription regulators (TRs) from 27 TR families, 26 mature miRNAs from 12 conserved miRNA families, and 16,811 potential lncRNAs. Moreover, four lncRNAs were predicted as endogenous target mimics (eTMs) for six miRNAs.
- A total of 4,107 EST-SSRs were discovered, out of which 166 were validated in a collection of 79 germplasm accessions of winged bean constituting eight populations from seven countries. Different clustering methods indicated that most African accessions tended to group, and their leftover members were spread across the hypothetical geographical populations, indirectly supporting the African origin of the winged bean.
- Ninety-eight germplasm accessions were screened, and a photo-insensitive genotype was identified in winged bean.
- The genome size of the winged bean was determined to be 710.94 Mbp against the reported size of 1.22 Gbp using propidium iodide staining followed by flow cytometry with a BD FACS Canto Flow Cytometer.
- The expression pattern of nine major allergenicity-related genes was analyzed in seeds and pods of winged bean at 5, 10, 16, and 30 days after anthesis (DAA). Most genes expressed maximally after 10 DAA in both seeds and pods.
- Evaluation of 147 mutants for agro morphological traits revealed distinguishable variation for early flowering (45-50 DAS), number of seeds per pod (1 to

बीज के आकार, बीज के रंग और पौधे की आकार-प्राकार के लिए भिन्नता का पता चला।

- भारतीय सरसों में लवणता तनाव/आघात स्थितियों के तहत अभिव्यक्त होने वाले 399 lncRNAs की पहचान की गई, और 4 miRNAs के लिए 5 lncRNAs को eTMs के रूप में पाया गया।
- धान में कम प्रकाश सहिष्णु किस्मों और अतिसंवेदनशील किस्मों के संकरण से उत्पन्न F2 पीढ़ी में चयन किया गया। पुनर्योगज अंतःप्रजनित वंशक्रमों के विकास के लिए चुने हुए संकरणों से अलग-अलग पौधों से बालियाँ एकत्र की गयी।
- जिन धान के पौधों में *Pup 1*, *qDTY 2.2* और *4.1* संमरूप अवस्था में उपस्थित पाये गये, उनका प्रदर्शन वर्षा आधारित सीधी बुवाई की परिस्थिति के लिए बेहतर पाया गया।
- बाकला के विभिन्न उत्तकों में मेटाबोलाइट्स की प्रोफाइलिंग करने पर पाया गया की डोपामाइन का जैवसंश्लेषण *L-DOPA* (3,4 डाइहाइड्रॉक्सी फेनिलएलनिन) के माध्यम से होता है। *L-DOPA* के प्रमुख संचायक फूल और पत्तियों के युवा उत्तक पाये गए, बीजों में सिर्फ डोपामाइन ही मिला।
- जस्ता की कमी के प्रति उत्तरदायी जीन *OsbZIP48 Zn,* धान के पौधों में जस्ता समस्थिति के लिए विशिष्ट भूमिका निभाता है।
- रामदाना के 115 जननद्रव्य प्राप्तियों का मूल्यांकन विभिन्न कृषि-रूपात्मक लक्षणों के लिए किया गया और एक कम बीज बिखरने वाले जीनोटाइप (IC-042277) की पहचान की गई।
- कुल्थी के 36 जननद्रव्य प्राप्तियों का 16 कृषि रूपात्मक और 12 पोषण संबंधी लक्षणों का मुल्यांकन करके अधिक उपज देने वाली (IC-23441), दाने में कम फाइटिक एसिड (IC-139460), कम टैनिन (IC-80943), उच्च लौह (IC- 80943 और IC-123022) और उच्च जस्ता (IC-53613) के लिए पहचान की गयी। दो प्रकाश असंवेदनशील प्राप्तियों (HPKM-11-72 और HPKM-11-74) की भी पहचान की गई।

20), pod morphology, seed size, seed colour and plant architecture in M1 generation of winged bean.

- Three hundred ninety-one lncRNAs expressing under salt stress/shock conditions were identified in Indian Mustard, and five lncRNAs were predicted as endogenous target mimics (eTMs) for four miRNAs.
- Selection performed in F2 populations generated from crossing low light tolerant genotypes and sensitive varieties. Panicles from individual plants collected from selected crosses for recombinant inbred lines development.
- Rice plants possessing *Pup1* and both *qDTY 2.2* and 4.1 in homozygous state exhibited superior performance than the plants carried either of the target QTLs under rainfed direct seed conditions.
- Metabolites profiling in different tissues revealed that the dopamine biosynthesis is mediated through L-DOPA (3,4 dihydroxy Phenylalanine) in Faba bean. The major accumulator of L-DOPA are young tissues of flower and leaves while seeds accumulates dopamine exclusively.
- Zinc deficit responsive gene *OsbZIP48* plays genotype based tissue specific role in Zn homeostasis.
- One hundred-fifteen germplasm accessions of grain amaranth were evaluated for various agro-morphological traits and one low seed shattering genotype (IC-042277) was identified.
- Thirty-six horse gram germplasm accessions were evaluated for 16 agro-morphological and 12 nutritional traits and identified genotypes with significantly high-yield potential (IC 23441), low phytic acid (IC 139460), low tannin (IC 80943), high iron (IC 123022) and high zinc (IC 53613). Two

- एक छोटे पैमाने पर किए गये प्रयोग के आधार पर पाया गया कि जिंक ऑक्साइड नैनोकणों 750 PPM मात्रा की जुट सड़ने के बाद अपशिष्ट जल में रंग के क्षरण के लिए उचित है।

- चूने की अनुशंसित मात्रा की तुलना में, नैनो–कैल्शियम की मात्र 1/50वीं मात्रा चने में अंकुरण और वृद्धि को प्रभावी रूप से बढ़ाती है तथा जल्दी फूल आने के लिए प्रेरित करती है। जड़ों की मिट्टी के विश्लेषण और जड़ों और तनों में कैल्शियम सिग्नलिंग पाथवे जीनों के ट्रांसक्रिप्टोमिक और जीन एक्सप्रेशन विश्लेषण ने भी दी गयी नैनो- कैल्शियम की प्रभावकारिता की पुष्टि की।

- रामगढ़ कोयला खद्यान जलाशय (परीक्षण) और गेतलसूद जलाशय (नियंत्रण) से लिए गये मिट्टी के नमूनों का शॉट गन मेटाजेनोमिक्स अनुक्रम विश्लेषण करके सुक्ष्मजीवीयों की विविधता की रूपरेखा ने इन जलीय संसाधनों की वर्गीकरण संरचना और कार्यात्मक क्षमता को समझने में महत्वपूर्ण सुराग प्रदान किया है; साथ ही अनुसंधान और व्यावसायिक अनुप्रयोग के लिए नवीन जीन और सूक्ष्म जीव मिलने की प्रयाप्त संभावनाएं भी हैं।

- स्वदेशी सूकरों के स्वाइन ल्यूकोसाइट एंटीजन (एसएलए) के प्रमुख और क्लासिकल Class-I और Class-II जीन के सीडीएस विशेषता की जाँच में पेप्टाइड बाइंडिंग साइट्स (पीबीएस) में प्रतिस्थापन बड़ी संख्या में देखे गए हैं।

- इंडिकस मवेशियों के एक्स और वाई-स्पर्मेटोजोआ के तुलनात्मक ट्रांस्क्रिप्टोमिक विश्लेषण से टॉप GO एनोटेशन के साथ सेक्स्ड स्पर्मेटोजोआ के लिए अद्वितीय ट्रांसक्रिप्ट का पता चला जो झिल्ली से जुड़े प्रोटीन पर विशेष ध्यान देने के साथ एक्स और वाई-स्पर्मेटोजोआ के बीच तुलनात्मक प्रोटिओम पर हमारे पिछले अवलोकन की पुष्टि करता है।

- मक्का की उष्णकटिबंधीय प्रभेद, रासी-4212 में परिपक्व बीज व्युत्पन्न नोडल एक्सप्लांट का उपयोग करके संयंत्र पुनर्जनन प्रोटोकॉल को अनुकूलित किया गया।

photo insensitive (HPKM-11-72 & HPKM-11-74) were also identified in horse gram

- In a small-scale experiment for standardization of doses of zinc oxide nanoparticles for degradation of colour in Jute retting waste water, a dose of 750 ppm nanoparticles was found optimum.

- Compared to the recommended dose of lime, 1/50th dose of nano-calcium significantly enhances germination and growth and induces early flowering in chickpea. ICP-OES analysis of the rhizospheric soil and transcriptomic and gene expression analysis of calcium signaling pathway genes in roots and shoots substantiated the efficacy of the dose.

- The profiling of microbial diversity of the soil samples from the Ramgarh coal void reservoir (Test) and Getalsud reservoir (Control) using shot gun metagenomics sequence analysis provided significant clues in understanding the taxonomic structure and functional potential of these aquatic resources with the possibility of getting novel genes and microbes for research and commercial application.

- CDS of major and classical Class I and Class II genes of swine leukocyte antigen (SLA) of indigenous pigs characterized, and large no. of substitutions are observed in peptide binding sites (PBS).

- Comparative transcriptomic analysis of X- and Y-spermatozoa of indicus cattle reveals transcripts unique to sexed spermatozoa with top GO annotations that corroborate our previous observation on comparative proteome between X- and Y-spermatozoa with special focus on membrane-associated proteins.

- Plant regeneration protocol optimized using mature seed derived nodal explant in tropical maize genotype, Rasi-4212.


सावित्रीबाई फुले छात्रावास
SAVITRIBAI PHULE HOSTEL

Research

GENOMICS AND MOLECULAR BREEDING

Development of transcriptome-based resources for indigenous agri-horticultural crops of eastern India

De novo transcriptome assembly for discovering SSRs and riboregulators in stone apple

Stone apple (*Aegle marmelos*), commonly known as bael, is an underexploited species of the family Rutaceae. It is a slow-growing, tough, medium-sized fruit-tree indigenous to India. It has minimal genomic resources limiting its efficient genetic improvement and conservation. We report developing comprehensive transcriptome data containing 40,886 unigenes with an N50 value of 2,289 bp. In the gene ontology (GO) analysis, a total of 597,708, and 501 unigenes of Aegle marmelos were assigned to biological processes (BP), molecular functions (MF), and cellular components (CC) GO categories, respectively. From 40,886 unigenes, we discovered 15,444 perfect SSRs (Fig. 1) with 192 distinct repeat motif types reiterating 4 to 21 times. Besides, we also identified 2,167 transcription factors (TFs) from 69 TF families, 415 transcription regulators (TRs) from 27 TR families, 26 mature miRNAs (Fig. 2) from 12 conserved miRNA families, 16,811 potential lncRNAs, and placed six functional eTMs in different lncRNA-miRNA pairs (Fig. 3A & 3B). The miRNA target prediction analysis using the psRNATarget online web server identified 176 unigenes as targets for 26 miRNAs with expectation values ranging from 0 to 2.5. The comparison of expression patterns of some selected miRNAs vis-à-vis their corresponding target genes is in progress.

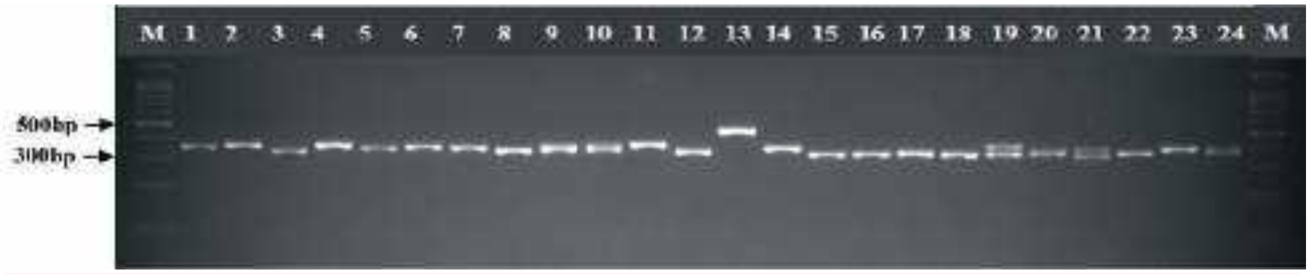

Fig. 1: *Validation of genic-SSR markers in Aegle marmelos germplasm accession IC209920. (1) IIAB-B1, (2) IIAB-B2, (3) IIAB-B4, (4) IIAB-B5, (5) IIAB-B6, (6) IIAB-B7, (7) IIAB-B8, (8) IIAB-B9, (9) IIAB-B10, (10) IIAB-B11, (11) IIAB-B13, (12) IIAB-B14, (13) IIAB-B15, (14) IIAB-B16, (15) IIAB-B18, (16) IIAB-B19, (17) IIAB-B22, (18) IIAB-B23, (19) IIAB-B25, (20) IIAB-B28, (21) IIAB-B29, (22) IIAB-30, (23) IIAB-31, (24) IIAB-32, M-100 bp DNA marker.*

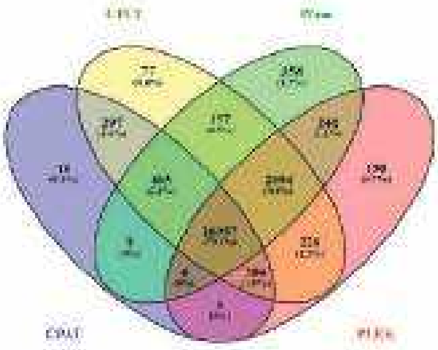

Fig 2: *VENN diagram representing the number of non-coding unigenes identified through different computational tools.*

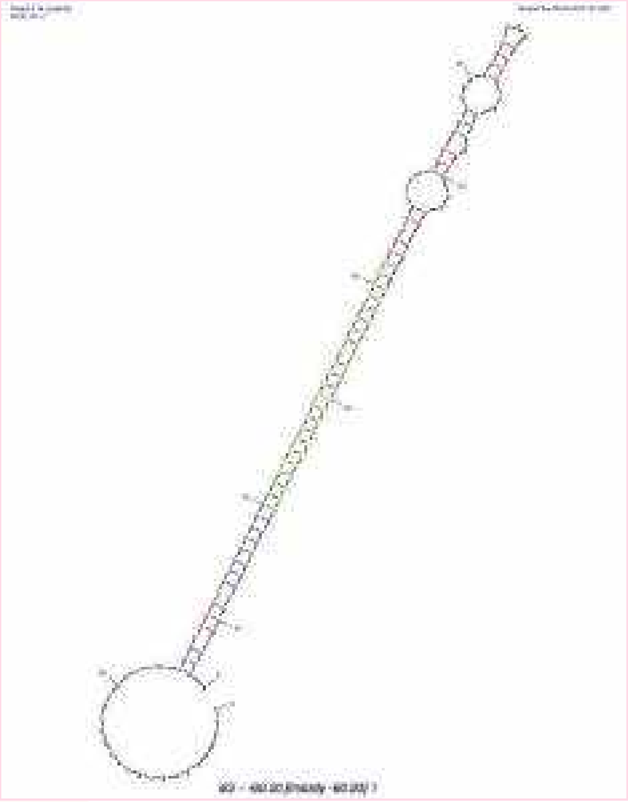

Fig. 3A: *Secondary structure of pre-miRNA sequences identified in the precursor miRNA transcript of Aegle marmelos.*

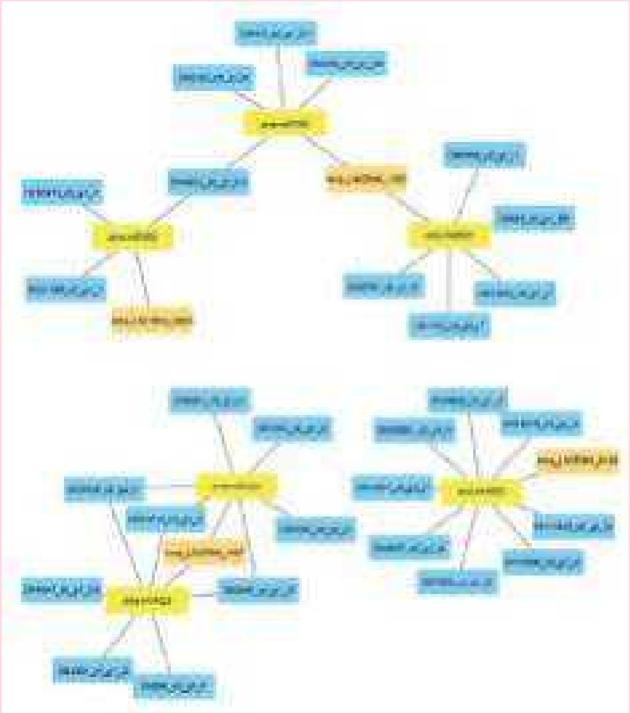

Fig. 3B: *Cystoscope network showing lncRNA-miRNA-target interaction in Aegle marmelos. The miRNAs are highlighted in yellow, lncRNAs are highlighted in brown, and target genes are highlighted in blue.*

Genetic mapping of the gene(s) /QTLs for photoperiod sensitivity in winged bean (Psophocarpus tetragonolobus L.)

Genetic diversity and population structure analysis in a global collection of winged bean

Winged bean (*Psophocarpus tetragonolobus* L.) is an underutilized tropical legume. It yields 14 quintals of dry seed and 115 quintal tubers per hectare and forms symbiotic associations with a broad-spectrum cowpea rhizobial group. We report the discovery of 4,107 perfect SSRs across the unigenes assembled from the publicly available winged bean RNAseq data sets. Seventy-eight of the 166 randomly selected SSRs amplified into a single band, of which 22 were polymorphic in 79 germplasm accessions of winged bean constituting eight populations from seven countries. Sixty alleles were found at the 22 polymorphic SSR loci, with a mean value of 2.73 per locus. The PIC values for the SSR loci ranged from 0.11 to 0.64, with a mean of 0.36. The maximum genetic diversity was recorded in advanced breeding lines (I = 0.67, He = 0.41), and the minimum genetic diversity in the germplasm accessions of Manipur (I = 0.44, He = 0.28). The AMOVA analysis indicated that within-population variation was significantly higher (85%) than between-population variation (15%). The pairwise Nm values between the populations ranged between 0.69 and -3.41, indicating the varying level of gene flow between them. The analysis of the population structure based on the Bayesian model-based clustering algorithm revealed two distinct groups among the eight populations with different levels of introgression (Fig. 4). The fuzzy clustering based on the Manhattan method also identified a similar number of groups, with 72% similarity between the two clustering methods. However, the Neighbour-Joining (NJ)-based clustering grouped all the accessions into four clusters (Fig. 5). Nevertheless, all three clustering methods unanimously indicated that most African accessions tended to group, and their leftover members were spread across the hypothetical geographical populations, indirectly supporting the African origin of the winged bean.

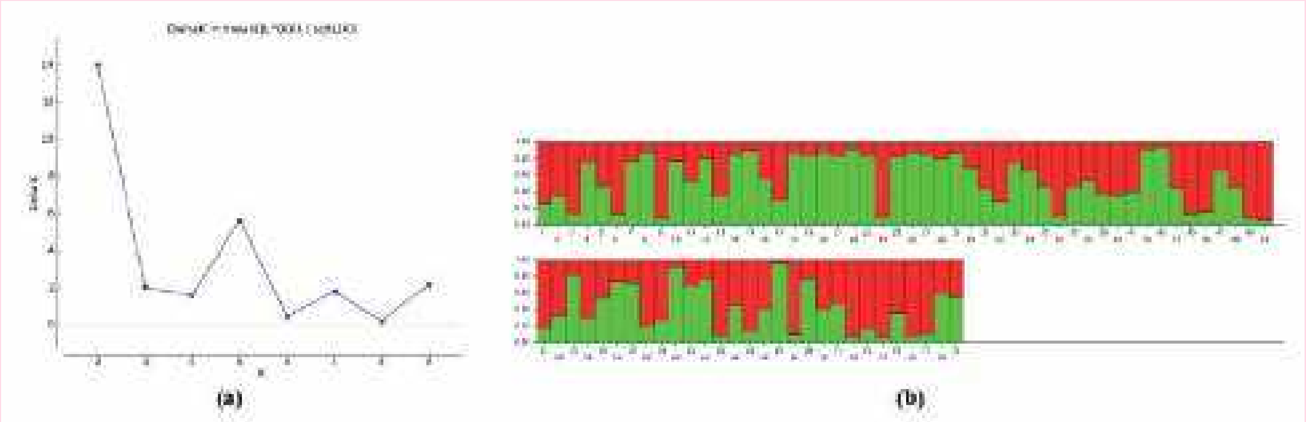

Fig. 4: *Population genetic structure based on 22 polymorphic genic-SSR markers in 79 germplasm accessions of winged bean. (a) ΔK graph showing peak value at $K = 2$, (b) population structure at $\Delta K = 2$.*

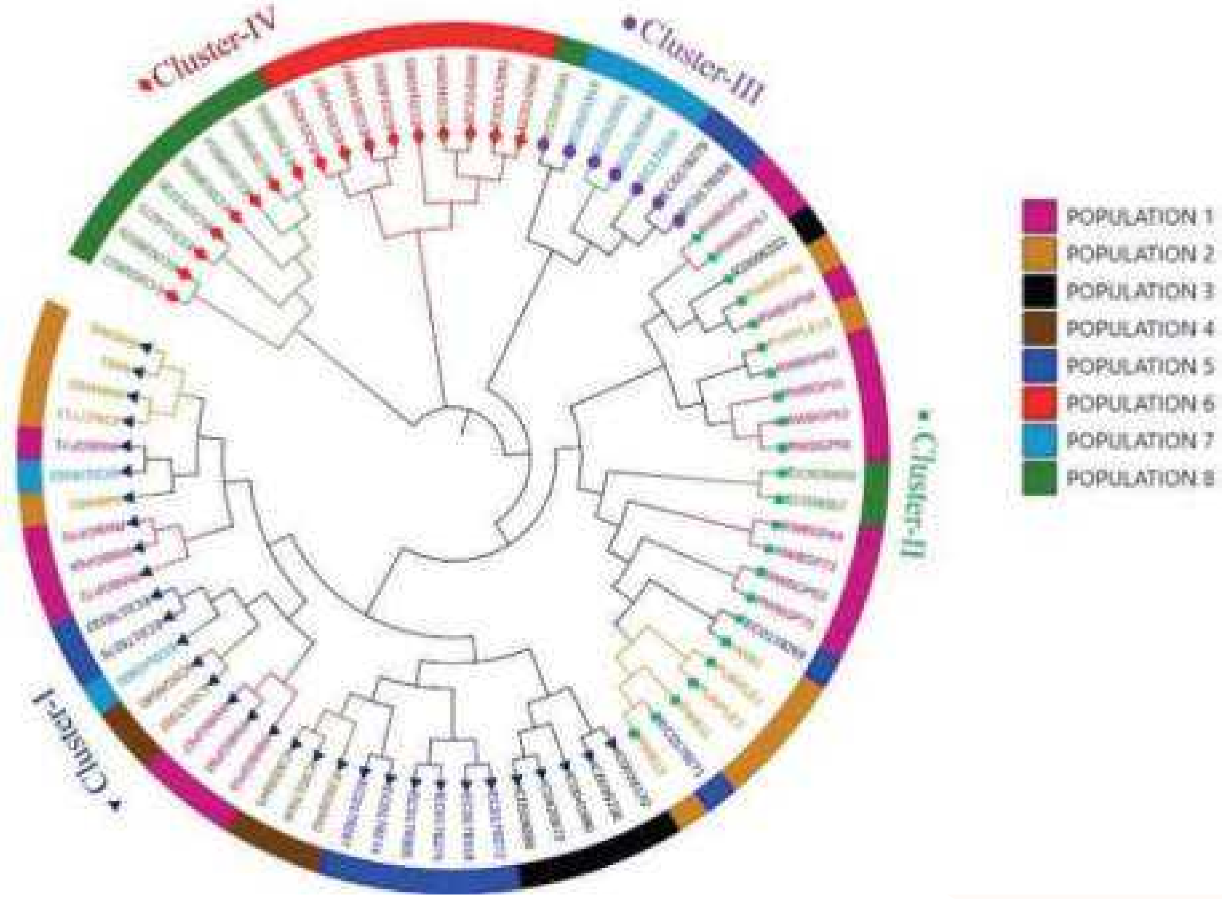

Fig. 5: *NJ tree showing the genetic relationships among the 79 germplasm accessions of winged bean*

Screening of winged bean germplasm for flowering under long-day conditions

Winged bean is primarily a self-pollinated crop. However, cross-pollination of up to 7.6% is reported. It is a short-day plant with an indeterminate growth habit. We screened a set of 98 germplasm accessions (92 collected from BAU, Ranchi, Jharkhand; six collected from, Shivrai, Vaijapur Tehsil, Aurangabad, Maharashtra) for flowering under long-day conditions. Sowing was carried out on 17th February 2021. Each accession was sown in a row of 2 m in length with a plant spacing of 60 cm. Two to three seeds were sown per hill and later thinned to one plant per hill. All crop management practices, including irrigation and plant protection, were provided as recommended. Out of the 98 accessions screened, five accessions (IIABPIS1, IIABWB2, IC0041980, EC0142652, EC0142654) flowered during the long-day conditions. However, pod-setting occurred only in one accession (IIABPIS1) (Fig. 6). The photo-insensitive nature of IIABPIS1 was confirmed through one more round of staggered sowing in the year 2022.

Fig. 6: *Screening of winged bean germplasm for flowering under long-day conditions. (A) photo sensitive genotype, (B) photo-insensitive genotype IIABPIS1.*

Genome analysis, linkage mapping, and identification of gene (s)/QTLs for seed oil and protein content in winged bean

Flow cytometry-based genome size determination of winged bean

The genome size of the winged bean was determined using propidium iodide staining followed by flow cytometry with a BD FACS Canto Flow Cytometer equipped with a 488 nm laser and 585/42 Band Pass filter. The winged bean nuclei, along with reference standard (Orzya Sativa; genome size 430 Mbp), isolated in 1 ml hypotonic propidium iodide lysis buffer having sodium citrate tribasic dehydrate, 2 mg/ml RNase A, 50 µg/ml propidium iodide, and 0.3 % (v/v) Tween-20 were co-stained, and the relative fluorescence was used to calculate the genome size of the winged bean. Three technical replicates were used in the study. The data was analyzed using FCS Express Software. The observed median peak for rice was 39140.42, while for the winged bean, the observed median peak was 64712.79. The observed CV for rice was 3.50%, while for winged bean it was 3.19% (Fig. 7). The genome size of winged bean was determined using the formula: sample genome size = reference genome size × (median value of sample G 0 /G 1 peak)/(median value of standard G0 /G1 peak). Following the formula, we determined the genome size of the winged bean to be 710.94 Mbp against the reported size of 1.22 Gbp.

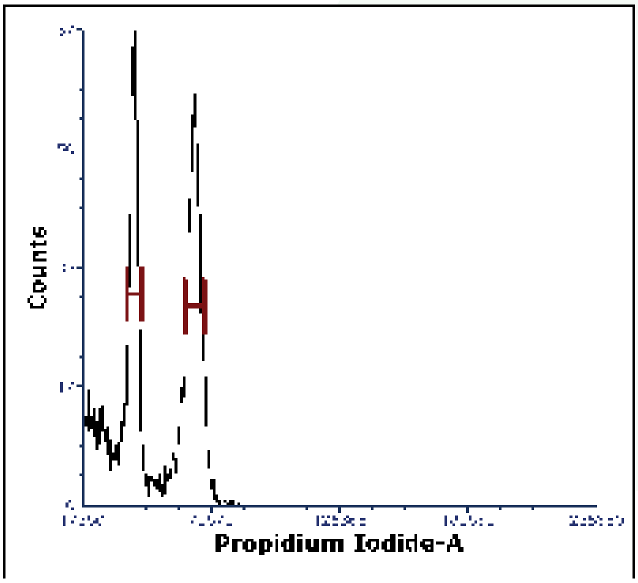

Fig. 7: *Genome estimation in winged bean using BD FACS Canto Flow Cytometer*

Spatio-temporal expression analysis of allergenicity-related genes in seeds and pods of winged bean

Winged bean is a high-protein potential leguminous crop. All parts of the plant are edible. However, tender pods are the principal economic parts eaten raw or as cooked vegetables. The mature beans are consumed as dried, roasted, or ground into flour to be combined with rice or other vegetables. As seen with most edible legumes, seeds and pods of winged bean also cause allergy to a significant proportion of the human population. Therefore, we analyzed the expression pattern of major allergenicity-related genes during seed and pod development in the winged bean. Seeds and pods from the AKWB-1 genotype were collected at four stages: 5, 10, 16, and 30 days after anthesis (DAA). Total RNA was extracted individually from seeds and pods of all four stages, and the cDNA synthesized from the total RNA was used as templates for analyzing the expression of nine allergenicity-related genes, as indicated in Fig. 8. The RT-qPCR-based spatiotemporal quantitative relative expression analysis of the allergenicity-related genes indicated that most genes expressed maximally after 10 DAA in both seeds and pods. Moreover, it was also evident that most of the allergenicity-related genes either do not express or express minimally on or before 5 DAA. This may be the primary reason for the use of seeds and pods of winged bean at an early stage for consumption.

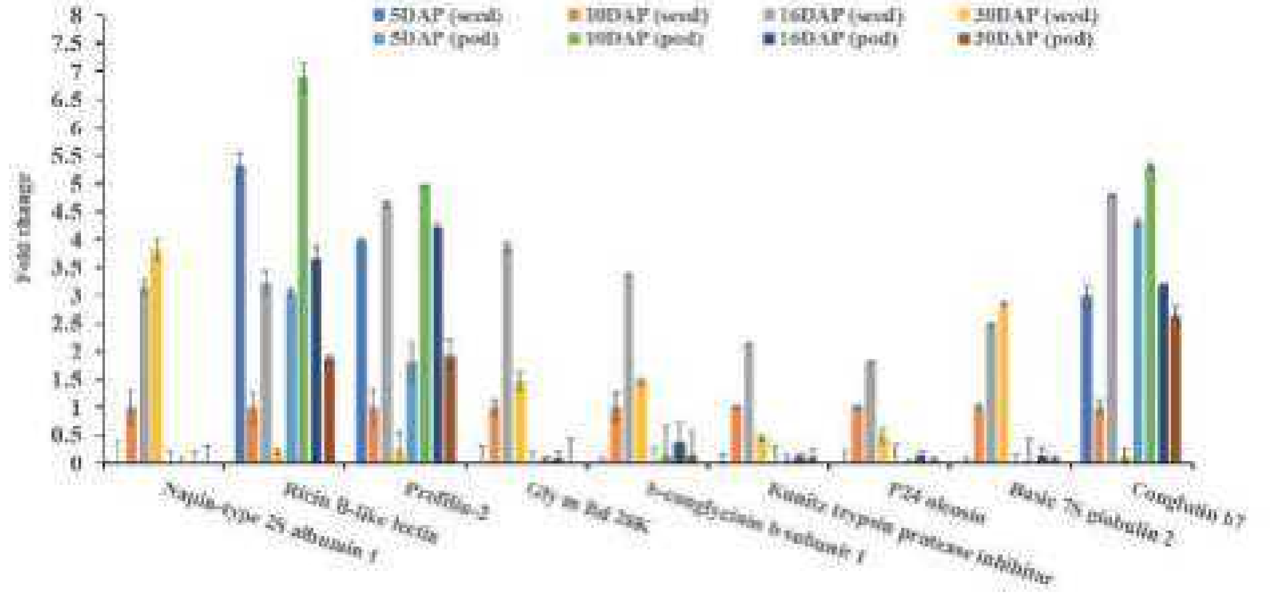

Fig. 8: *Bar graph showing RT-qPCR-based quantitative expression of (1) Napin-type 2S albumin 1, (2) Ricin B-like lectin, (3) Profilin-2, (4) Gly m Bd 28K, (5) b-conglycinin b subunit 1, (6) Kunitz trypsin protease inhibitor, (7) P24 oleosin, (8) Basic 7S globulin 2, and (9) Conglutin b7 in seeds and pods of winged bean at 5, 10, 16, and 30 DAA.*

Molecular dissection of plant architecture traits in winged bean through mutagenesis and genomic approaches

Generation of mutants in winged bean

A total of 147 mutants were generated through gamma irradiation in winged bean genotype AKWB 1 (with the help of BARC, Trombay). Some of the distinguishable phenotypes observed during the M1 generation mutants were early flowering (45-50 DAS), single-seeded pod, pod with a very high number of seeds (up to 20), flat pod with small sized seeds (suitable for the vegetable purpose), bold-seeded pods, bushy type plant with high numbers of pods, seed coat color variation (Fig. 9 & 10) etc.

S. No.	Gamma rays dose (Gy)	No. of seed irradiated	No. of seeds germinated	Percent survival
1.	100	500	64	3.20
2.	150	500	45	2.25
3.	200	500	24	1.20
4.	300	500	14	0.70

Fig. 9: *Seed-coat color M1 generation variants of winged bean*

Fig. 10: *Pod size and no of seeds per pod M1 generation variants of winged bean*

Improvement of rice yield under low light intensity condition

Eastern and northeastern India are the major rice-growing regions of the country. However, the crop's productivity is lowest in these regions primarily due to the low incidence of solar radiation coupled with fluctuating light due to the overcast sky during the wet season. Different institutions have identified several low-light-tolerant rice germplasm over the last couple of years. Some notable low-light tolerant rice germplasms are IRCTN 91-84, IRCTN 91-94, Rhyllo Red, Mahisugandha, Danteswari, Megha Rice 1 and Swarnprabha. We used these germplasms to develop low-light tolerant breeding lines and F2 mapping populations through their crossing with some of the popular rice varieties of the region. The initial crosses were made during kharif, 2020, and after the confirmation of the F1s using morphological and molecular markers, these were advanced to the next generation. During kharif 2022, F2 populations derived from the crosses (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) were planted along with parents and single panicle were harvested from each individual for generation advancement. Selected populations will be used for genotyping and phenotyping during kharif 2023, for mapping low-light tolerance QTLs, while others will be advanced for further selection.

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

Low nutrient availability in acidic soils coupled with drought and severe incidences of blast in rainfed ecology of Jharkhand are major bottleneck in realizing potential yield in rice. This project aims to introgress *Pup1* a major QTL for P-uptake, combinations of *DTYs* and gene(s) for blast resistance for the development of drought tolerant and phosphorus use efficient high yielding rice varieties resistant to blast. In this endeavor, 758 selections (F3) pertaining to seven crosses and segregating for *Pup1* and *DTYs* were evaluated under direct seeded rainfed conditions and based on *per se* performance, 832 selections were made during kharif 2022. Two hundred fifty F2 populations (single crosses, backcrosses, three-way crosses) segregating for QTLs viz., *Pup1, DTYs* and blast genes (*Pi2, 9, 54*) were also evaluated under direct seed rainfed conditions and 4651 selections based on per se performance were made. Total 326 plants of populations segregating for *Pup1* and *DTYs* (*2.2* and *4.1*) were screened with the help of tightly linked markers. Twenty two plants possessing both the *qDTYs* in homozygous condition and *Pup1* were identified. On comparison of performance of plants possessing different QTL combinations, it was found that plants having *Pup1* and both the *DTYs* in homozygous conditions recorded highest average grain yield per plant indicating towards positive synergy between *Pup1* and *qDTYs* and eventually scope of enhancing rice yield in rainfed low input conditions.

F1s generated by crossing Swarna and Lalat with highly drought tolerant accession of *Oryza rufipogon* (IIABWR1) were raised and backcrossed with respective varietal parents for developing mapping populations. Similarly, MTU 1210 a high yielding variety released for lowland exhibited high level of drought tolerance, involved in crosses with lowland varieties and F2s were raised under direct seeded conditions. Differential response of F2s were observed under drought stress at reproductive stage. All the F2s (4 nos) were forwarded through SSD for developing RILs for mapping genomic reasons conferring drought tolerance.

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

Metabolite profiling of catecholamine intermediates

The identification and quantification of catecholamine intermediates (CI), viz., L-DOPA, L-tyrosine, dopamine and tyramine were carried out using HPLC (High-Performance Liquid Chromatography) by comparing their retention time with that of authentic standards (Fig.

11A). The concentration of CI was quantified in various tissues of Faba bean, viz., very young leaves (VYL), young leaves (YL), matured leaves (M), flower bud (FB), open flower (F), pods and seeds. Significant variation in the CI content was observed across the tissues. The amount of L-Tyrosine and Tyramine content in all the tissues was very less (0.1 to 0.15% on a dry weight basis). The L-DOPA content in dry tissues of YL and FB were 5-6 % and 7.5-10 %, respectively (Fig. 11B). During the process of the ontogeny of flower and leaves, the amount of L-DOPA content gradually decreased with the maturity of the tissues suggesting its possible conversion to other metabolic forms. Quantification of L-DOPA and dopamine content at different stages of pod development indicated that the accumulation of L-DOPA is restricted to pod skin. On the other hand, a progressive accumulation of dopamine along with an unknown peak was observed towards seed tissue maturation (Fig. 11C). The progressive decrease of L-DOPA content towards tissue maturity and concomitant increase in dopamine content towards seed maturity reflects that dopamine production in Faba bean is mediated through L-DOPA only. A study is being carried out to understand the molecular regulation of L-DOPA accumulation in different contrasting tissues.

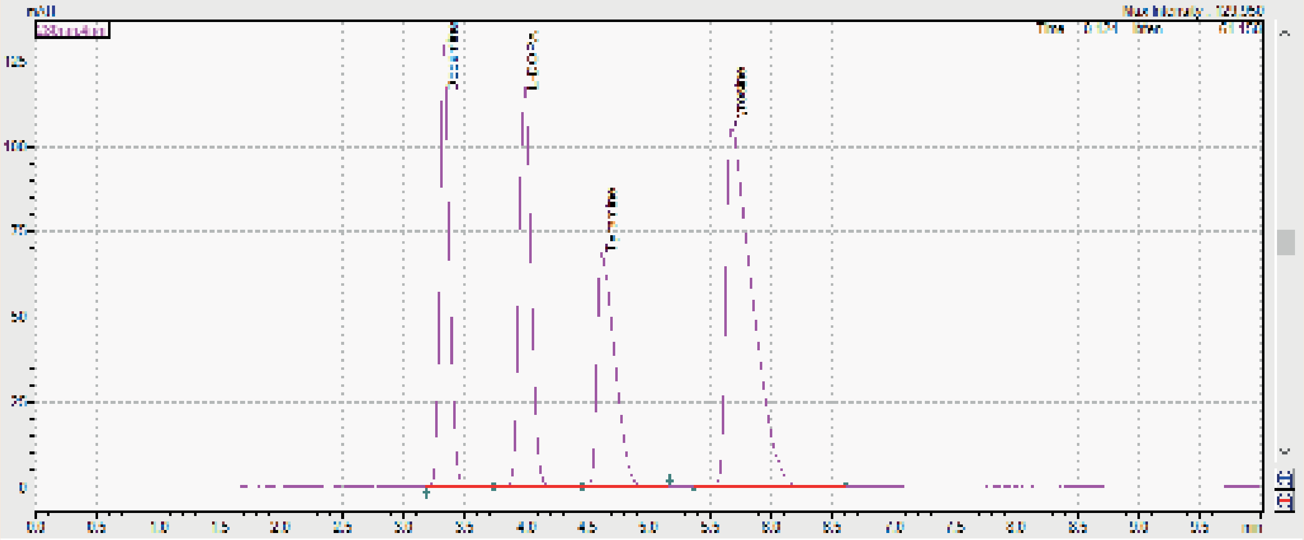

Fig. 11A: *Chromatogram showing separation of Dopamine, L-DOPA, Tyramine, and L-Tyrosine standards for 100 ppm conc.*

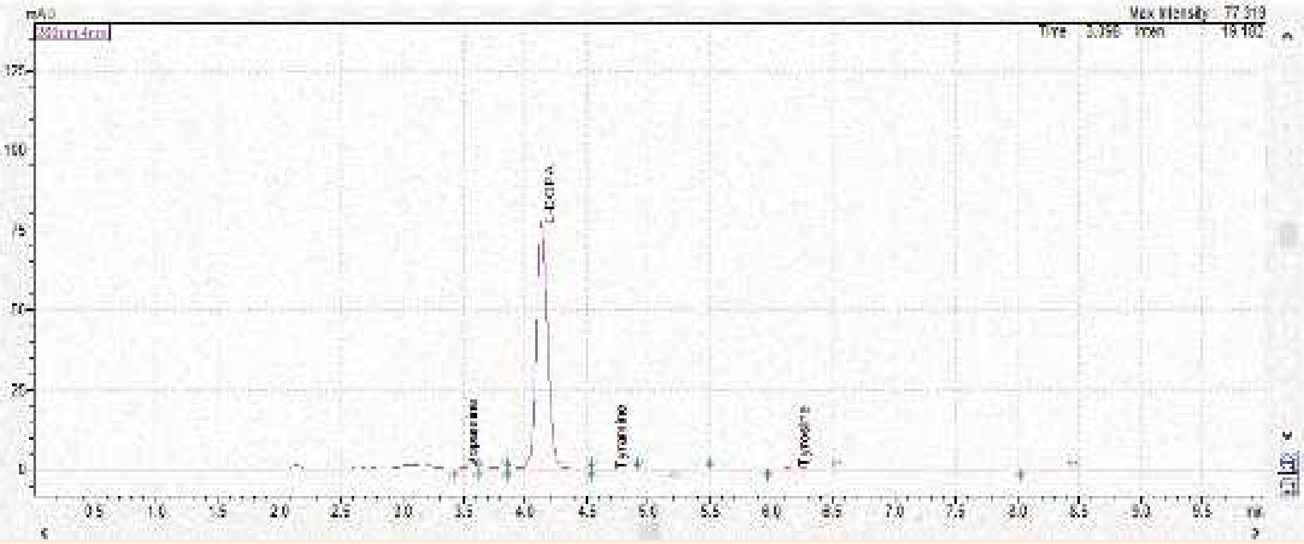

Fig. 11B: *A representative chromatogram showing the presence of L-DOPA in young leaves*

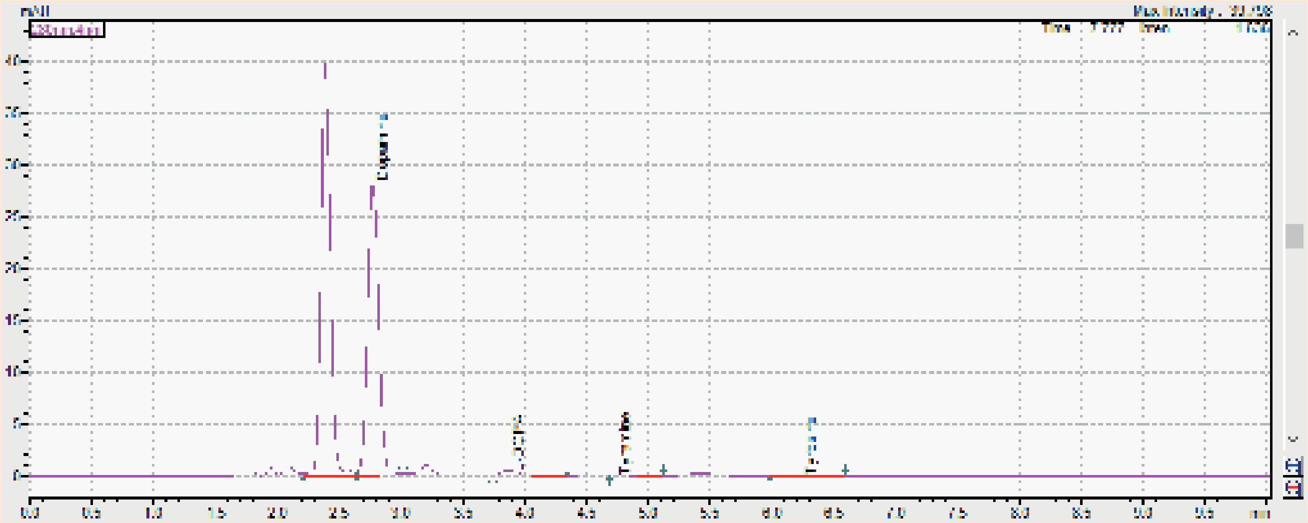

Fig. 11C: *Chromatogram showing the presence of dopamine and an unknown peak in mature seed tissue.*

Fig. 11: *HPLC based catecholamine intermediate profiling in various Faba bean tissues, The values in X-axis of the chromatograms indicate the retention time in minutes and Y-axis refer to the response of absorbance in mAU.*

Identification of genes responsible for Zinc homeostasis in rice (Oryza sativa L.)

Expression profiling of Zn deficiency responsive genes in rice

The present study was conducted to understand the differential expression pattern of three zinc-responsive genes, viz., OsbZIP48, OsbZIP53 and Os03g22810 under Zn deficit (0.005µM) and control conditions (5 µM) in rice. Two rice genotypes differing in seed Zn content, viz., BKS 41 (high) and Sadabahar (low), were grown under hydroponic condition. Samples were collected from both root and shoot tissues of 10-day old seedlings for RNA isolation and subsequent gene expression assay. Zn deficiency induced OsbZIP48 differential tissue specific expression. A significant up regulation (about 13-fold) of OsbZIP48 was observed only in root of BKS 41, while its induction was not observed in Sadabahar root. On the contrary, the shoot tissues showed significant induction of OsbZIP48, while its counterpart showed insignificant changes in its expression. Further, an opposite induction pattern of Os03g22810 was observed in the shoot tissues of both genotypes (Fig. 12). For example, while a significant induction of the gene was observed in BKS 41, there was a significant reduction in Sadabahar, suggesting its vital function in Zn homeostasis. This preliminary study indicated the intricacy of the gene regulation for Zn homeostasis in rice which needs further elaborate study.

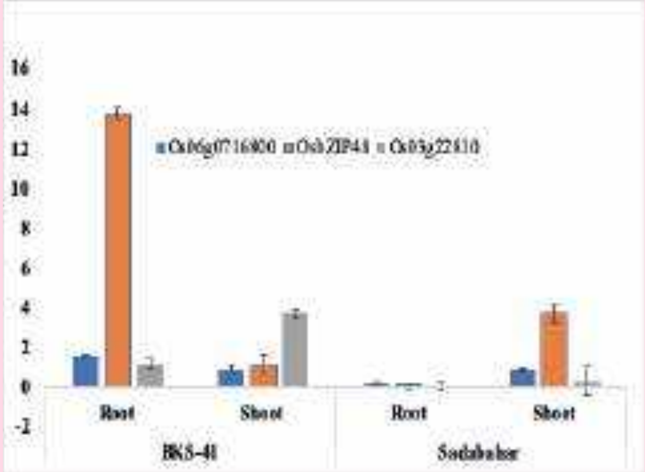

Fig. 12: *Graph showing RT-qPCR-based relative expression of zinc responsive genes (Os06g0716800, OsbZIP48 and Os03g22810) under Zn deficit condition in root and shoot tissues of contrasting rice genotypes differing in seed Zn content. The data is mean of three replicates and the line on each bar is ± SE. The value in Y-axis represents relative fold change in gene expression as compared to control.*

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

Genotype identified for low seed shattering trait in Amaranthus

A total 115 germplasm were grown and various morpho-physiological traits like days to 50% flowering, percentage seed shattering etc. were recorded. Seed shattering percentage ranged from 0.5 – 48% across the germplasm. Five low seed shattering (<5%) and eight high seed shattering (>40 %) germplasm were identified. One germplasm (IC 042277) with the least seed shattering (<1 %) was identified which is being evaluated further.

Ideotype breeding in horse gram for Jharkhand region

Assessment of genetic diversity in horsegram for agro-morphological and nutritional attributes

A core collection of thirty-six horsegram (Macrotyloma uniflorum) germplasm accessions and two checks were evaluated during kharif, 2021, at ICAR-IIAB, Ranchi, and analyzed for 16 agro-morphological and 12 nutritional traits. It also revealed that seed yield per plant, number of clusters per plant, number of primary & secondary branches, plant height, tannin content, nitrogen content, and sulfur content had very high heritability. Path analysis showed maximum positive direct effect towards seed yield by the number of primary branches followed by days to 85% maturity, SPAD chlorophyll meter reading, carbohydrate content, number of clusters per plant, nitrogen content, iron content, number of seeds per pod, number of pods per cluster, seed width, hydrogen content, protein content, seed length, zinc content, and reducing sugar and phytic acid contents. Genetic diversity through Mahalanobis D2 analysis identified a diverse group of genotypes (IC 139367 & IC 23441 and IC 110666 & IC 23441) suitable for generating transgressive segregants through hybridization. IC 23441 (12.21g/plant) showed a significantly higher yield than the best check, HPKM 317 (10.82 g/plat). IC 139460 had the lowest phytic acid (8.21mg/g) content, while IC 80943 recorded the minimum tannin (0.89g/100g) content. IC 123022 recorded the highest iron content (0.07mg/g), while IC 53613 had the highest zinc content (0.05mg/g).

Identification of photo-insensitive lines in horsegram

Horsegram is an underutilized crop with limited cultivation due to its poor plant architecture traits like spreading, twining, indeterminate growth habit and photosensitivity. It is a short-day plant and is generally grown in the kharif season. Identification of photo-insensitive genotypes could lead to the cultivation of horsegram throughout the year. A germplasm set of 210 accessions (procured from ICAR-NBPGR, New Delhi and HPKV, Palampur) were evaluated for flowering under long-day conditions. Sowing was carried out on the second week of February (15th February 2022) and grown under recommended agronomic practices. Out of 210 accessions screened, two accessions (HPKM 11-72 & HPKM 11-74) recorded complete flowering and seed set under long-day conditions. The photo-insensitive nature of these genotypes could be utilized in the breeding program for the development of elite photo-insensitive, high-yielding varieties or for developing a mapping population to map QTLs/genes.

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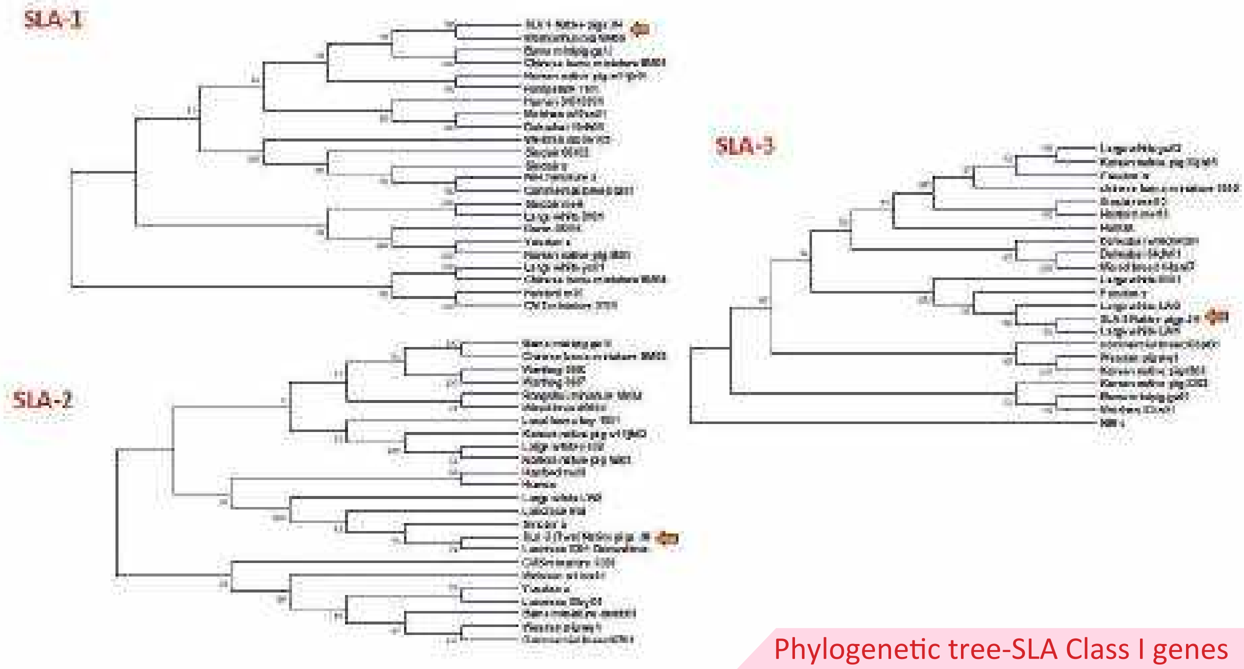
GENETIC ENGINEERING

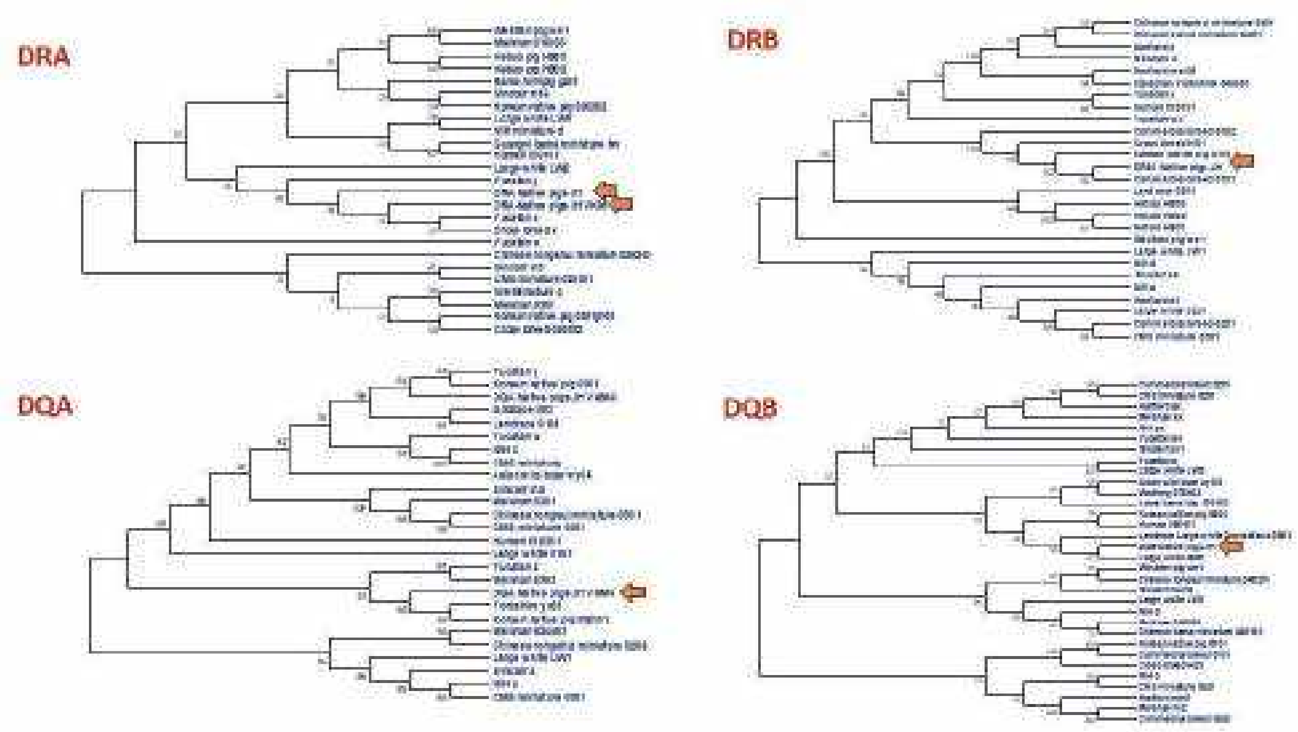
Exploring Swine Leucocyte Antigens (SLA) as candidate genes for improvement of immune response in swine

Swine Leukocyte Antigen (SLA), the Major Histocompatibility Complex (MHC) of domestic pig (Sus domesticus), plays a central role in the body defence and immunity. Recent outbreaks of Classical Swine Fever (CSF) and African Swine Fever (ASF) in different parts of India call for dissection of immunity at molecular level vis-à-vis (anecdotal) claim of disease resistance in indigenous domestic pigs. Molecular characterization of the SLA genes of the indigenous pigs were carried out during the year. The major constitutively expressed classical SLA genes, namely SLA-I, SLA-II and SLA-III of Class-I, and DRA, DRB, DQA and DQB of Class-II were cloned and sequenced followed by bioinformatic analysis. The PCR amplicons of 1,109 (SLA-1), 1,118 (SLA-2) and 1,728 bp (SLA-3) of Class-I, and 799 (DRA), 907 (DRB), 793 (DQA) and 1,103 bp (DQB) of Class-II were produced, and we obtained ORF of 876 (SLA-1), 1,095 (SLA-2) and 927 bp (SLA-3) of Class-I and 759 (DRA), 801 (DRB), 765 and 768 (DQA) and 786 bp (DQB) of Class-II SLA genes. The rates of nonsynonymous substitutions per site were higher for antigen-binding sites (ABS). This is supposed to confer advantage in immunity function. The important residues at N-glycosylation site, disulfide bond, etc. were invariant.

The sequence homologies varied between 90.39 and 99.91% for Class-I genes, and 93.70 and 100.00% for Class-II genes when compared with respective gene of domestic and commercial pigs as well as closely related other pig species around the world. The SLA-1 gene of indigenous pigs was phylogenetically closer to Asian pig breeds and miniature pigs whereas SLA-2 and SLA-3 genes were closer to western pig breeds and their crosses. The Class-II genes were closer to western breeds and commercial crosses although DRB and DQA were also closer to few Asian native pigs. The information revealed by this study indicates diversity in allelic architecture and haplotypes in MHC of domestic pigs that shall aid disease resilience.



Phylogenetic tree-SLA Class I genes



Phylogenetic tree-SLA Class II genes

Standardization of efficient regeneration protocol in tropical maize

Six tropical maize genotypes were evaluated for callus induction and plant regeneration. The callus induced from mature seed derived split nodal explants and maximum callus induction takes place in supplemented Murashige and Skoog medium (MS) containing 2.5mg/L 2,4-Dichlorophenoxyacetic acid (2,4-D). Out of 6 genotypes evaluated, the embryogenic callus obtained in three hybrids, viz., Rasi 4212, SV521, NU XCEL, while only non-embryogenic Calli produced in remaining genotypes. Among all the genotypes, the best callusing efficiency (50%) and regeneration efficiency (44%) takes place in Rasi 4212 (Fig. 13).

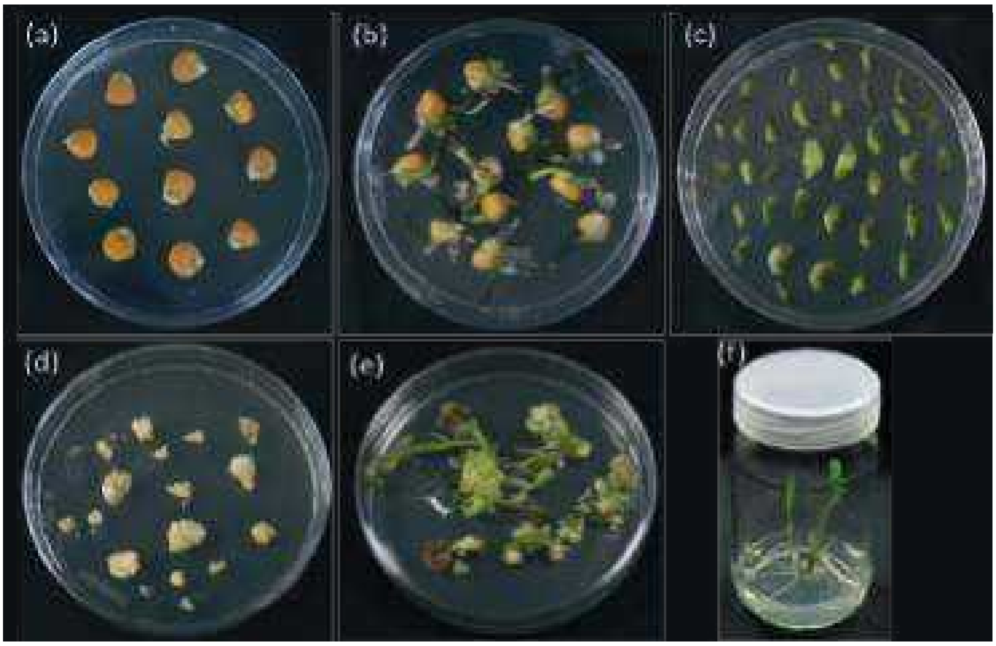


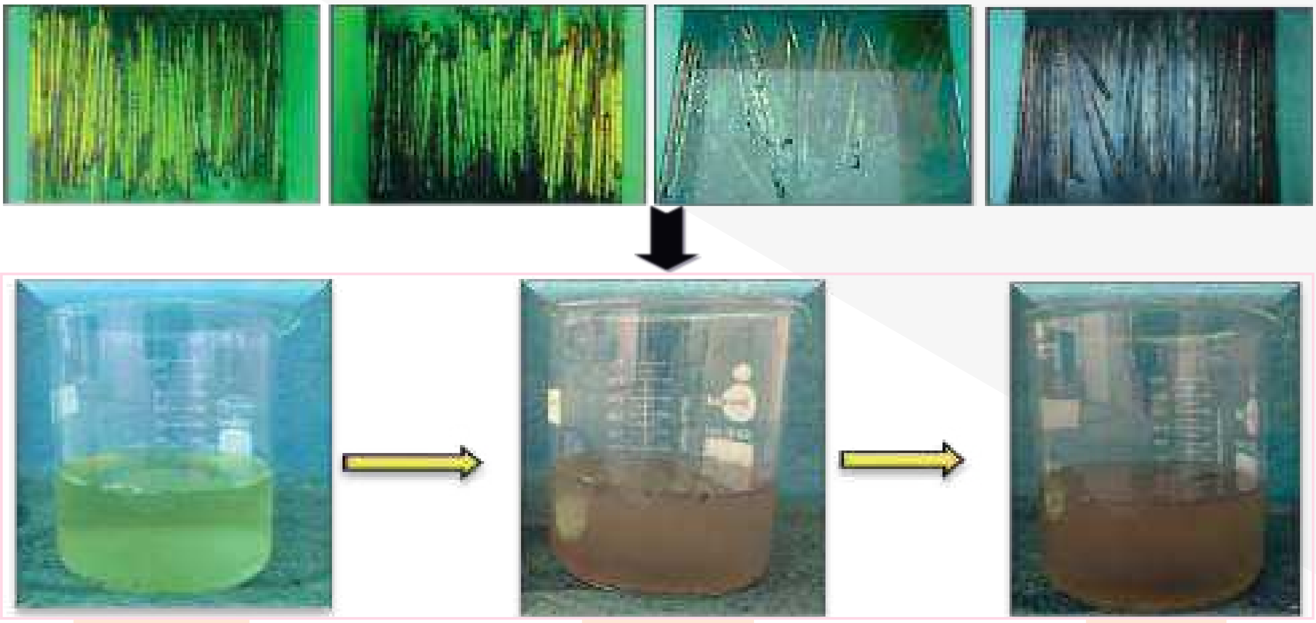
Fig. 13: *Schematic representation of various steps in callusing and plant regeneration in tropical maize using mature seed derived nodal explant (Rasi 4212). a mature seed b swollen internode c split internodal portion d callus e regeneration f rooting.*

MOLECULAR DIAGNOSTICS, PROPHYLACTICS AND NANO–BIOTECHNOLOGY

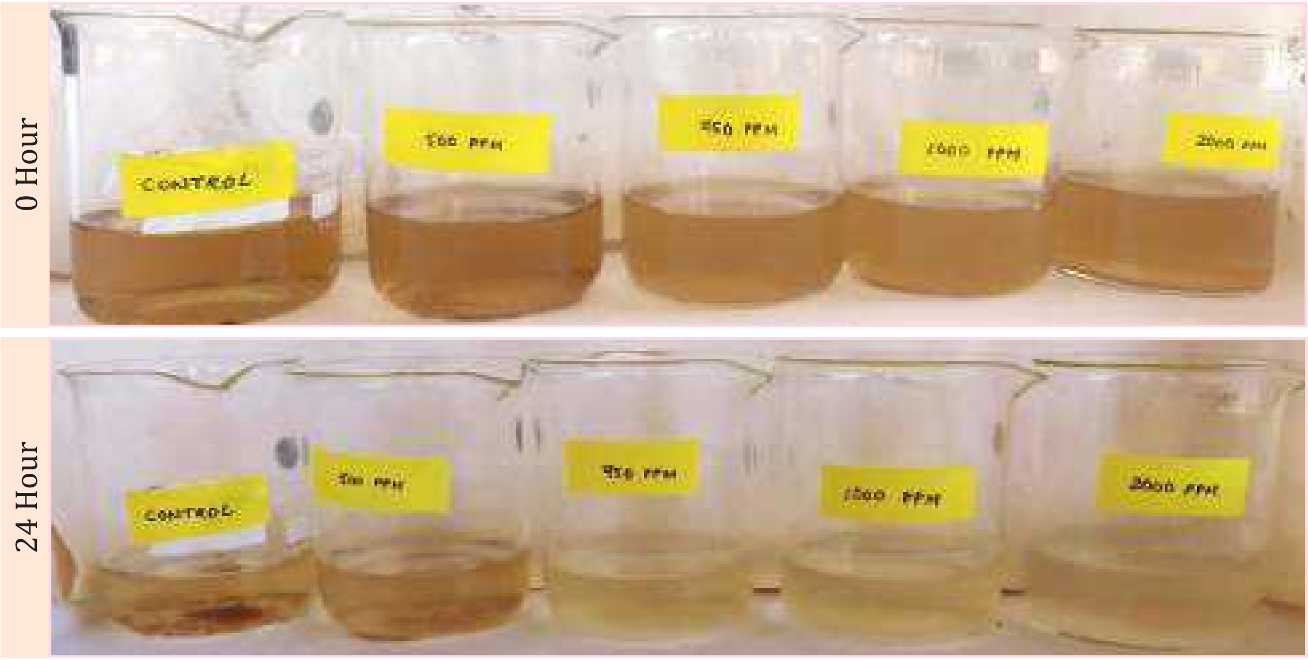
Evaluating the nano-inspired degradation of aquatic pollutants with special reference to lac dye and Jute retting waste-water

Method for evaluating the nano-inspired degradation of Jute retting waste-water

Nano remediation is an efficient approach to eradicate the aquatic pollutants from the environment. Jute industries are facing major problems with the generation of wastewater during the process of jute retting. The microbial driven retting process leads to accumulation of scum and degraded products of jute fibers which cause eutrophication and adversely affects the quality of jute and associated aquatic ecosystems. To address this problem, nanoparticles are employed to remediate the jute wastewater due to its unique attributes which includes large surface area and high photocatalytic activity and the sustainability of biological indicator are monitored. Experimental trials were initiated to generate the jute wastewater, where 4 kg jutes was suspended in 40 L of water in a FRP tank (100 L), with the addition of 60 gm CRIJAF Sona at its recommended dose (15g/kg Jute). The change in color of the jute wastewater was regularly monitored. Zinc oxide nanoparticles (ZnO NPs) was previously synthesized by using co-precipitation method and was characterized. ZnO NPs @ 500, 750, 1000 and 2000 ppm, respectively, contained in micro containers were incorporated in the jute wastewater (100 ml) of 10 days. All treatments including control was incubated in the sunlight (approx. at 33°C in the month of mid-October having sunlight intensity of 30,000 lux), and stirred well in an hourly interval and change in the color was noted. Microbial load was examined by using plate count method (Reasoner, 2004) on the 1st and 10th days of incubation. All treatments showed the effective results by completely degrading the jute wastewater in 24 hrs. The viable number of microorganisms was observed in 750 ppm ZnO NP after the 24 hrs. of incubation. After 10 days, microbial load was counted and the number of microbial populations, which was increased in all four treatments. The effective concentration of ZnO NPs was obtained in 750 ppm ZnO NP as compared to other treatments, which indicated the complete degradation of jute retting wastewater with low bactericidal effects in the incubation period of the 24 hrs (Fig. 14).



3rd. Day 10th. Day 21st. Day



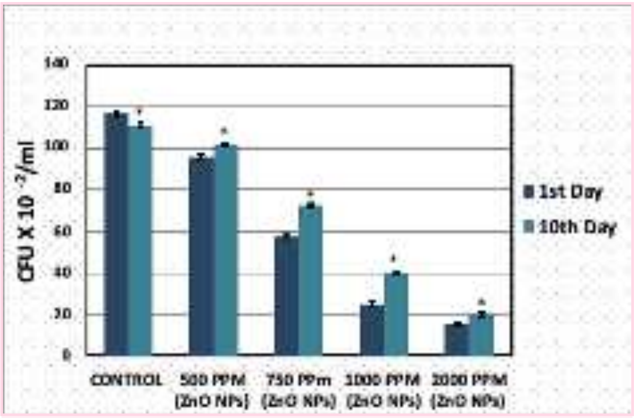
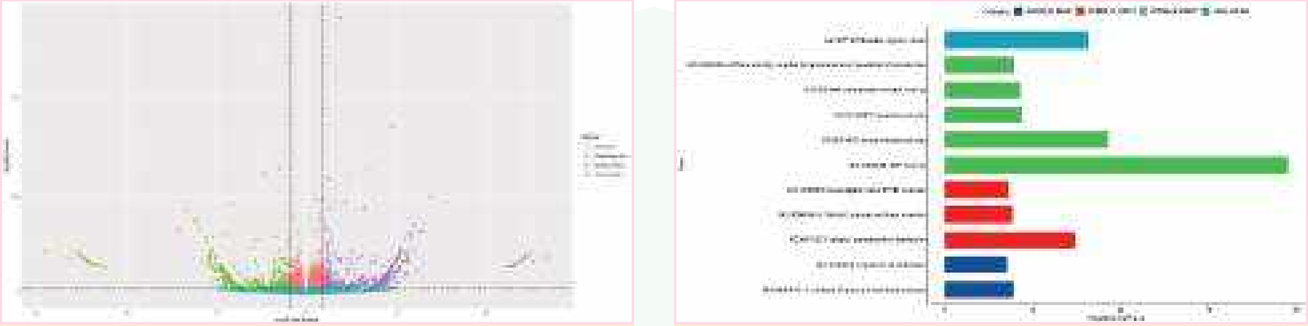


Fig. 14: *Graphical representation of microbial load in different doses of ZnO NPs in jute wastewater on 1st day and 10th day*

Development and evaluation of the efficacy of novel nanoparticles for enhancing yield in rice and Indian major carp

Evaluating the doses impact of Calcium Oxide Nanoparticles on the gene expression profile of Chickpea

Nanotechnology provides an innovative insight on developing tools for precision farming. Current research is designed to decipher the molecular mechanism behind the dose dependent role of calcium oxide nanoparticles (CaO NPs) in chickpea cultivation under acidic soil conditions. Initially, CaO NPs are synthesized and characterized via FTIR, XRD, FE-SEM, and EDS. Experimental pots were prepared and chickpea seeds var. Chirag were sown following the standard protocol. The CaO NPs was delivered in the rhizospheric region of the soil by using spraying methods at different doses i.e., Nano 1/50th, Nano 1/100th and Nano1/150th including a positive control (2g Lime/pot) and a negative control (without treatment). The morphological developments as well as physiological indices were regularly monitored. Higher germination, growth and early flowering were observed in Nano 1/50 dose followed by Nano 1/100 doses. Transcriptomics analysis of the chickpea plants was carried out using RNAseq technology, which showed 271389 transcripts and 215631 unigenes, the N50 values obtained were 1886 bp and 814bp, respectively and calcium regulations related genes i.e., calmodulin-binding transcription activator 2-like isoform X1, calcium-transporting ATPase 8, exhibit up regulation in the treatment groups in comparison with the controls. Through volcano mapping, differentially expressed genes between the treatment group 1/50th and P.C are shown and gene ontology represents molecular functions of the upregulated genes in the treatment group 1/50th (Fig. 15). Furthermore, ICP-OES analysis of the rhizospheric soil and chickpea plants roots as well as shoots showed higher accumulation of CaO NPs at the dose of

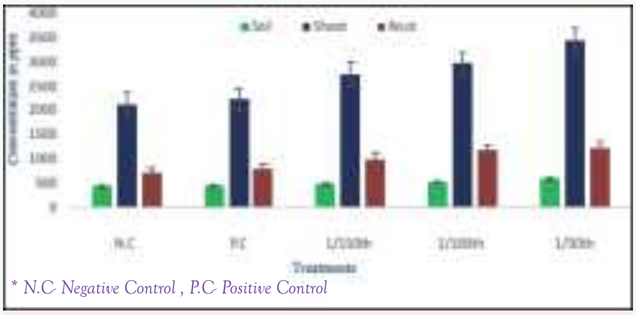


A

B

Fig. 15: *Transcriptomics Analysis (A.) Volcano Plot (B.) Gene Ontology*

1/50th (Fig. 16). Hence, it can be concluded that CaO NPs at the minimum doses i.e., 1/50th can be a viable substitute for the lime application in the chickpea cultivation



** N.C- Negative Control , P.C- Positive Control*

Fig. 16: *ICP-OES analysis of soil, shoots and roots of chickpea from different doses of CaO NPs treatments*

Investigation on soil microbiome profile of coal mine aquatic ecosystem of Ramgarh, Jharkhand

Mining activities adversely affect the fertility of the soil. Many heavy metals present at the mining site alter the microbial activity of the soil resulting from significant changes in the microbial diversity. In the present study, two different sites namely the Ramgarh coal void and Getalsud reservoir were selected as the test and control sites, respectively to investigate the soil microbial community structure. The concentrations of heavy metals present in the soil and water samples were analyzed by inductively coupled plasma mass spectrometry (ICP-MS). In the soil samples no significant differences in Li, Be, V, Co, Cu, Zn, Se, Ag and Fe were recorded. However, significant difference was found in the concentrations of Cr, Mn and Ni. Similarly, no significant differences were observed in the concentrations of Be, V, Mn, Co, Se and Ag in the water samples. However, significant differences ($p<0.05$) were found in Li, Cr, Ni, Cu, Zn and Fe. The concentration of heavy metals was found to be higher at the test site than the control.

Bacteria and Archea were found to be most abundant domains in the soil samples collected from Ramgarh and Getalsud (Table.1). However, the contribution of Archae was significantly higher in the soil sample of test site. Though, Proteobacteria contribution was dominant in both the experimental group, the percentage abundance was higher from the coal void site. Among the Proteobacteria, Deltaepsilon and Beta proteobacteria were observed to be major class in both groups with higher percentage contribution at the coal void site (Fig. 17).

Table 1: Major microbial domain of the soil sample collected from Test and control site

Domain	Control	Test
Bacteria	97.33 ± 0.33	96.66 ± 1.20
Archae	2.66 ± 0.33	3.33* ± 1.20
Viruses	0.23 ± 0.07	0.25 ± 0.04
Others	0.02 ± 0.01	0.04 ± 0.03

*Data represents Mean± Se, n=3, * indicates significance difference ($p<0.05$)*

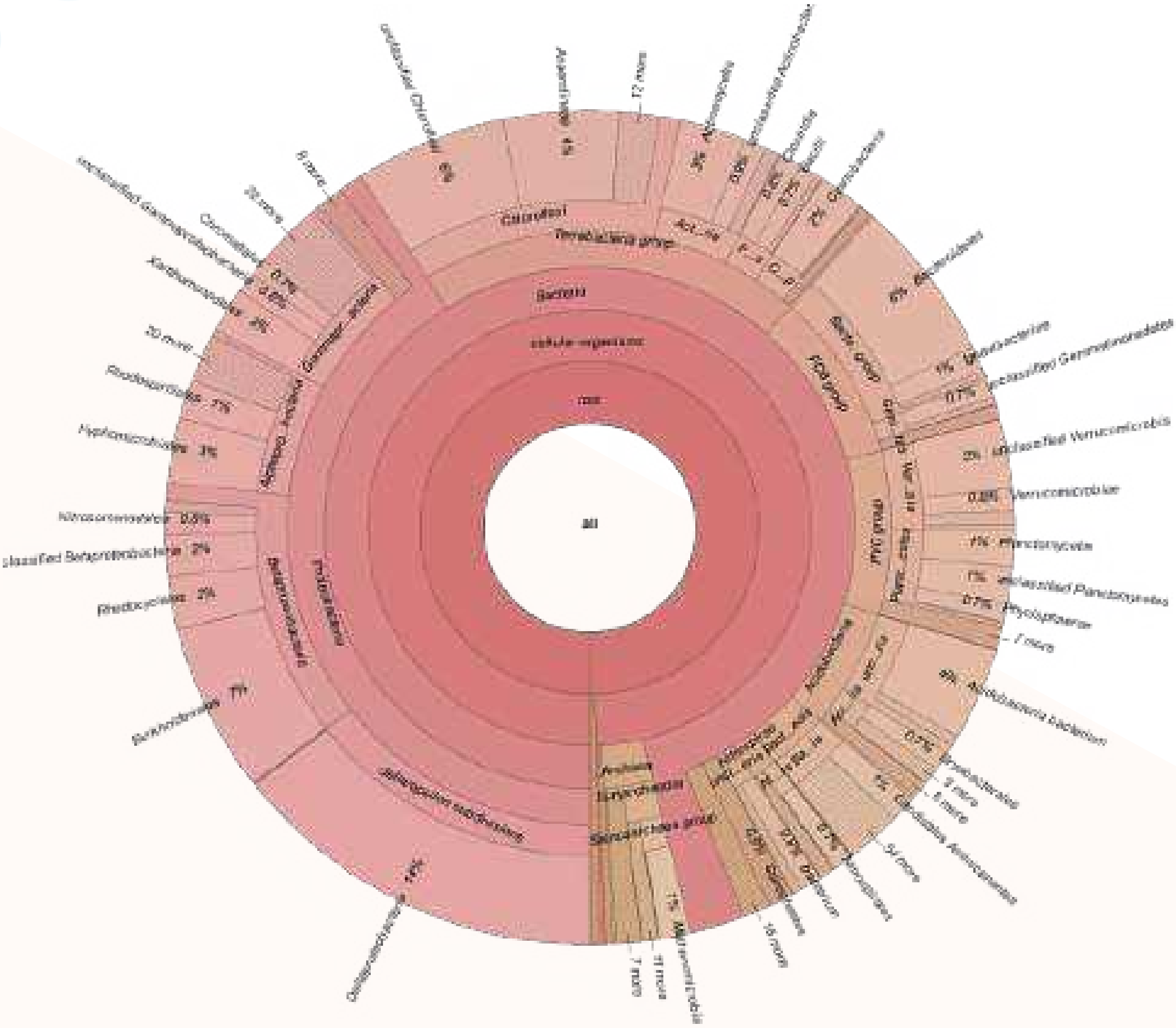
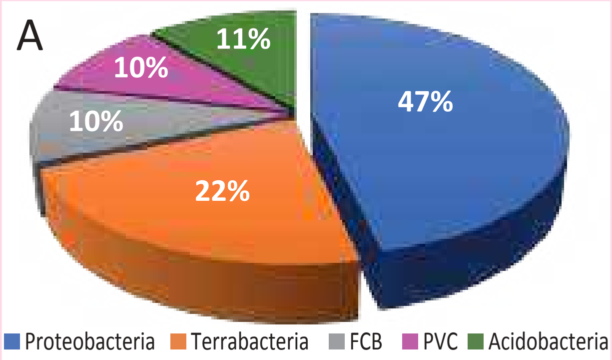


Fig. 17: *Krona chart displays the major microbial community composition in the soil sample of test site.*

The bacterial groups, Proteobacteria were recognized as the dominating phylum compared to Terrabacteria and FCB bacteria in both control and test samples (Fig. 18 A&B). Two proteobacteria class such as deltaepsilon and beta proteobacteria was observed to be major class in both the groups. The Terrabacteria, Chloroflexi and Actinobacteria class was the most dominant in the soil samples from the both groups. At species level, Acidobacteria bacterium were most abundant in soil samples collected from the Getalsud Reservoir (6%), and Ramgarh Coal Mine (2.33%) Fig. 19. At genus level, Sulfuricurvum comprised of maximum number of OTU (3.67%) contribution in the soil samples collected from coal. At phylum level, Proteobacteria was the most abundant in the soil samples collected from coal void (46.6), followed by Chloroflexi (11%). The Euryarchaeota was recognized as the major phylum of the Archaea domain followed by Track group, with higher abundance at the control site.



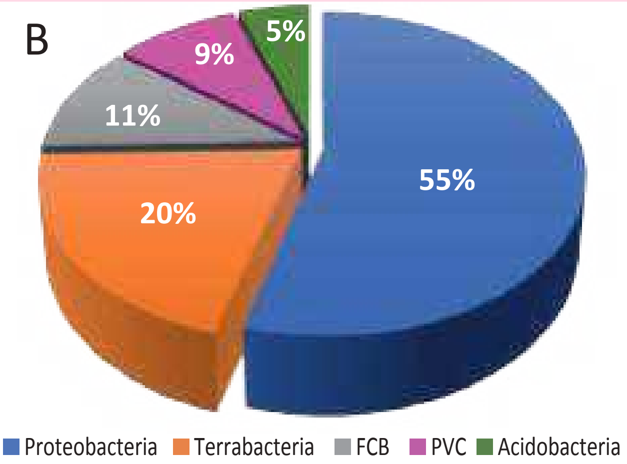


Fig. 18: *Phylum of Bacterial Domain, A. (Control), B. (Test)*

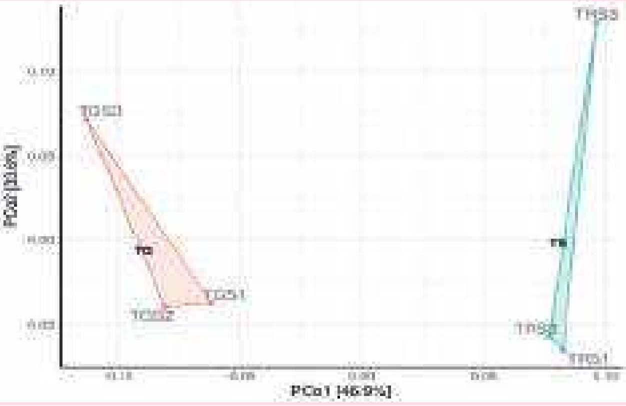


Fig. 19: *Principal coordinate analysis (PCoA) of test and control site showing separate cluster of bacterial community composition*

No significant (p> 0.05) difference was observed in the Shannon and Fischer alpha-diversity indices of soil samples collected from Ramgarh coal void whereas significant impact was seen in terms of Simpson index. Principal coordinate analysis (PCoA) was used to compare the similarity between the two groups that revealed a clear separation of bacterial community composition (Fig. 20). Further functional metagenomics approaches might shed light to decode heavy metal resistance genes.

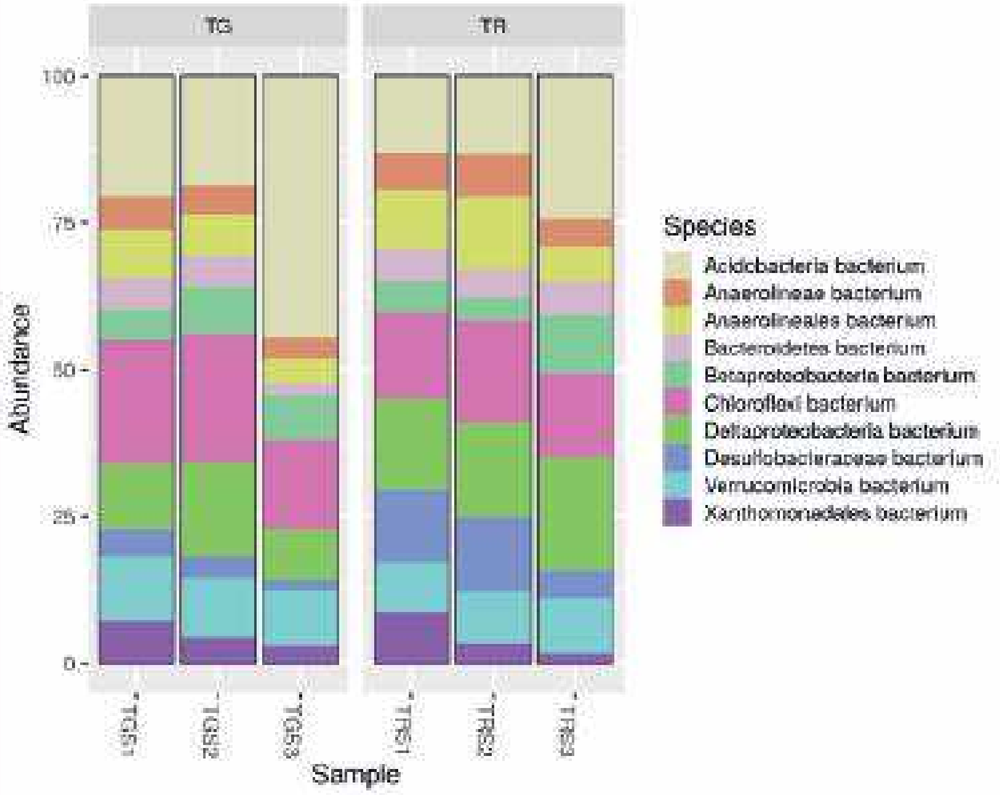


Fig. 20: *Heatmap displays metagenome abundance by the method of color-coding. At species level, Acidobacteria bacterium were most abundant in soil samples collected from the Getalsud Reservoir (6%), and Ramgarh Coal Mine (2.33%)*

EXTERNALLY FUNDED PROJECT

Exploring cell surface biomarkers of cattle spermatozoa for sex-specific segregation through proteomic and genomic approach (OXX04775, DST-SERB funded)

Spermatozoa is by large transcriptionally inactive; the RNA content is approx. 1/1,000 times of a typical mammalian somatic cells. It is further complicated by the frequent presence of spermatozoal DNA (spDNA) and RNA derived from somatic cells, leucocytes, epithelial cells, etc. present in the semen. Thus, isolation of quality spermatozoal RNA (spRNA) for downstream applications is a formidable challenge. Through use of a cocktail of chaotropic agents, we have standardized a protocol yielding quality RNA for downstream applications. The quality of derived spRNA was ensured by different genetic markers like protamine 1 and 2, PTPRC, CDH1, KIT, etc. The spRNA yielded from the unsorted spermatozoa, X-spermatozoa and Y-spermatozoa of indicus cattle (Bos indicus) were used for transcriptome sequencing using Illumina HiSeqX NGS Platform. The high-quality reads were aligned against NCBI Reference of Bos indicus (assembly Bos_indicus_1.0). The overall alignments were 80-83, 71-80 and 74-77% for unsorted spermatozoa, X-spermatozoa and Y-spermatozoa, respectively. Differential Gene Expression (DGE) and Gene Ontology (GO)-analysis were performed. The differential expression revealed upregulation of 737 transcripts and downregulation of 1,016 transcripts in Y-spermatozoa as compared to X-spermatozoa ($p<0.05$). The transcripts unique to X-spermatozoa have top GO annotations for cell and plasma membrane integrity, protein heterodimerization, transcription and histone packaging while the ones unique to Y-spermatozoa have top GO annotations for glucose metabolism, mitochondrial translation and cytochrome p450. This is very interesting vis-a-vis our observation on comparative proteome between X- and Y-spermatozoa with special focus on membrane-associated proteins of indicus cattle that revealed abundance of differential proteins in Y-spermatozoa which are presumed to support sperm capacitation and sperm migration velocity and differential abundance of X-specific proteins associated with structural molecule activity. Thus, our results serve to follow a proteogenomic approach for biomarker discovery for immunosorting of cattle semen.

Additionally, the differences in fertility among the bulls of exotic (eg. Holstein Friesian (HF) and Jersey), crossbred (eg. HF/Jersey x Sahiwal) and indigenous (eg. Sahiwal) cattle breeds that are well-documented at phenotypic levels was studied by qPCR in terms of regulation of expression of few important and prospective candidate genes involved in mitochondrial function (COX5A and COX3) and fertility and embryogenesis (YWHAZ, CHMP5 and GTSF1L). The COX5A gene revealed significant upregulation ($p<0.05$) in the spermatozoa of exotic and crossbred cattle as compared to indigenous cattle. The differential gene expression of YWHAZ, CHMP5 and GTSF1L genes in exotic and crossbred bulls showed a significant upregulation ($p<0.05$) than the indigenous bulls. The significant upregulation of genes related to mitochondrial function and fertilization and embryogenesis in the spermatozoa of exotic and crossbred cattle may indicate towards the differences in the fertility vis-s-vis indigenous cattle leading to varying reproductive success. (images Top GO terms for X- and Y-spermatozoa of indicus cattle, Differential expression of genes related to mitochondrial function, fertility and embryogenesis in different genetic groups of cattle)

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ACADEMIC ACTIVITIES

Eight of the nine M.Sc. Students (4-Molecular Biology and Biotechnology; 4-Genetics and Plant Breeding; 1-Biochemistry) of 2020-21 batch have completed their degree during the period. One student from non-agricultural background is continuing the extra courses. Five students of 2020 batch qualified CSIR-UGC, DBT JRF/NET exams and achieved high ranks in ICAR SRF and Ph.D. entrance examination, out of them three students secured admissions at IARI, New Delhi and one each at NIPGR, New Delhi and CCS HAU, Hisar. One student is selected as Agriculture Development Officer in Govt of Haryana. One of the students (….name) secured Ph.D. admission in several reputed institutions (IISER, Thiruvananthapuram, IIT, Gandhinagar, TIFR-DBT-Instem, IIT Guwahati, IISER Bhopal ICGEB, New Delhi and MEXT, Japan).

In the session 2021-22, ten students (6 of Molecular Biology and Biotechnology and 4 of Genetics and Plant Breeding) of Master Degree programme are pursuing M.Sc. degree. From academic session 2022-23 B. Tech. (Botechnology) programme with 30 students is being initiated at the institute.

Academic session: 2021-22, Master Degree Program			
Sl. No.	**Name**	**Research topic**	**Research guide**
Molecular Biology and Biotechnology			
1	Ms. Sradhanjali Jena	Understanding the biochemical and molecular basis of L-Dopa biosynthesis in Faba bean (*Vicia faba* L.)	Dr Biplab Sarkar
2	Mr. Sudheer Bishnoi	Investigating the molecular role of seed-coated nanoscale iron in chickpea	Dr Biplab Sarkar
3	Mr. Pratik Prasad Singh	Molecular insight into the protective role of green copper nanoparticle against *Fusarium oxysporum* in chickpea.	Dr Biplab Sarkar
4	Mr. Ankit Raj	Identification and characterization of long non-coding RNAs (lncRNAs) related to pod and seed development in winged bean (*Psophocarpus tetragonolobus* L.)	Dr. Kishor U Tribhuvan
5	Mr. Shivakumaraswamy M	Identification and characterization of salt-stress-related lncRNAs in Indian Mustard (*Brassica juncea* L.)	Dr Binay Kumar Singh
6	Mr. Mustafa N	Genome-wide identification and characterization of PEBP family genes in winged bean (*Psophocarpus tetragonolobus* L.)	Dr Binay Kumar Singh
Genetics and Plant Breeding			
7	Mr. Koppula Satya Sai Kumar	Molecular characterization of rice genotypes using candidate gene markers for NUE and PUE	Dr Avinash Pandey
8	Ms. Jaya Kothapelly	Genetic and molecular characterization of rice germplasm for yield and nutritional quality traits	Dr. Vijai Pal Badana
9	Ms. Adepu Priyadarshini	Assessment of genetic diversity in Horsegram germplasm by using SSR markers	Dr Sudhir Kumar
10	Mr. Mukesh Raj	Development of SSR markers and their application in revealing genetic diversity in Adzuki bean (*Vigna angularis*)	Dr Avinash Pandey

OUTREACH ACTIVITIES

Scheduled Tribe Component (STC)

Distribution programme

Under the Scheduled Tribe Component (STC), ICAR-IIAB supported 2,280 tribal farm families from 80 villages in five districts of Jharkhand, namely East Singhbhum, Chatra, Ranchi, Gumla, and Ramgarh. Critical agricultural inputs and training on improved production technologies for field crops, horticulture and piggery were provided to the tribal farmers(Fig. 21), which include (1) promotion of cultivation of drought-tolerant high-yielding rice variety DRR Dhan 42 along with the other high-yielding rice varieties, viz., TRC 15-5, Swarna Sherya, Swarna Shakti Dhan, Swarna Samriddhi Dhan and Sahbhagi Dhan recommended for the state; (2) promotion of cultivation of high-yielding Indian Mustard variety NRCHB 101 in the rice fallows for increasing the cropping intensity and farm income; (3) distribution of an early maturing, finger and neck blast-resistant cultivar of finger millet, viz., VL Mandua 352; (4) popularization of improved breeds of pig (Jharsuk); (5) distribution of light-weight VL metallic hand tools for smooth intercultural operations, battery-operated sprayers for promoting integrated pest and nutrient management in the field and horticultural crops. Besides, farmer-scientist interaction meetings, on-farm training, field days, on-farm trials, farmers' fairs and outstation exposure visits were also organized to increase knowledge and awareness among the tribal farmers.

Fig. 21: *Seed distribution under STC programme (a) Distribution of paddy seeds among ST farmers in Bero (Ranchi) (b) Distribution of paddy seeds among ST farmers of Gumla district at the Piggery farm of BAU, Ranchi*

Training on value addition in finger millet

Finger millet (Eleusine coracana), also known as ragi or mandua, is one of the oldest food grains known to humankind. In Jharkhand, it is consumed mostly as pancakes, particularly during the winter season. Because of a high degree of drought tolerance and resilience to climatic change, finger millet is extensively grown in almost all 24 districts of Jharkhand. The crop is particularly important to the South Eastern Plateau (agro-climatic sub-zone VI) comprising the districts of East Singbhum, Saraikela, and West Singbbhum. During the year, ICAR-IIAB organized six 5-day residential training programs for the farmers of tribal communities of Jharkhand (Table 2). The objective of the training was to create awareness among the farm women about the nutritional value of the finger millet and the skill of preparing value-added products from it. The programs were organized at the Department of Home Science, Birsa Agricultural University (BAU), Ranchi. One hundred forty-two farmers from Ranchi, Latehar, Lohardaga, Khunti, Gumla, East Singhbhum, Simdega, Chatra, Hazaribag, and Ramgarh districts of Jharkhand attended the training programs.

मडुआ से विभिन्न उत्पाद बनाने का प्रशिक्षण लेती महिलाएं।

सारणी 2: प्रशिक्षण कार्यक्रमों का विवरण

क्रमिक संख्या	प्रशिक्षण कार्यक्रम का नाम	अवधि	प्रतिभागियों की संख्या
1	मोटे अनाजो के विशेष सन्दर्भ में खाद्य प्रसंस्करण	जुलाई 4 से 8, 2022	25
2	खाद्य प्रसंस्करण द्वारा मिलेट,एवं फल व सब्जियों का मूल्य संवर्धन	जुलाई 11 से 15, 2022	22
3	मंडुआ के विशेष सन्दर्भ में खाद्य प्रसंस्करण	जुलाई 26 से 30, 2022	23
4	पोषक अनाजों के विशेष सन्दर्भ में खाद्य प्रसंस्करण	सितम्बर 12 से 16, 2022	24
5	मिलेट के विशेष सन्दर्भ में खाद्य प्रसंस्करण	नवंबर 29 से दिसंबर 3, 2022	25
6	खाद्य प्रसंस्करण द्वारा पोषक अनाजों एवं फल व सब्जियों का मूल्य संवर्धन	दिसंबर 13 से 17, 2022	23

प्रशिक्षुओं की कुल संख्या, 142

Training on piggery

ICAR-IIAB organized four 5-day residential training programs on scientific pig farming at the College of Veterinary Sciences & Animal Husbandry, Birsa Agricultural University (BAU), Ranchi The objective of the training was to sensitize the tribal farmers about scientific pig farming and create avenues for entrepreneurship development in Jharkhand. One hundred ninety-seven farmers from Ranchi and the adjoining districts attended the training program (Table 3).

सारणी 3: प्रशिक्षण कार्यक्रमों का विवरण

क्रमिक संख्या	प्रशिक्षण कार्यक्रम का नाम	अवधि	प्रतिभागियों की संख्या
1	सुअर पालन प्रशिक्षण कार्यक्रम	फरवरी 18 से 22, 2022	49
2	सुअर पालन प्रशिक्षण कार्यक्रम	मार्च 7 से 11, 2022	51
3	सुअर पालन प्रशिक्षण कार्यक्रम	मार्च 21 से 25, 2022	50
4	सुअर पालन प्रशिक्षण कार्यक्रम	मार्च 26 से 30, 2022	47

प्रशिक्षुओं की कुल संख्या, 197

Fish seed distribution program

A fish-seed distribution program was organized on 27h August 2022 for the tribal farmers of Kharsidag, Garhkhatanga, and Tetri villages of Ranchi district. The farmers were sensitized about balance nourishment and additional feeding in fish farming. Moreover, they were provided with total of advance fingerlings with the composition Catla (50%), Rohu (30%), and Mrigal (20%) for stocking in their ponds (Fig. 22).

Fig. 22: *Scientists of ICAR-IIAB providing advance Fingerlings to the tribal farmers*

Scheduled Caste Sub-Plan (SCSP)

Distribution programme

Over 2,600 scheduled caste farmer families were supported in 2022 under the Scheduled Caste Sub Plan (SCSP). These farmers belonged to nearly 70 villages in four districts of Jharkhand, viz., Chatra, Palamu, Latehar, and Ranchi. The Institute provided improved production technologies for field crops, piggery and fishery to the farmers. The activities taken up were (1) the distribution of the quality seeds of drought-tolerant/aerobic high-yielding rice variety IR 64drt1, Swarna Sherya, Swarna Shakti Dhan, Swarna Samriddhi Dhan recommended for the state of Jharkhand; (2) the distribution of Indian Mustard varieties namely NRCHB 101, PM 26 and PM 27 in the rice fallows for doubling the cropping intensity and promoting crop rotation; (3) the promotion of improved breeds of pig (Jharsuk) and popularization of the use of area-specific mineral mixtures for promoting the productivity of the animals; (4) distribution of VL metallic hand tool sets to ease the different cultural practices during farming and distribution of portable incubators and hatchery to promote backyard poultry and self-employment; (6) popularization of the use of quality fish feed mixtures for enhancing fish production. The Institute also organized several need-based farmers-scientists interaction meetings and on-farm training. It also organized on-farm trials, farmers' fairs, and outstation exposure visits.

Fig. 23: *Distribution of paddy seeds among the farmers of the SC community*

Farmer-Scientist Interaction meet cum advisory and fish feed distribution program

During 2022, the institute organized several fish feed distribution programs and benefitted 95 farmers of the SC community of Jharkhand. Besides, farmer-scientist interaction meet cum advisory programs for the scientific management of aquaculture were organized for the farmers of Maheshpur of Angada block of district Ranchi, Ara Sarubera of Mandu block of district Ramgarh, Sukurhutu of Kanke block of Ranchi, and Palkot of Gumla district. The program aimed at capacity building of SC farmers to improve livelihood and income generation. During the program, farmers were sensitized about the role of balance nutrition and supplementary feeding for aqua-culturable fish. In addition, they were made aware that nutritionally supplemented feed provides better fish development and prevents diseases caused by weakened immunity.

Fig. 24: *Organization of farmer-scientist interaction and fish feed distribution program under SCSP*

Northeastern Hill (NEH) programme

Northeastern Hill (NEH) Region

The NEH component of the institute was implemented in Tripura in collaboration with ICAR Tripura Centre. Through the KVKs planned activities were carried out in East Khasi Hill district of Meghalaya, Peren district of Nagaland, Morigaon district of Assam and in collaboration with Agriculture College (CAU), Pasighat in Arunachal Pradesh. In order to promote farm mechanization as a measure to enhance efficiency of farm and reduce drudgery of farm labour in agricultural operations in remote hill areas of NEH, one 50 HP Tractor along with one each of Hydraulic Trailer, Cultivator and Disc Plough costing more than Rs. 10.0 lakhs were provided in Nagaland through KVK, Peren and Digital Soil Testing Mini Lab, Micro-Weeder, Power Reaper, Three Tinned Furrow Opener and Tree Pruner altogether worth Rs.19.5 lakhs were provided through KVK East Khasi Hill district of Meghalaya. Field demonstrations with 400 quintals of quality seeds of five improved varieties of rice, viz., Gomati, Khowai, Hauchuk 2, Tripura Nirog and Tripura Chikan Dhan were organized in all the eight districts of Tripura involving 2600 farmers. Besides, 12500 hermetic bags were also provided to the beneficiary farmers for safe storage of seeds. In Nagaland, 10,000 hermetic bags of various capacities for safe storage of seeds in high humidity conditions were provided to the farmers of 21 villages of Peren district. To encourage vegetable production in backyard for improved livelihood and nutritional security, farmers of Peren district were also provided 100 Sprayers, Watering cans and need based organic pesticides.

In Assam, 3000 saplings of Assam Lemon (a seedless variety) and vermicompost (50 qtls) were distributed to the farmers of Morigaon district in collaboration of KVK Morigaon. Four capacity building programmes involving 100 beneficiary farmers of Pasighat area in Arunachal Pradesh were organized at Agriculture College, Central Agricultural University, Pasighat. In addition, demonstrations on vermicompost preparation, production of sesame, mushroom and winter vegetables were organized involving 4, 5, 10 and 25 farmers, respectively in Pasighat, Arunachal Pradesh.

Thirty homestead piggery-cum-breeding units were established by providing two months old genetically superior piglets (1 male: 2 female) in eight different villages of Peren district of Nagaland. Veterinary medicines, food supplements like, mineral mixtures, vitamin and calcium were also distributed. In addition, training programme on scientific piggery covering various topics like importance of pig rearing for breeding purpose, care and management of newborn piglets, healthcare and measures to be taken to control parasitic infections in piglets in different seasons and scientific management practices for better production and increased productivity of animals was organized for the beneficiaries. The programme was implemented in collaboration with KVK Peren, ICAR-RC for NEH Region, Nagaland Centre, Jalukie.

Fig. 25: *Micro-weeder, Power reaper and Tree pruner provided in East Khasi Hill district of Nagaland*

Fig. 26: *Distribution of sprayers and watering cans in Peren, Nagaland.*

Fig. 27: *Training on scientific pig farming and piglet distribution among NEH farmers in Nagaland*

Mera Gaon Mera Gaurav (MGMG)

Two multidisciplinary teams of scientists from ICAR-IIAB conducted awareness programs on natural and organic farming for sustainable and eco-friendly agriculture; general sensitization on improved crop production technologies, protected cultivation of high-value crops, swachhta abhiyan, climate change, crop insurance, avoiding the burning of crop residues, etc. under MGMG targeting nine villages from Chatra and Ranchi districts of Jharkhand. Awareness cum training programs were also organized on direct seeded rice, utilization of paddy fellow land for rabi season, water conservation, and use of low-cost small farm tools for efficient management of weed and intercultural practices. Demonstration cum sensitization programs on deworming of pigs, vaccination of cattle, use of mineral mixture for animals, etc., for getting a high remunerative return in animal husbandry were also organized. Awareness programs were also conducted on aquaculture, cage culture, ornamental fish farming, and the value addition of fish products. Technical support was provided to the farmers through meetings, discussions, and mobile advisory on various aspects of agriculture & allied activities.

Fig. 28: *Farmer-scientist interaction at Chandaghasi village of Namkum Block of Ranchi*

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INSTITUTIONAL ACTIVITIES

Institute Research Council (IRC) meeting

The Institute Research Council (IRC) meeting of the ICAR-Indian Institute of Agricultural Biotechnology (IIAB), Ranchi, was held on September 23-24, 2022, under the chairmanship of Dr A. Pattanayak, Director, ICAR-IIAB to review the progress of ongoing research projects (Fig. 29). Dr Sushil Prasad, Dean, Ranchi Veterinary College, BAU, Ranchi, was the expert (Animal Sciences), Dr A.K. Singh, Associate Dean, College of Fisheries Science, Gumla, Jharkhand, participated at the meeting as an expert (Fisheries Science), and Dr Manoj Kumar, Associate Professor & Head, School of Life Sciences, Central University of Jharkhand, Brambe, Ranchi, attended the meeting as an expert (Agril. Biotechnology). A total of 19 in-house projects were reviewed, out of which six projects were concluded. Overall, the Chairman and the experts expressed satisfaction with the progress made in the projects and made appropriate suggestions and recommendations for improving the research projects.

Fig. 29: *Interactions among scientist during IRC meeting*

Swachh Bharat Abhiyan

The Swachhta Pakhwada was organized by the ICAR-IIAB, Ranchi during 16-31 Dec 2022. Swacchta Pakhwada started with Swachhta pledge. The scientist, staff and students taken the Swachhta pledge and after the pledge, the awareness was spread towards cleanliness and personal hygiene. Several cleanliness drive and Swachhta awareness campaign organized in the institute premises (Fig.30), nearby villages, parks, school. Also, Face masks, sanitizer and dustbin distributed among the villagers and youth were sensitized about hygiene and cleanliness. Nodal officer, scientists and other staff of institute significantly contributed in cleanliness drive.

Fig. 30: *Swacchta Pakhwada celebrated at ICAR-IIAB*

Kisan Diwas

ICAR-Indian Institute of Agricultural Biotechnology, Ranchi organized a workshop on the occasion of Farmer Day on 23rd December, 2022 and also marked the swachhta pakhwada which is being celebrated from Dec 16-31, 2022 at the institute. The programme started with welcome speech by Dr. Shambhu Krishan Lal, Scientist, ICAR-IIAB. He emphasized the role of farmer in the economic development of a country. The director of the institute, Dr. Sujay Rakshit motivated the farmers on utilization of improved technology in agriculture (Fig. 31). He suggested way to enhance farmers's income. Also, he emphasizes the need to inculcate the habit of cleanliness that contribute to the development of country. Dr. Arunava Pattanayak, Principal Scientist, ICAR-IIAB spoke on the government schemes for upliftment of socio-economic status of the farmers. In this workshop, other scientists, Dr. V.P. Badhana, Dr. S. Naskar, Dr. Sudhir Kumar, Dr. Sanjay Kumar, Dr. Madan Kumar, Dr. K. Tribhuvan delivered lectures on various topics like efficient utilization of water resources, scope and advantages of natural farming, swachhta programme initiated by govt. of India, animal and fish health.

Scientists have suggested to adopt natural farming and its use in modern agriculture. Also, they suggested to make self-help group for selling of milk and other animal product to co-operative society and make animal husbandry a profitable business.

Fig. 31: *Director IIAB interacting with farmers on Kisan Diwas*

Parthenium Awareness

Parthenium Awareness Week (PAW) was organized during 16-22 Aug 2022,. The farmers and staff of the institute were sensitized about harmful effects of Parthenium hysterophorus/ Gazar Ghas (Fig. 32). The parthenium plants present in the institute premises are uprooted and dumped in earthen pit to get converted into manure.

Fig. 32: *Scientists imparting awareness about Pathenium among farmers*

World Pulse Day

ICAR-Indian Institute of Agricultural Biotechnology, Ranchi organized a seminar and farmers' meeting on the occasion of 4th World Pulses Day on 10.02.2022. In this program, Dr. Vijai Pal Bhadana, Principal Scientist, while presenting the welcome speech, congratulated the present farmers, , guests and employees on this day and in brief, increased knowledge about the usefulness of pulses. On this occasion, the chief guest Dr. A. K. Singh, in-charge, ICAR RC ER, Plandu Ranchi Centre stressed on the quality of pulses and its immense potential in Jharkhand. Dr. A. Pattanayak, Director, ICAR-Indian Institute of Agricultural Biotechnology, Ranchi highlighted the usefulness of pulses as it is rich in nutrients as well as beneficial for soil health. Dr. C. Chattopadhyay, Joint Director (Academic) provided information about disease and pest management of pulse crops to the farmers on this occasion. On this occasion, the seeds of improved variety of moong (Virat) were distributed among the farmers by the institute. The keynote speaker of the seminar, Dr. R.S. Pan, Principal Scientist, presented a detailed lecture on Vegetable Pulses. During the Kisan Goshthi, there was a dialogue between the farmers and the scientists about the management of pulses, selection of varieties, and its uses as animal feed (Fig. 33). Dr. Soumen Naskar, Principal Scientist emphasized that the use of husk and peel of pulses are important in increasing animal health, milk production and quality. Dr. Sudhir Kumar, Scientist, Dr. Madan Kumar, Scientist and Dr. Shambhu Krishna Lal, Scientist played an important role in the implementation of this program.

Fig. 33: *Scientist-farmers interaction on World Pulse Day*

Vigilance awareness week

ICAR-IIAB, Ranchi, Jharkhand, enthusiastically celebrated "Vigilance Awareness Week" from October 31st to November 6th, 2022, with the theme "Corruption Free India for a Developed Nation." The awareness week started with an "Oath-taking ceremony" on October 31st at 11 AM. All staff members (permanent, contractual, research scholars, and supporting staff) took the oath during this occasion after the Director of ICAR-IIAB read out the vow (Fig. 34). During the week, various programs were organized at the institute, which was participated by the staff members and students. On November 6th, during the closing ceremony, a group discussion was organized wherein all the institute's staff members participated. Dr Sujit Kumar Bishi, Vigilance officer, ICAR-IIAB, explained the types and nature of corruption. He also explained different means to prevent it for helping to make India a developed country and underlined that employees must uphold their integrity and the organization's standards to prevent corruption. Views from other participants were also heard with patience by the present audience. In his closing remarks, Dr A Pattanayak, Director, emphasized the need for self-introspection, discipline, and integrity for total personal growth, which can ultimately contribute to moving the country closer to being a developed nation.

Fig. 34: *Vigilance Oath taking ceremony at ICAR-IIAB*

संस्थान के राजभाषा संबंधी गतिविधियाँ

संस्थान की राजभाषा प्रकोष्ठ संस्थान के कार्यान्वयन में राजभाषा के उपयोग के प्रोत्साहन तथा भारत सरकार की राजभाषानीतियों का अनुकरण व प्रसार में अहम् भूमिका निभाती है। हिन्दी के प्रयोग तथा प्रधानता के आधार पर राजभाषा विभाग भारत सरकार द्वारा विभक्त किए गए तीन भौगोलिक क्षेत्रों में, हमारी संस्थान 'क' क्षेत्र में स्थित है। राजभाषा अधिनियम व राजभाषा नियम के अनुसार राजभाषा संबंधी कार्यो की समीक्षा तथा राजभाषा के प्रयोग को गति प्रदान करने हेतु संस्थान के निदेशक महोदय की अध्यक्षता में राजभाषा कार्यान्वयन समिति गठित है।

राजभाषा संबंधी कार्यकलापों की समीक्षा की गई तथा राजभाषा कार्यान्वयन में आनेवाली बाधाएँ एवं उनके निदान के उपायों पर चर्चा एवं सुझाव लिये गए। राजभाषा कार्यान्वयन समिति भारत सरकार के राजभाषा विभाग द्वारा निर्धारित वार्षिक कार्यक्रम के लक्ष्यों की प्राप्ति हेतु समुचित योजना को सुनिश्चित करती है तथा समय–समय पर किए गए की समीक्षा पूर्व मार्गदर्शन भी करती है।

हिंदी दिवस एवं हिंदी पखवाड़ा 2022

संस्थान में 14 सितम्बर 2022 को हिंदी दिवस के उद्‌घाटन समारोह के शुभारम्भ के साथ दिनांक 14-30 सितम्बर 2022 की अवधि में हिंदी पखवाड़ा का आयोजन किया गया, जिसमे संस्थान के निदेशक महोदय डॉ. अरुणव पट्टनायक ने सभा को संबोधित करते हुए हिंदी दिवस की बधाई दी, उपस्थित कर्मचारियों को कार्यालय का अधिकतम काम काज हिंदी में करने के लिए प्रेरित किया (चित्र 35)। संयुक्त निदेशक (शैक्षणिक) डॉ. विजय पाल भडाना एवं डॉ. सुजित कुमार बिशी ने हिंदी भाषा के सहजता व सरलता पर अपने मौलिक विचार सभा में रखे। राजभाषा प्रभारी श्री परितोष कुमार गुप्ता ने सभा में उपस्थित सभी को हिंदी पखवाड़े के दौरान आयोजित होने वाले विभिन्न कार्यक्रमों की रूप रेखा के बारे में अवगत कराया एवं प्रतिभागियों से भाग लें कर कार्यक्रम को सफल बनाने के लिए आग्रह किया।

पखवाड़े के दौरान विभिन्न प्रतियोगिताओं का आयोजन सफलतापूर्वक किया गया, जिसमें हिन्दी प्रारूप व टिप्पण लेखन, वाद विवाद प्रतियोगिता, आशुभाषण प्रतियोगिता, निबंध लेखन प्रतियोगिता, अन्ताक्षरी प्रतियोगिता इन सभी कार्यक्रम में केवल हिन्दी भाषा का ही प्रयोग किया गया। उक्त पखवाड़े में संस्थान के समस्त वैज्ञानिकगण, अधिकारीगण, कर्मचारीगण, विद्यार्थीगण इत्यादि ने बढ़ चढ़ कर भाग लिया।

समापन एवं पुरस्कार वितरण समारोह में निदेशक महोदय डॉ अरुणव पट्टनायक ने अध्यक्ष व मुख्य अतिथि के तौर पर पखवाड़े के दौरान आयोजित विभिन्न प्रतियोगिताओं के विजेताओं को मान्यवरों के करकमलों द्वारा पुरस्कृत किया गया। कार्यक्रम का संचालन प्रभारी राजभाषा श्री परितोष कुमार गुप्ता द्वारा किया गया।

चित्र 35: हिन्दी अधिकारी द्वारा राजभाषा संबंधित गतिविधियों का विवरण

TRAINING AND CAPACITY BUILDING

Details of training and workshop attended during 2022

S.N.	Name	Duration	Host Institute	Participants
1.	Advanced statistical techniques for data analysis using R"	03-15 Jan.	ICAR-Indian Institute of Rice Research, Hyderabad	Dr Kishor U. Tribhuvan Dr Madan Kumar Dr. Sudhir Kumar
2.	Biosecurity and Biosafety: Policies, Diagnostics, Phytosanitary Treatments and Issues" during	02-11, Aug.	ICAR-NBPGR, New Delhi	Dr. V P Bhadana
3.	RNA world: advance bioinformatics for deciphering regulatory molecules	03-09, Nov.	ICAR-Indian Agricultural Statistics Research Institute, New Delhi	Dr Kishor U. Tribhuvan
4	Advanced Analytical and simulation techniques in chemical engineering applications	21-27, Nov.	Department of chemical engineering, BIT MESRA, Ranchi	Dr Sujit Kumar Bishi Dr Madan Kumar
5.	New Crop Breeding Technologies	21, Nov. -11, Dec.	ICRISAT, Patancheru, Hyderabad	Dr Sudhir Kumar

MoUs SIGNED

- Shaheed Mahendra Karma Vishwavidyalaya, Bastar, Jagdalpur, Chhathisgarh on 22nd Jan. 2022
- ICAR- Indian Veterinary Research Institute (Deemed University) Izatnagar on 12th May 2022
- Amity Institute of Biotechnology - Amity University Jharkhand, Ranchi on 1st Nov. 2022

PARTICIPATION IN CONFERENCES/MEETINGS/ SEMINARS/SYMPOSIA DURING 2022

S. No.	Event	Venue	Period	Participants
1.	Climate Change Concerns: Challenges for Agriculture Sector and Food and Nutrition Security	Karnataka Agri-professional Association in collaboration with ICAR-Indian Institute of Millets Research, Hyderabad	14-15, May	Dr. V P Bhadana
2	Bilateral International Conference (ICEES-2022)	Khulna University, Khulna, Bangladesh.	19-20, Oct.	Dr.Biplab Sarkar
3	VIIth International Conference on "Global Research Initiatives for Sustainable Agriculture & Allied Sciences"	Birsa Agricultural University, Ranchi	21-23, Nov.	Dr Kishor U. Tribhuvan Dr Sujit Kumar Bishi Dr Madan Kumar Dr Sanjay Kumar Gupta Dr Sudhir Kumar
4	National Conference on Biotechnology for Sustainable Development and Human Welfare	Jamia Hamdard, New Delhi,	23-24, Nov.	Dr Sujit Kumar Bishi
5	National Symposium on Emerging Innovations in Plant Molecules for Achieving Food and Nutritional Security (EIPMAFNS)	Navsari Agricultural University, Navsari, Gujrat,	22-23, Sept.	Dr Sujit Kumar Bishi

PUBLICATIONS

Patent

1. Biplab Sarkar. A Roy Chowdhury, S Bhattacharjee, Arnab Sen, A Pattanayak (2022) Alcoholic Nano-silver having Anti-Viral and Anti-Biofilm Efficacy and Method of Preparation thereof (File no. TEMP/ E1/69397/2021- DEL).

Research/ Review Articles

1. Agarwal, S., Prasad, S., Kumar, R., Naskar, S., Chandra, S. and Agarwal, BK. (2022). Characterization of native chickens of Ranchi district of Jharkhand. Indian Journal of Animal Sciences 92(2):18–21.
2. Barman K, Konwar D, Sarma DK, Thomas R, Naskar S, Pegu SR, Banik S, Mohan NH, Tamuli MK, Kaushik Purabi, Rajkhowa S. 2022. Effect of supplementation of methionine chelated trace minerals on growth, nutrient utilization and blood profiles in crossbred (Hampshire X Ghungroo) finisher pigs. Animal Nutrition and Feed Technology. 22(1):31-39.
3. Choudhary, SB., Gurjar, SC., Singh, BK., Singh, DK., Sharma, HK., Horo, S., Kumari, N., Amrapali, S., Ahlawat, SP., Singh, K. (2022). Morphology and genic-SSRs-based diversity analysis and georeferencing of economic traits in natural populations of Jack (Artocarpus heterophyllus Lam.) from Eastern India. Scientia Horticulturae 295:110852.
4. Devi, YS., Pandey, A., Kumar, A., Rai, M., Tyagi, W., Aochen, C. (2022). Genetic variability and population structure analysis in ricebean (Vigna umbellata) genotypes from northeast India). Indian Journal of Genetics and Plant Breeding 82(4): 448-457.
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2. Singh, AK., Naskar, S., Ramteke, PW., Kumar, R. (2022). Nucleic Acid Sequence-Based Amplification (NASBA) methods and CRISPR/Cas13 system to detect pig viral diseases. Protocols for the Diagnosis of Pig Viral Diseases. Deb R et al. (Eds). Springer Protocols Handbooks. Pp. 151-157.

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3. Lal, SK., Kumari, R., Potam, P., Pattanayak, A., Pandey, A., Prasad, K., Kumar S., Kumar M. (2022) Multiple shoot regeneration in indica rice (*Oryza sativa.* L) genotypes. In Abstract, Proceeding Book of VIIth International Conference on "Global Research Initiatives for

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AWARDS AND RECOGNITIONS

1. Dr Biplab Sarkar, Principal Scientist, was awarded honorary fellow of the “Institute of Ecotoxicology and Environmental Sciences (IE&ES)”, India during bilateral international conference (ICCEES-2022) at the Khulna University, Bangladesh organized between 19-20 October, 2022
2. Dr Madan Kumar, Senior Scientist received ‘Scientist of the Year’ award for his outstanding contribution in the field of Plant Physiology in VIIth International Conference on "Global Research Initiatives for Sustainable Agriculture & Allied Sciences" organised by Astha foundation, Meerut during 21-23 November, 2022 at BAU, Ranchi.

3. Dr. Sanjay Kumar Gupta received the best oral presentation award in VIIth International Conference on "Global Research Initiatives for Sustainable Agriculture & Allied Sciences" organised by Astha foundation, Meerut during 21–23 November, 2022 at BAU, Ranchi.
4. Dr. Sudhir Kumar received ‘Excellence in Research Award’ for his outstanding contribution in the field of Genetics & Plant Breeding in VIIth International Conference on "Global Research Initiatives for Sustainable Agriculture & Allied Sciences" organised by Astha foundation, Meerut during 21–23 November, 2022 at BAU, Ranchi.

JOINING / TRANSFER / RETIREMENT

Dr. Sujay Rakshit,
Joined as the Director of ICAR-IIAB on 09th Dec. 2022

Dr. A. Pattanayak,
Principal Scientist and *Ex*-Director, ICAR-IIAB superannuated on 31st Dec. 2022

Dr. Sujatha TP,
Scientist (Agrl. Biotech.) relieved on 20th Aug. 2022 to join at ICAR-CTCRI on transfer

Dr. C. Chattopadhyay,
Principal Scientist (Plant Pathology.) relieved on 12th Aug. 2022 to join at ICAR-CRIJAF on transfer

ONGOING RESEARCH PROJECTS

Sl. No.	Project Title	Principal Invigilator
	School of Genomics and Molecular Breeding	
1.	Molecular breeding for the development of rice varieties with inbuilt resistance/tolerance to drought, low soil P, and blast.	Dr V.P. Bhadana
2.	Genome analysis, linkage mapping, and identification of gene(s) / QTLS for seed oil and protein content in winged bean (*Psophocarpus tetragonolobus* L.).	Dr B.K. Singh
3.	Genetic mapping of gene(s)/QTLs for photoperiod sensitivity in winged bean (*Psophocarpus tetragonolobus* L.)	Dr Kishor U. Tribhuvan
4.	Improvement of rice yield under low light intensity conditions	Dr Avinash Pandey
5.	Understanding the biochemical and molecular mechanism of L-DOPA and tannin biosynthesis in faba bean (*Vicia faba* L.)	Dr Sujit Kumar Bishi
6.	Identification of genes/QTLs responsible for zinc homeostasis in rice	Dr Madan Kumar
7.	Understanding the morpho-physiological and molecular mechanism of seed shattering in grain amaranths (*Amaranthus spp*.)	Dr Madan Kumar
8.	Ideotype breeding in horse gram for Jharkhand region	Dr Sudhir Kumar
9.	Molecular dissection of plant architecture traits in winged bean through mutagenesis and genomic approaches	Dr Sudhir Kumar
	Genetic Engineering	
10.	Molecular characterization of the Major Histocompatibility Complex (MHC) genes of indigenous pig (*Sus scrofa*).	Dr Soumen Naskar
11.	Investigating the role of purine degrading pathway genes of hemibiotroph fungal pathogens during host-pathogen interaction and their potential to confer disease resistance in maize	Dr S. K. Lal
	Molecular Diagnostics, Prophylactics and Nano-Biotechnology	
12.	Evaluating the nano-inspired degradation of aquatic pollutants with special reference to lac dye and jute retting wastewater	Dr Biplab Sarkar
13.	Evaluation of extrinsic and intrinsic parameters for sustainable breeding and culture of Clarias magur in captivity	Dr Sanjay Gupta
14.	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 biofloc system	Dr Sanjay Gupta

BUDGET ALLOCATION AND UTILIZATION (2022)

(Figure in lakhs)

Head	R.E. 2021-22 (Rs. in Lakhs)	Total Expenditure in Percentage	B.E. 2022-23 (Rs. in Lakhs)	Total Expenditure (Up to Dec-2022) in Percentage
Grants in Aid - General	454.00	100	200.00	80.78
Grants in Aid -(Capital)	1257.93	100	1000.00	64.98
TSP	65.25	100	25.00	66.60
NEH (General)	43.00	100	35.00	36.06
NEH (Capital)	30.51	100	--	--
SCSP (Capital)	150.00	100	100.00	10.00
SCSP (General)	50.00	100	100.00	52.06
Revenue Generated during 2022 : Rs. 4,63,247/-				

NODAL OFFICERS FOR INSTITUTE'S DIFFERENT PORTFOLIOS

Name of the Nodal Officer	Responsibilities
Dr. Avinash Pandey	Krishi Portal
Dr. Biplab Sarkar	Agriculture Technology Foresight Centre (ATFC), CPGRMS, CPIO/RTI, TSP
Dr. B K Singh	ITMU, ABI, PME, PMS, Permisnet-II, Innovation Excellence Indicators for Public Funded R & D Organizations Coordinated by SA to PM
Dr. S K Bishi	ARMS, Vigilance, HRD
Dr. Soumen Naskar	ICAR-MIS, ERP
Dr. Sudhir Kumar	Public Information Officer/RTI, SCSP, MGMG
Dr. S K Lal	Swatch Bharat Abhiyan
Dr. V P Bhadana	NEH, AEBAS
Mr S R Singh	GeM Purchase, Store
Mr. Paritosh Gupta	Rajbhasha Implementation

INFRASTRUCTURE DEVELOPMENT

Sl. No.	Name of the Work	Estimated Cost (Rs. In Lakhs)	Present status
CIVIL WORKS			
1.	Mess Building	352.22	Completed
2.	Boys' Hostel	852.39	Completed
3.	Girls' Hostel	852.39	Completed 85% construction; bathroom tiling, painting, plumbing and misc. work is in progress and likely to be completed by 30 Jun 2023
4.	Water Harvesting Structure of Site D	76.84	Completed
5.	Water Harvesting Structure of Site A	146.94	Digging work is completed
6.	Administrative/Institute Building	3584.99	90 % completed
7.	Vertical extension of Administrative/ Institute Building (from 12.6 meters to 30.6 meters –Laboratory side only)	1192.78	60 % completed
8.	Construction of Internal roads, Drainage, Water Supply and Electrical Lighting (Developmental works)	522.78	30% work completed
9.	Type-V Six Nos. staff residential quarters (One block with stilt parking)	630.88	30% work completed
10.	Overhead Water Tank (2 lakh litre capacity) in Farm A	148.11	Work just started
11.	Water Treatment Plant at Farm A	49.30	Tender process completed
12.	Boundary Wall and Security Room of Director's residence	19.98	Tender process completed
ELECTRICAL WORKS			
1.	Installation and commissioning of Lifts in Hostels (4 nos)	78.81	Tender is floated
2.	LT Feeder Panel, Electric Cables for charging different buildings Farm A	510.41	20 % completed


सावित्रीबाई फुले छात्रावास
SAVITRIBAI PHULE HOSTEL


ANNAPURNA MESS

NOTES

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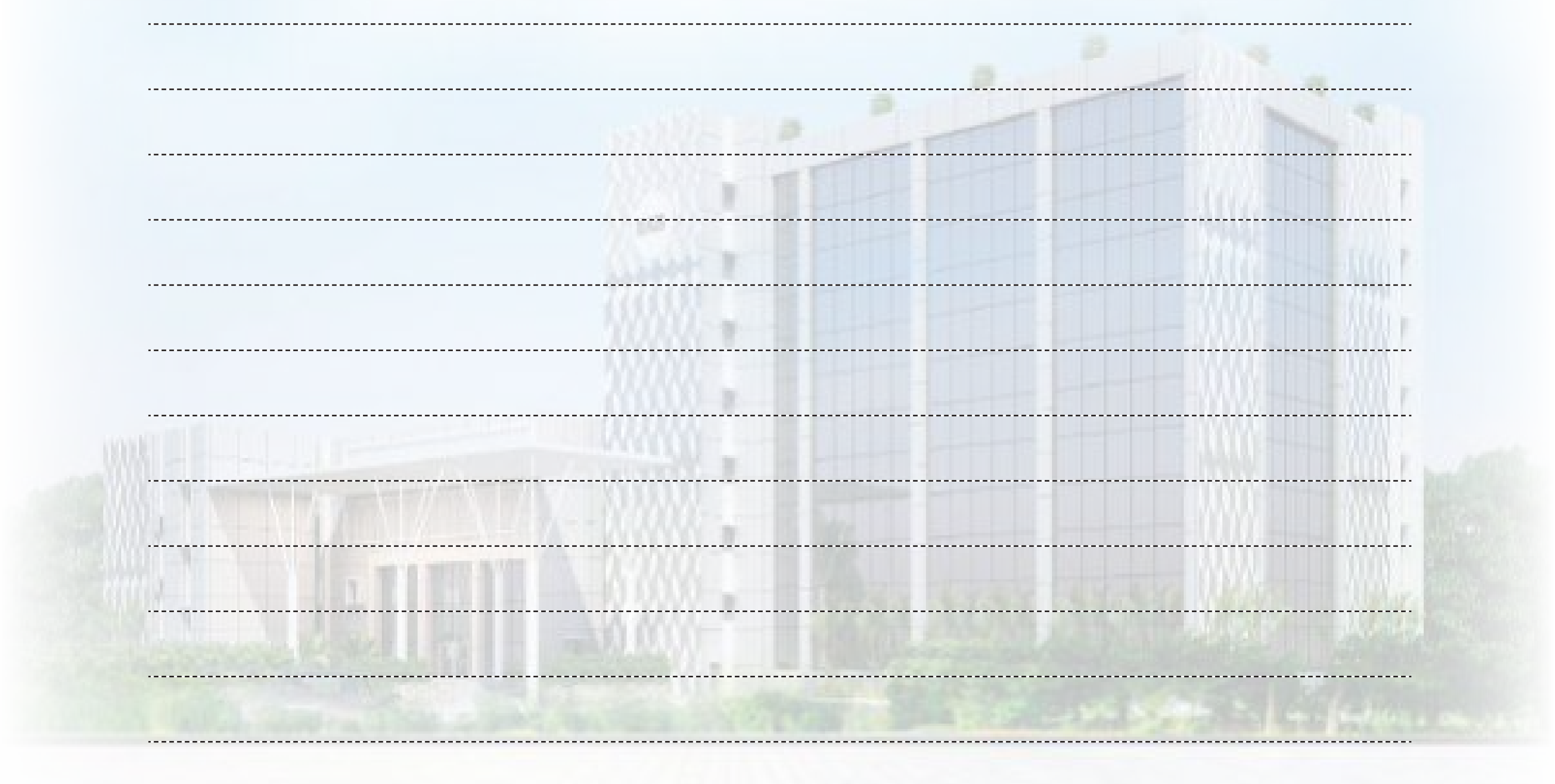

Unlocking the potential of Biotechnology through plant-animal-fish-microbe interface research and human resource development

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