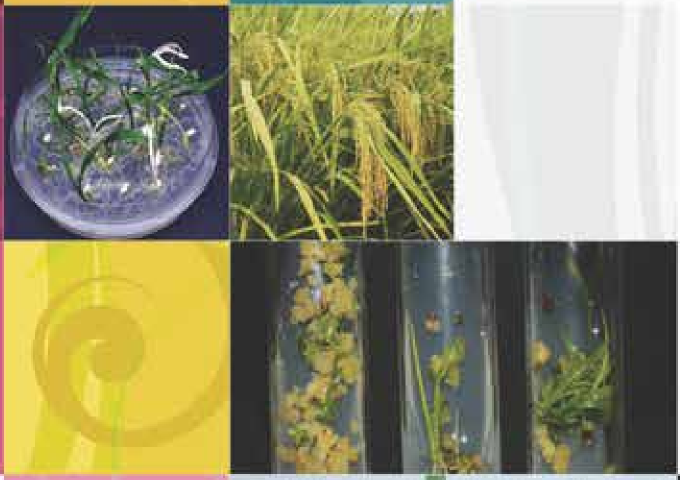

ANNUAL REPORT 2025

भाकृअनुप
ICAR

भाकृअनुप–केंद्रीय चावल अनुसंधान संस्थान
कटक, ओड़िशा
ICAR-Central Rice Research Institute
Cuttack, Odisha

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CRRI

वार्षिक प्रतिवेदन
Annual Report
2025

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ICAR

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कटक (ओडिशा) 753006, भारत

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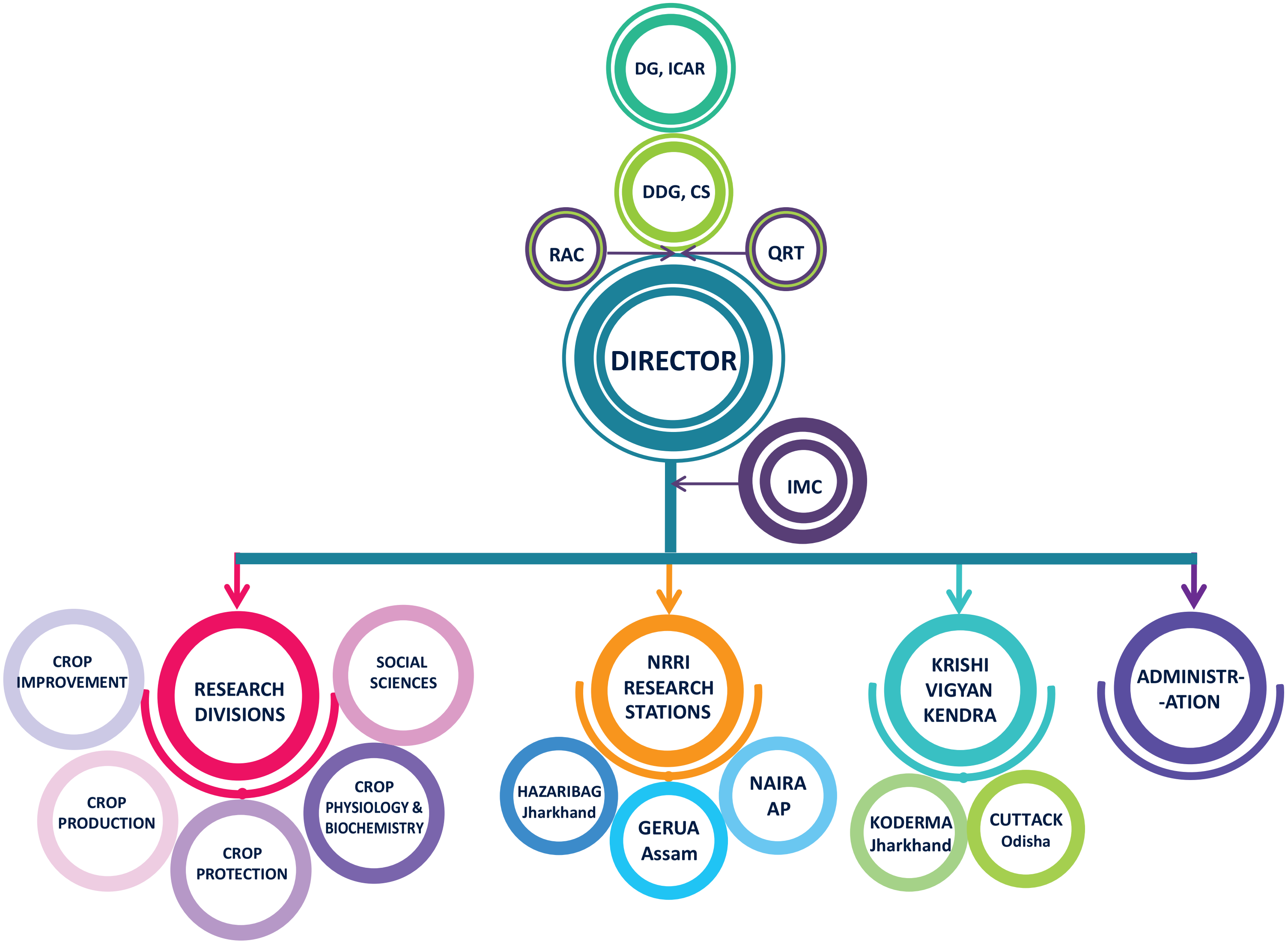
Contents

Organogram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ADMINISTR- -ATION

PREFACE

It gives me immense pleasure to present the *Annual Report 2025* of the **ICAR–Central Rice Research Institute, Cuttack**, encapsulating the major scientific, technological, and institutional achievements accomplished during the year.

The year 2025 has been particularly significant for the Institute. A total of **eight new rice varieties**, including **two hybrids**, were released and notified through CVRC and SVRC for cultivation in multiple states. Among them, **CR Dhan 812**, a herbicide-tolerant variety suited for direct-seeded rice (DSR) systems, marks an important milestone in addressing the challenge of weedy rice. In addition, **423 elite entries** were nominated under AICRP trials, and several promising lines were registered with PPV&FRA and ICAR-NBPGR, strengthening our national germplasm portfolio.

More than **2,000 germplasm accessions** were evaluated for trait discovery, and a **digital database of ~50,000 rice accessions** was developed and hosted online to facilitate efficient utilization of genetic resources. The Institute produced **17.89 quintals of nucleus seed of 134 varieties** and **471.0 quintals of breeder seed of 76 varieties**, along with **489.95 quintals of Truthfully Labeled (TL) seed**, significantly contributing to quality seed availability. Two patents and three non-varietal technologies were granted during the year, underscoring the Institute's leadership in advanced breeding, genome editing, and doubled haploid technologies.

In crop production and natural resource management, long-term experiments and precision nutrient management strategies enhanced input use efficiency, while microbial interventions, conservation agriculture, and climate modelling studies strengthened resilience in rice-based systems. Crop protection research led to the identification of novel QTLs and resistant genotypes against major pests and diseases, along with innovations in hyperspectral disease detection and bio-formulations. Advances were also made in abiotic stress tolerance, low glycaemic index rice, nutritional enhancement, and C4 rice research.

Socio-economic research, value-chain development, digital extension through *CRRI Barta*, mechanization studies, and policy-oriented groundwater vulnerability assessments further reinforced the Institute's commitment to sustainable and inclusive rice sector development.

These accomplishments are the result of the dedicated efforts of our scientists, technical staff, administrative personnel, and regional research stations working in close coordination with AICRP centres and partner institutions.

I express my profound gratitude to the **Director General, ICAR & Secretary, DARE**, for his visionary leadership and continuous encouragement. I sincerely acknowledge the invaluable guidance and support of the Deputy Directors General of Crop Science, Natural Resource Management, Agricultural Extension, Agricultural Engineering, and other divisions of ICAR. I also place on record my appreciation to the concerned Assistant Directors General for their constructive review, facilitation, and strategic direction in advancing our research and outreach programmes.

I gratefully acknowledge the support extended by ICAR Headquarters, the Ministry of Agriculture & Farmers Welfare, Government of India, State Agricultural Universities, collaborating institutions, and national and international partners.

I place on record my special appreciation to the **Publication Unit of ICAR-CRRI** for their meticulous efforts in compiling, editing, and designing this Annual Report 2025 in a comprehensive and timely manner.

I am confident that the scientific achievements and policy insights documented herein will further strengthen India's rice research ecosystem and contribute meaningfully to sustainable, climate-resilient, and nutrition-sensitive rice-based agri-food systems.

(G.A.K. Kumar)
Director, ICAR-Central Rice Research Institute

Executive Summary

The Crop Improvement Programme made significant advancements in 2025, marked by the development, release and notification of eight new rice varieties. The varieties namely, CR Dhan 812, CR Dhan 417 and one hybrid CR Sankar Dhan 706 were released by CVRC for multiple states and the varieties like CR Dhan 215, CR Dhan 325, CR Dhan 335, CR Dhan 912 and a hybrid CR Sankar Dhan 705 were released by SVRC, Odisha. In addition, 423 elite entries were nominated for evaluation under AICRP on Rice trials of 2025. Eight Varieties CR Dhan 312, CR Dhan 323, CR Dhan 414, CR Dhan 704, CR Dhan 707, CR Dhan 809, CR Dhan 324, CR Dhan 911 were submitted for registration in PPV&FRA. Two promising DH lines CR 4423-14 (INGR 25044): osmotic dehydration tolerance at seedling stage with higher shoot dry weight under severe osmotic stress (2%) and CR4423-17 (INGR 25005) with multiple abiotic stress tolerance such as osmotic, drought, salinity and with high anaerobic germination got registered in ICAR-NBPGR. The herbicide-tolerant rice variety CR Dhan 812 was notified for cultivation in multiple states which provides an effective solution for managing weedy rice in direct-seeded rice (DSR) systems. Two patents, one for its breakthrough innovation **'Systems and Methods for Targeted Genome Editing in Plants'**, centred on a miniature RNA-guided nuclease **TnpB (**Patent No. 570650) and another patent **'Vacuum based anther culture device and method of doubled haploid production'** (Patent No. 574471) were granted during 2025. Three non-varietal technologies were granted and certified by ICAR on 16th July, 2025. Those are i) DH technology titled 'Genotypic independent Androgenic Protocol in Indica rice for the development of doubled haploids', ii) Genome editing technology titled 'Novel Single Guide RNA scaffolds for efficient plant genome editing' and iii) 'Protocols for protoplast isolation and transfection in monocots and dicots with a pause point'. Extensive evaluation of more than 2,000 rice germplasm accessions and breeding lines was undertaken to strengthen trait discovery and varietal development. A digital database of ~50,000 rice germplasm accessions could be developed and hosted online, enabling efficient documentation, retrieval, and utilization of genetic resources for rice improvement by the researchers across the country. In response to the increasing demand for high-quality seed, 17.89 quintals of nucleus seed of 134 varieties and 471.0 quintals of breeder seed of 76 varieties were produced. Through participatory seed production, 489.95 quintals of Truthfully Labeled (TL) seed were produced. To maximise the effective utilization of genetic resources, a total of 464 rice germplasm accessions were supplied to researchers, including 295 accessions within the institute and 169 to external organizations. A wide range of trait-specific genetic resources was developed for targeted breeding. Lines carrying *Dro1*, *Dro3*, and *Pup1* were identified for deep rooting and phosphorus-use efficiency. Elite lines for direct-seeded rice (DSR) systems and aerobic conditions were identified based on early vigor and yield performance. Biofortified lines with high iron, zinc, and protein content were developed. The variety, Improved Chakhao derivatives possessing semi-dwarf stature, lodging resistance, and high antioxidant content were also developed. Significant progress was made in hybrid rice development and parental line improvement. The CMS line CRMS 61A was developed, and several maintainer and restorer lines were improved through introgression of key genes for BPH resistance, bacterial blight resistance, and herbicide tolerance. Several improved varieties and near-isogenic lines (NILs) with enhanced resistance and tolerance were identified and developed. Multiple Swarna NILs (PW 767-1, PW-773, PW-150, PW- 484, and SW-225) exhibited improved bacterial blight resistance and submergence tolerance. Similarly, herbicide-tolerant NILs and BPH-tolerant NILs of Pooja were identified and promoted in AICRIP trials. A substantial number of quantitative trait loci (QTLs) and genes associated with key agronomic traits were identified. More than 40 QTLs linked to important traits, including reproductive-stage salinity tolerance (spikelet sterility, grain number, panicle length, grain weight, and ion balance), submergence survival and elongation, bakanae disease resistance (qBK5.1), and yield-related traits (grains per panicle, panicle length, spikelet fertility, plant height, and grain yield), were identified through diverse mapping approaches. Genome-wide association studies further revealed 137 marker–trait associations and 234 significant SNPs for early vigour and yield traits. Expansion of A-genome markers to the other genomes of genus *Oryza* identified 240 and 81 transferable markers from *O. punctata* (BB) and *O. coarctata* (KKLL), respectively, with 42 markers common across AA, BB, and KKLL genomes. Interaction among *Sub1A*, *SNORKEL1*, *SNORKEL2*, and *sd1* genes was studied using 489 RILs, identifying 12 gene combinations and a minor QTL on chromosome 9 for submergence tolerance. The programme successfully utilized CRISPR–Cas9 to develop semi-dwarf, lodging-resistant lines of the aromatic landrace Nua-Kalajeera by targeted editing of the *OsSD1* gene, resulting in significant plant height reduction without compromising yield or grain quality. Advanced genome-editing platforms, including PAiD-Cas9 (AI-designed Cas9) and intronized TnpB-based editors, were developed and optimized to enhance editing efficiency, enabling applications such as gene knockout, base editing, and prime editing. These next-generation tools demonstrated comparable or improved performance over conventional Cas9 systems. Gene prospecting and epigenetic studies identified key genes associated with stress tolerance and yield in rice. Haplotype analysis of drought-responsive genes (*OsCYP72A32, OsNCX5.2, OsSPX2, OsSTA104, OsRING313, Os3BGlu6*) revealed superior alleles in tolerant genotypes such as NCS 901 A, H 15-23-DA, LOHAMBITRO, and MEJANES-2. Candidate genes for brown planthopper resistance (RPM1, LRR proteins, ZOS4-01) and potassium transporter genes for salinity tolerance were also identified.

The Crop Production Programme on enhancing productivity, sustainability and resilience of rice based production system integrates nutrient management, precision agronomy, weed and water management, microbial interventions, ecosystem services, vulnerability analysis, agro-waste management, value addition, farm mechanization approaches to enhance input use efficiency, rice productivity and environmental sustainability in rice-based systems. Calibration of GreenSeeker based nitrogen management in long-duration rice (Pooja, Swarna) demonstrated agronomic NUE of 21.2–24.3 kg grain kg^{-1} N, statistically *at par* with recommended nitrogen dose, enabling NDVI-based nitrogen topdressing strategy for rice. Transcriptomic analysis showed about 26% higher gene involvement in protein synthesis, signalling and metabolic pathways under nano-urea compared to conventional urea application. In 52-year long-term fertility experiment, metagenomic analysis revealed enrichment of glutamate synthetase (GlnA) and co-enrichment of nitrification (AmoCAB), DNRA (NrfAH), and denitrification (NirK) proteins under FYM-based systems. Rice-groundnut systems achieved the highest system productivity (11.89 t ha^{-1}), with organic farming outperforming natural farming (9.76 vs. 8.98 t ha^{-1}). The Vulnerability analysis of Bolangir and Dhenkanal districts showed total rainfall may not increase substantially but the intensity of single-day and extreme rainfall events are projected to rise. Green manuring with 75% of recommended dose of N significantly enhanced labile K and exchangeable K, improving soil K availability under both DSR and TPR systems. Seed treatment with *Trichoderma*, application of PSB with 50% recommended dose of P along with brown manuring and need-based mechanical weeding emerged as the best practice in terms of grain yield, net returns and B:C ratio. Mid-century (2035–2064) DSSAT simulations project rice yield declines up to 44.79% (SSP370) relative to 1986–2013, driven by rising Tmax/Tmin and shortened crop duration. Under RCP 4.5, Tmax is expected to rise 1.4–2.2°C (2050) and 1.9–2.9°C (2080), with increased rainfall in about 13 states, while reduced rainfall in 17 states by 2050 than the base period. GHG emissions from food production and consumption across India showed livestock products contributed disproportionately to total emissions (89.81%) relative to crop-based foods (10.19%), primarily due to enteric fermentation and feed production. CR-Composter reduced GHG emissions during straw decomposition by 25.6%, while bioethanol production from lime with microbial pre-treatment achieved 19–21% recovery efficiency. Microbial inoculant CRRI-Endo N delivered about 10% average yield increase with 25% nitrogen savings. AMF inoculation at nursery stage achieved 68–83% root colonization and enabled 25% phosphorus reduction while maintaining yields of 5.44–5.58 t ha^{-1}, comparable to recommended dose. Conservation agriculture with herbicide tolerant rice variety achieved 8.42 t ha^{-1} system productivity and >90% weed suppression, improving B:C ratio by 25% over DSR-ZT systems. In dose response study, moderate resistance to bispyribac sodium herbicide was recorded in 14 *Echinochloa colona* accessions. A solar-powered, automated bird scaring device that uses ultrasonic sound stimuli to was designed and developed to deter birds from rice fields with efficiency of > 90%. Projected groundwater recharge (2000–2024) showed +521 mm average *kharif* recharge offsetting −516 mm *rabi* depletion.

The Crop Protection Programme on Biotic stress management in rice addressed various aspects of insect, disease, and nematode pest management. Screening and identification of resistance sources is being carried out regularly against major biotic stresses. One genotype namely IC 316446 has been found moderately resistant against both BPH and WBPH. Marker-trait association of 152 genotypes found that, RM 1313 (*Bph 9*), and RM 7 (*Qbph3*) were significantly associated with BPH resistance. Similarly, Salkathi, ARC-5758, ARC-5768, ARC-10973, ARC-11434, CR Dhan-801, CR Dhan-310, RKM-6, Ramakrishna, CR Dhan 310, Champa-6, Kalia Lendi, Kalia Kaincha, Kala Mulia, Balangir Kala Krishna and PTB 33 were found moderately resistant to yellow stem borer. GWAS analysis of 115 diverse rice accessions against gall midge resistance identified 50 significant MTAs across all the rice chromosomes except chromosome 11. Promising varieties like Chandrama, CR Dhan 205, CR Dhan 311, Abhishek, few germplasm ARC collections like ARC 5759, ARC 5937, ARC 6033, ARC 6097 were found moderately resistant to sheath blight disease under artificial inoculated condition. While screening against false smut resistance, it was found that ARC collections namely, ARC- 5769, 5776, 5842, 5937, 5940, 5975, 5982, 6005, 6006, 6609, 6628, 7009, 7035, 7085, and NGB accession, IC466660, IC114371, IC435159, IC324679, IC379843, IC595241 were resistant under natural conditions in three locations. For sheath rot, the ARC lines like 9002, 9004, 9038, 9044, 9052, 9058, 9064, 9067, 9070, 9074, 9076, 9086, 9102, 9118, 9119, and 9136 were found resistant. Gene expression analysis in blast resistant and susceptible aromatic rice land races found that, significantly enhanced activities of key defense-related enzymes, including peroxidase, phenylalanine ammonia lyase, polyphenol oxidase, superoxide dismutase, and catalase observed in resistant genotypes compared with the susceptible genotypes. A novel QTL, qBK5.1 (gene id locus Os05g0518800) has been identified on chromosome 6 against bakanae disease from a bi-parental mapping population. Twenty one Odisha land races were found resistant to bacterial leaf blight disease. Varieties like Phalguni, CR Dhan 203, CR Dhan 209, Sahbhagidhan and Kalinga-II were moderately resistant to rice root knot nematode. Mitochondrial *COX2* gene-based genetic diversity analysis revealed substantial genetic variation among the yellow stem borer (YSB) populations across countries as well as within India.

Potassium silicate treatment enhanced phenol and lignin contents and increased the activity of defense-related enzymes across the tested rice varieties. An up-regulation of defense-related gene expression was also observed in the susceptible variety following potassium silicate amendment against both YSB and BPH, indicating enhanced induced resistance. Potassium silicate treated plants showed an increased presence of repellent compounds with altered levels of short-range attractants and oviposition-stimulant compounds, and these changes in volatile profiles might have contributed to the disrupted host-selection behavior of YSB females. The hyperspectral analysis of rice canopies using ASD data successfully identified sensitive spectral regions and optimal bands for early detection of rice brown spot (RBS) disease through a combination of derivative analysis, sensitivity analysis, continuum removal, and feature selection algorithms. The complete genome of *Streptomyces caeruleatus* S14 revealed that, the genome comprises 9,191 predicted protein-coding genes, 68 tRNA genes, and 6 rRNA genes, with a high G+C content of 71.03%. VOCs like p-Cymene, n-Pentadecanol, Heptadecane, n-Tridecan-1-ol, Dodecanal, and Tetradecane were found in higher quantities in the bacterial leaf blight resistant varieties. Rapid and simplified detection of Sclerotium rolfsii from seedling and soil has been developed using LAMP technique. Field evaluation of *Streptomyces*-based bioformulations for the management of rice blast found promising with reduced disease. Seed priming with Melatonin was found effective against rice root knot nematodes with enhanced defense enzyme activities. Lignin-degrading fungal strains isolated from biomixture for myco-remediation of pesticides and all the isolates exhibited tolerance to bispyribac-sodium (BS), carbendazim (CAR), and imidacloprid (IMI), across concentrations ranging from 1 to 10 ppm. Sublethal concentrations of acephate shortened developmental duration and enhanced fecundity, while higher concentrations lowered fecundity, reduced longevity.

A multiple abiotic stress-tolerant *aus* rice germplasm accession was registered with NBPGR as a unique genetic stock. Sixty lowland rice genotypes were evaluated under prolonged submergence and stagnant flooding. Genotypes tolerant to three weeks of submergence carried both *SUB1* and *SNORKEL* alleles, while genotypes possessing only *SNORKEL* alleles performed better with lower yield under stagnant flooding conditions. It was observed that the combined stress of saline water flooding was more damaging than individual stresses. Genotypes tolerant to flooding generally performed better under combined stress, while salt-tolerant genotypes were poor at tolerating saline water flooding stress. Potassium retention and flooding tolerance were key determinants of combined stress tolerance in rice. It was identified that root aerenchyma may act as a sink for sodium storage in rice roots and thus aid in salt tolerance. Application of melatonin (100 µM) was found to impart seedling stage drought tolerance. Fifty genotypes were evaluated for viviparous germination, out of which five genotypes were identified as tolerant. Previous studies indicate that lower PEP Km and reduced feedback inhibition were key evolutionary changes in C4 PEPC. Using prime editing tools, PEPC from C3-like to C4-like functionality was achieved. Edited PEPC lines showed reduced malate sensitivity, higher catalytic activity, and exhibited increased chlorophyll content, higher photosynthetic rate, and improved light use efficiency compared to the wild type. More than 100 genotypes were evaluated for greater biomass production ability and net assimilation rate, out of which two were identified for high yield and photosynthetic efficiency.

Rice genotypes with high resistant starch (RS) and low glycaemic index (GI) were evaluated to understand the roles of amylose and amylopectin structure in starch digestibility. Among 110 genotypes, significant variation in GI, RS, and amylose content was observed. Molecular analysis of three contrasting lines revealed that low-GI genotype IG 23 carried a promoter mutation in Pullulanase, enhancing its expression and promoting longer amylopectin chains, higher starch crystallinity, and increased RS. The impacts of different methods of rice grain processing were tested, and it was found that prolamin (a less digestible protein fraction) content increased significantly under different hydrothermal processing conditions in rice grain. Non-destructive estimation of proteins and different amino acid contents in rice grain was standardized with more than 90% accuracy of the prediction models. Pigmented and non-pigmented rice accessions were characterized for phytochemical composition and antioxidant activity. Two landraces were identified as promising for nutritional enhancement. The anthocyanin extraction method was standardized from pigmented rice, and *in vitro* incorporation of the extracted anthocyanin pigment during the cooking process substantially enhanced nutritional parameters of cooked rice. The effect of moisture content on stabilization efficiency and oil quality of rice bran was tested, and it was found that microwave stabilization is more effective when rice bran retains its normal moisture content.

The programme undertook an integrated outlook of capacity building, technology dissemination, and policy-oriented socioeconomic research to enhance farm income, sustainability, and resilience of rice stakeholders across India. Project RECAP strengthened stakeholders' socio-economic capacities through dissemination of rice technologies, training programmes, and development of rice value-chain models such as 'arORIce' to enhance export-oriented production and farm income, thereby promoting market-linked growth and value addition. The drudgery assessment project demonstrated women-friendly farm machineries and quantified their impact using the Human Physical Drudgery Index, showing significant reduction in physical strain and improved work efficiency among tribal women, thus advancing gender-inclusive mechanization and labour efficiency. A robust Kirkpatrick-based evaluation framework was developed to scientifically assess the effectiveness of farmer training programmes in terms of knowledge gain, behavioural change, and livelihood outcomes, ensuring systematic evaluation and continuous improvement of capacity-building interventions. The analysis of the CRRI e-extension platform 'CRRI Barta' evaluated audience engagement and effectiveness of video-based advisories across different crop stages, strengthening digital outreach and enhancing timely access to technical knowledge among stakeholders. These initiatives collectively improved technology dissemination, gender inclusivity, training effectiveness, and digital outreach to enhance the socio-economic well-being of rice stakeholders, while also creating a strong foundation for evidence-based policy research. In this context, the groundwater vulnerability assessment project analysed 472 districts using the IPCC framework and PCA-based index, revealing that nearly half of the districts face high to very high vulnerability to groundwater depletion, especially in Punjab, Haryana, and major rice-growing states, thereby highlighting critical sustainability challenges and the need for adaptive water management strategies. Under Project WINGS, rice-producing districts were classified based on productivity levels, showing that 26% of rice area falls under low productivity while about 54% lies at or above the national average, highlighting regional disparities and scope for targeted interventions to improve productivity and resource use efficiency. A rice yield forecasting project developed and validated statistical and machine learning models using weather variables for Bargarh district, with LASSO and Elastic Net emerging as the most accurate models for yield prediction, thereby strengthening scientific planning and risk management in rice production systems. The farm mechanization project in Odisha analysed machinery distribution, subsidy effectiveness, and gender inclusion, demonstrating increased access, improved equity, and significant cost savings due to DBT-enabled subsidy delivery, which contributed to enhanced efficiency and reduced cultivation costs. These projects collectively provided critical policy insights on water sustainability, productivity enhancement, yield forecasting, and mechanization, thereby strengthening rice sector planning, improving resource-use efficiency, and enhancing farm income and livelihood resilience in the rice-based production systems.

Programme 6 focused on developing climate-resilient rice technologies for rainfed upland, rainfed lowland, and coastal saline ecologies by promoting stress-tolerant varieties and integrated crop management practices for small and marginal farmers. CR Dhan 111 (DRV07) was released for direct-seeded conditions, and promising DSR and aerobic lines were identified, while genetic studies on anaerobic germination, seed vigour, nutrient stress, cold tolerance, and disease resistance supported resilient breeding efforts. Agronomic and pest management interventions, including brown manuring, nano urea, integrated weed management, and native biocontrol agents, were evaluated at CRURRS, Hazaribag. During 2024–25 and kharif 2025, RRLRRS, Gerua strengthened rainfed lowland production through germplasm conservation, evaluation of flood-tolerant varieties, and large-scale seed production, with CR Dhan 801 and CR Dhan 802 performing well under submergence. In the coastal ecosystem, the Regional Coastal Rice Research Station at Srikakulam produced quality breeder, nucleus, and TL seeds, and varietal evaluations showed performance comparable to local checks. Improved nitrogen management enhanced productivity in direct-seeded rice, while advanced pest forecasting models and the patented NoctiLens device supported effective pest surveillance. Validation of IPM practices in farmers' fields in Andhra Pradesh further improved yields and reduced pest incidence, demonstrating the overall success of integrated, climate-resilient rice production strategies.

कार्यकारी सारांश

फसल उन्नयन प्रभाग ने वर्ष 2025 में उल्लेखनीय प्रगति की, जिसमें आठ नई धान किस्मों का विकास, विमोचन एवं अधिसूचना शामिल है। इनमें CR धान 812, CR धान 417 तथा एक संकर किस्म CR संकर धान 706 को कई राज्यों के लिए केंद्रीय किस्म विमोचन समिति द्वारा जारी किया गया। इसी प्रकार, CR धान 215, CR धान 325, CR धान 335, CR धान 912 तथा संकर किस्म CR संकर धान 705 को राज्य किस्म विमोचन समिति, ओडिशा द्वारा जारी किया गया।

इसके अतिरिक्त, वर्ष 2025 में अखिल भारतीय समन्वित चावल उन्नयन कार्यक्रम के अंतर्गत परीक्षण हेतु 423 विशिष्ट प्रविष्टियाँ नामित की गई। आठ किस्में—CR धान 312, CR धान 323, CR धान 414, CR धान 704, CR धान 707, CR धान 809, CR धान 324 तथा CR धान 911—को पौध किस्म और कृषक अधिकार संरक्षण प्राधिकरण में पंजीकरण हेतु प्रस्तुत किया गया।

दो आशाजनक डबल्ड हैप्लॉइड (DH) किस्में—CR 4423-14 (INGR 25044), जिसमें अंकुर अवस्था पर ऑस्मोटिक निर्जलीकरण सहनशीलता तथा तीव्र ऑस्मोटिक तनाव (2%) में अधिक शूट ड्राई वेट पाया गया, और CR 4423-17 (INGR 25005), जिसमें ऑस्मोटिक, सूखा, लवणता तथा उच्च एनेरोबिक अंकुरण सहित बहु-अजैविक तनाव सहनशीलता पाई गई—को भा.कृ.अनु.प – राष्ट्रीय पादप आनुवंशिक संसाधन ब्यूरो में पंजीकृत किया गया।

इसके अलावा, खरपतवार-प्रतिरोधी धान किस्म CR धान 812 को कई राज्यों में खेती के लिए अधिसूचित किया गया, जो प्रत्यक्ष बुवाई धान (DSR) प्रणाली में खरपतवार धान के प्रभावी प्रबंधन के लिए एक कारगर समाधान प्रदान करती है।

वर्ष 2025 में दो पेटेंट प्राप्त हुए । इनमें पहला पेटेंट ‘पौधों में लक्षित जीनोम संपादन के लिए प्रणालियाँ और विधियाँ’ से संबंधित था, जो लघु RNA-निर्देशित न्यूक्लीएस TnpB पर आधारित है (पेटेंट संख्या 570650), तथा दूसरा पेटेंट ‘वैक्यूम आधारित एथर कल्चर डिवाइस और डबल्ड हैप्लॉइड प्रोडक्शन का तरीका’ (पेटेंट संख्या 574471) से संबंधित था।

इसके अतिरिक्त, 16 जुलाई 2025 को भारतीय कृषि अनुसंधान परिषद द्वारा तीन गैर-किस्मीय प्रौद्योगिकियों को स्वीकृति एवं प्रमाणन प्रदान किया गया। ये प्रौद्योगिकियाँ हैं—

i) DH तकनीक: ‘इंडिका चावल में डबल्ड हैप्लोइड्स के विकास के लिए जीनोटाइपिक स्वतंत्र एंड्रोजेनिक प्रोटोकॉल,

ii) जीन संपादन तकनीक: ‘पौधों के जीनोम को बेहतर तरीके से एडिट करने के लिए नए सिंगल गाइड RNA स्कैफोल्ड’, तथा

iii) ‘एकबीजपत्री और द्विबीजपत्री में प्रोटोप्लास्ट अलगाव और संक्रमण के लिए विराम बिंदु के साथ प्रोटोकॉल’।

गुणधर्म खोज एवं किस्म विकास को सुदृढ़ करने के लिए 2,000 से अधिक धान जर्मप्लाज्म प्रबिष्टियों एवं प्रजनन किस्मों का व्यापक मूल्यांकन किया गया।

लगभग 50,000 धान जर्मप्लाज्म प्रबिष्टियों का एक डिजिटल डेटाबेस विकसित कर ऑनलाइन होस्ट किया गया, जिससे देशभर के शोधकर्ताओं को धान सुधार के लिए आनुवंशिक संसाधनों का प्रभावी दस्तावेजीकरण, पुनर्प्राप्ति एवं उपयोग संभव हो सका।

उच्च गुणवत्ता वाले बीज की बढ़ती मांग को ध्यान में रखते हुए, 134 किस्मों के 17.89 क्विंटल नाभिकीय बीज तथा 76 किस्मों के 471.0 क्विंटल प्रजनक बीज का उत्पादन किया गया। सहभागी बीज उत्पादन के माध्यम से 489.95 क्विंटल बिशयसनीय (TL) बीज तैयार किए गए।

आनुवंशिक संसाधनों के अधिकतम एवं प्रभावी उपयोग के लिए कुल 464 धान जर्मप्लाज्म प्रबिष्टियों शोधकर्ताओं को उपलब्ध कराए गए, जिनमें 295 संस्थान के भीतर तथा 169 बाहरी संगठनों को प्रदान किए गए।

लक्षित प्रजनन के लिए गुण-विशेष आधारित आनुवंशिक संसाधनों की एक विस्तृत श्रृंखला विकसित की गई। गहरी जड़ प्रणाली एवं फॉस्फोरस उपयोग दक्षता के लिए Dro1, Dro3 तथा Pup1 जीन युक्त किस्मों की पहचान की गई।

प्रारंभिक वृद्धि शक्ति और उपज प्रदर्शन के आधार पर प्रत्यक्ष बुवाई धान (DSR) प्रणाली तथा एरोबिक परिस्थितियों के लिए उन्नत किस्मों की पहचान की गई। उच्च लौह, जिंक एवं प्रोटीन युक्त जैव-संपुष्ट (बायोफोर्टिफाइड) किस्मों का विकास किया गया।

इसके अलावा, अर्ध-बौने कद, गिरने के प्रति प्रतिरोध तथा उच्च एंटीऑक्सीडेंट गुणों वाली ‘इम्प्रूव्ड चकहाओ’ की व्युत्पन्न किस्मों का भी विकास किया गया।

संकर धान विकास तथा जनक किस्मों सुधार में उल्लेखनीय प्रगति हुई। CMS लाइन CRMS 61A का विकास किया गया तथा BPH प्रतिरोध, जीवाणु झुलसा रोग प्रतिरोध एवं खरपतवारनाशी सहनशीलता से जुड़े प्रमुख जीनों के अंतःस्थापन (इंट्रोग्रेशन) द्वारा कई मेंटेनर एवं रिस्टोरर किस्मों में सुधार किया गया।

उन्नत प्रतिरोध एवं सहनशीलता वाले कई सुधरे हुए किस्मों तथा नियर-आइसोजेनिक किस्मों (NILs) की पहचान कर उनका विकास किया गया। स्वर्णा की कई NILs (PW 767-1, PW-773, PW-150, PW-484 तथा SW-225) में जीवाणु झुलसा रोग के प्रति बेहतर प्रतिरोध तथा जलमग्नता सहनशीलता पाई गई।

इसी प्रकार, पूजा की खरपतवारनाशी-सहनशील NILs तथा BPH-सहनशील NILs की पहचान की गई और उन्हें अखिल भारतीय समन्वित चावल उन्नयन कार्यक्रम के परीक्षणों में प्रोत्साहित किया गया। इसके अलावा, प्रमुख कृषि-गुणों से संबंधित बड़ी संख्या में मात्रात्मक लक्षण स्थलों (QTLs) एवं जीनों की पहचान की गई। विविध मैपिंग विधियों के माध्यम से 40 से अधिक QTLs की पहचान की गई, जो महत्वपूर्ण लक्षणों से जुड़े थे। इनमें प्रजनन अवस्था पर लवणता सहनशीलता (स्पाइकलेट बाँझपन, दानों की संख्या, बाली की लंबाई, दाने का वजन एवं आयन संतुलन), जलमग्नता में जीवित रहने एवं बढ़वार क्षमता, बैकाने रोग प्रतिरोध (qBK5.1) तथा उपज से संबंधित लक्षण (प्रति बाली दानों की संख्या, बाली की लंबाई, स्पाइकलेट उर्वरता, पौधे की ऊँचाई एवं दाना उपज) शामिल हैं।

जीनोम-वाइड एसोसिएशन अध्ययन (GWAS) से प्रारंभिक वृद्धि शक्ति और उपज लक्षणों के लिए 137 मार्कर–लक्षण संबंध तथा 234 महत्वपूर्ण SNPs की भी पहचान हुई।

इसके अलावा, Oryza वंश के अन्य जीनोमों में A-जीनोम मार्करों के विस्तार से O. punctata (BB) से 240 तथा O. coarctata (KKLL) से 81 स्थानांतरित होने योग्य मार्करों की पहचान की गई, जिनमें से 42 मार्कर AA, BB और KKLL जीनोमों में समान पाए गए।

489 रिकॉम्बिनेंट इनब्रेड किस्मों (RILs) का उपयोग करते हुए Sub1A, SNORKEL1, SNORKEL2 तथा sd1 जीनों के बीच अंतःक्रिया का अध्ययन किया गया, जिससे जलमग्नता सहनशीलता के लिए 12 जीन संयोजनों तथा गुणसूत्र 9 पर एक लघु QTL की पहचान हुई।

कार्यक्रम के अंतर्गत CRISPR–Cas9 तकनीक का सफलतापूर्वक उपयोग कर सुगंधित देशी किस्म Nua-Kalajeera में OsSD1 जीन के लक्षित संपादन द्वारा अर्ध-बौनी एवं गिरने के प्रति प्रतिरोधी किस्मों विकसित की गई। इससे उपज और दाना गुणवत्ता से समझौता किए बिना पौधे की ऊँचाई में उल्लेखनीय कमी आई।

संपादन दक्षता बढ़ाने के लिए उन्नत जीन-संपादन प्लेटफॉर्म विकसित एवं अनुकूलित किए गए, जिनमें PAiD-Cas9 (AI-डिज़ाइन किया गया Cas9) तथा इंट्रोनाइज्ड TnpB-आधारित एडिटर शामिल हैं। इन प्लेटफॉर्मों से जीन नॉकआउट, बेस एडिटिंग तथा प्राइम एडिटिंग जैसे अनुप्रयोग संभव हुए। इन नवीन उपकरणों ने पारंपरिक Cas9 प्रणालियों की तुलना में समान या बेहतर प्रदर्शन दिखाया।

जीन प्रॉस्पेक्टिंग एवं एपिजेनेटिक अध्ययनों के माध्यम से धान में तनाव सहनशीलता और उपज से संबंधित प्रमुख जीनों की पहचान की गई। सूखा-संवेदनशील जीनों (OsCYP72A32, OsNCX5.2, OsSPX2, OsSTA104, OsRING313, Os3BGlu6) के हैप्लोटाइप विश्लेषण से NCS 901 A, H 15-23-DA, LOHAMBITRO तथा MEJANES-2 जैसे सहनशील जीनोटाइपों में श्रेष्ठ एलील पाए गए।

इसके अतिरिक्त, ब्राउन प्लांट हॉपर प्रतिरोध (RPM1, LRR प्रोटीन, ZOS4-01) तथा लवणता सहनशीलता के लिए पोटैशियम ट्रांसपोर्टर जीनों की भी पहचान की गई।

फसल उत्पादन प्रभाग का उद्देश्य धान-आधारित उत्पादन प्रणाली में उत्पादकता, स्थिरता एवं लचीलापन बढ़ाना है। इसके अंतर्गत पोषक तत्व प्रबंधन, सटीक कृषि, खरपतवार एवं जल प्रबंधन, सूक्ष्मजीव हस्तक्षेप, पारिस्थितिकी तंत्र सेवाएँ, संवेदनशीलता विश्लेषण, कृषि-अपशिष्ट प्रबंधन, मूल्य संवर्धन तथा कृषि यंत्रीकरण जैसी विधियों को एकीकृत किया गया, जिससे इनपुट उपयोग दक्षता, धान उत्पादकता और पर्यावरणीय स्थिरता में वृद्धि हो सके।

दीर्घ अवधि वाली धान किस्मों (पूजा, स्वर्णा) में ग्रीनसीकर आधारित नाइट्रोजन प्रबंधन के अंशांकन से 21.2–24.3 किग्रा दाना प्रति किग्रा नाइट्रोजन की कृषि उपयोग दक्षता (NUE) प्राप्त हुई, जो अनुशंसित नाइट्रोजन मात्रा के सांख्यिकीय रूप से समान थी। इससे NDVI-आधारित नाइट्रोजन टॉप-ड्रेसिंग रणनीति को अपनाने में सहायता मिली। ट्रांसक्रिप्टोमिक विश्लेषण से यह पाया गया कि पारंपरिक यूरिया की तुलना में नैनो-यूरिया के उपयोग से प्रोटीन संश्लेषण, सिग्नलिंग तथा चयापचय मार्गों में जीनों की भागीदारी लगभग 26% अधिक रही। 52 वर्षों के दीर्घकालीन उर्वरता प्रयोग में किए गए मेटाजीनोमिक विश्लेषण से गोबर खाद आधारित प्रणालियों में ग्लूटामेट सिंथेटेज (GlnA) तथा नाइट्रीफिकेशन (AmoCAB), DNRA (NrfAH) और डिनाइट्रीफिकेशन (NirK) प्रोटीनों का सह-समृद्धिकरण पाया गया।

धान–मूंगफली प्रणाली में सर्वाधिक प्रणाली उत्पादकता (11.89 टन प्रति हेक्टेयर) प्राप्त हुई, जिसमें जैविक खेती ने प्राकृतिक खेती की तुलना में बेहतर प्रदर्शन किया (9.76 बनाम 8.98 टन प्रति हेक्टेयर)।

बलांगीर और ढेंकानाल जिलों की संवेदनशीलता विश्लेषण से यह स्पष्ट हुआ कि कुल वर्षा में बहुत अधिक वृद्धि की संभावना नहीं है, लेकिन एक ही दिन में होने वाली भारी वर्षा तथा अत्यधिक वर्षा घटनाओं की तीव्रता में वृद्धि होने का अनुमान है। विशेष रूप से, बलांगीर और ढेंकानाल जिलों में चरम वर्षा की घटनाएँ बढ़ने की संभावना जताई गई है। अनुशंसित नाइट्रोजन मात्रा के 75% के साथ हरी खाद के उपयोग से लैबाइल पोटाश तथा विनिमेय पोटाश में उल्लेखनीय वृद्धि हुई, जिससे DSR और TPR दोनों प्रणालियों में मृदा में पोटाश की उपलब्धता में सुधार हुआ।

बीज उपचार में ट्राइकोडर्मा का उपयोग, फॉस्फोरस की 50% अनुशंसित मात्रा के साथ PSB का प्रयोग, ब्राउन मैन्यूरिंग तथा आवश्यकता आधारित यांत्रिक निराई को दाना उपज, शुद्ध लाभ और लाभ–लागत अनुपात (B:C) की दृष्टि से सर्वोत्तम प्रबंधन पद्धति के रूप में पहचाना गया।

मध्य-शताब्दी (2035–2064) के DSSAT सिमुलेशन के अनुसार, 1986–2013 की तुलना में SSP370 परिदृश्य में धान की उपज में अधिकतम 44.79% तक गिरावट का अनुमान है, जिसका मुख्य कारण अधिकतम एवं न्यूनतम तापमान (Tmax/Tmin) में वृद्धि तथा फसल अवधि में कमी है।

RCP 4.5 परिदृश्य के अंतर्गत, Tmax में वर्ष 2050 तक 1.4–2.2°C तथा वर्ष 2080 तक 1.9–2.9°C वृद्धि होने की संभावना है। साथ ही, लगभग 13 राज्यों में वर्षा बढ़ने तथा 2050 तक 17 राज्यों में आधार अवधि की तुलना में वर्षा घटने का अनुमान लगाया गया है।

भारत में खाद्य उत्पादन एवं उपभोग से होने वाले ग्रीनहाउस गैस (GHG) उत्सर्जन के विश्लेषण से यह पाया गया कि पशुपालन उत्पादों का कुल उत्सर्जन में अनुपातहीन रूप से अधिक योगदान (89.81%) रहा, जबकि फसल-आधारित खाद्य पदार्थों का योगदान केवल 10.19% था। इसका मुख्य कारण जुगाली प्रक्रिया (एंटरिक फर्मेंटेशन) तथा पशु आहार उत्पादन है। यह प्रवृत्ति पूरे भारत में देखी गई।

सीआर-कंपोस्टर के उपयोग से पराली अपघटन के दौरान ग्रीन हाउस गैस उत्सर्जन में 25.6% की कमी आई, जबकि सूक्ष्मजीवी पूर्व-उपचार के साथ चूने से जैव-एथेनॉल उत्पादन में 19–21% पुनर्प्राप्ति दक्षता प्राप्त हुई। सूक्ष्मजीवी इनोकुलेंट CRRI-Endo N के प्रयोग से औसतन लगभग 10% उपज वृद्धि हुई तथा 25% नाइट्रोजन की बचत संभव हुई। नर्सरी अवस्था में AMF इनोकुलेशन से 68–83% जड़ उपनिवेशण प्राप्त हुआ और 25% फॉस्फोरस की बचत के साथ 5.44–5.58 टन प्रति हेक्टेयर की उपज बनी रही, जो अनुशंसित मात्रा के समान थी। खरपतवारनाशी-सहनशील धान किस्म के साथ संरक्षण कृषि अपनाने से 8.42 टन प्रति हेक्टेयर प्रणाली उत्पादकता प्राप्त हुई तथा 90% से अधिक खरपतवार नियंत्रण संभव हुआ, जिससे DSR-ZT प्रणालियों की तुलना में लाभ–लागत अनुपात में 25% की वृद्धि हुई। डोज-रिस्पॉन्स अध्ययन में *Echinochloa colona* की 14 प्रबिष्टियों में बिसपाइरिबैक-सोडियम खरपतवारनाशी के प्रति मध्यम स्तर का प्रतिरोध दर्ज किया गया। धान खेतों में पक्षियों को भगाने के लिए अल्ट्रासोनिक ध्वनि पर आधारित एक सौर-ऊर्जा चालित स्वचालित उपकरण का डिजाइन एवं विकास किया गया, जिसकी प्रभावशीलता 90% से अधिक पाई गई। वर्ष 2000–2024 के दौरान अनुमानित भूजल पुनर्भरण से यह स्पष्ट हुआ कि खरीफ मौसम में औसतन +521 मिमी पुनर्भरण हुआ, जिसने रबी मौसम में −516 मिमी की कमी की भरपाई की।

धान में जैविक तनाव प्रबंधन पर फसल सुरक्षा कार्यक्रम में कीट, रोग और नेमाटोड कीट प्रबंधन के विभिन्न पहलुओं को शामिल किया गया है। प्रमुख जैविक तनावों के विरुद्ध प्रतिरोधक क्षमता के स्रोतों की स्क्रीनिंग और पहचान नियमित रूप से की जा रही है। एक जीनोटाइप, IC 316446, BPH और WBPH दोनों के प्रति मध्यम रूप से प्रतिरोधी पाया गया है। 152 जीनोटाइपों के मार्कर-लक्षण संबंध से पता चला है कि RM 1313 (Bgh 9) और RM 7 (Qoph3) BPH प्रतिरोधक क्षमता से महत्वपूर्ण रूप से जुड़े हुए हैं। इसी प्रकार, सालकाठी, एआरसी-5758, एआरसी-5768, एआरसी-10973, एआरसी-11434, सीआर धान-801, सीआर धान-310, आरकेएम-6, रामकृष्ण, सीआर धान 310, चंपा-6, कालिया लेंडी, कालिया कैंची, काला मुलिया, बलांगित काला कृष्णा और पीटीबी 33 पीले तना छेदक के प्रति मध्यम रूप से प्रतिरोधी पाए गए हैं। गॉल मिज के प्रति प्रतिरोधकता हेतु 115 विविध चावल किस्मों के जीडब्ल्यूएस विश्लेषण में गुणसूत्र 11 को छोड़कर सभी चावल गुणसूत्रों में 50 महत्वपूर्ण एमटीए की पहचान की गई। चंद्रमा, सीआर धान 205, सीआर धान 311, अभिषेक जैसी आशाजनक किस्में और एआरसी 5759, एआरसी 5937, एआरसी 6033, एआरसी 6097 जैसे कुछ जर्मप्लाज्म संग्रह कृत्रिम रूप से संक्रमित परिस्थितियों में शीथ एलाइट रोग के प्रति मध्यम रूप से प्रतिरोधी पाए गए। आभासी कंड झूठे स्मट प्रतिरोध के खिलाफ स्क्रीनिंग करते समय, यह पाया गया कि एआरसी संग्रह, अर्थात् एआरसी-5769, 5776, 5842, 5937, 5940, 5975, 5982, 6005, 6006, 6609, 6628, 7009, 7035, 7085, और एनजीबी अभिगम, आईसी466660, आईसी114371, आईसी435159, आईसी324679, आईसी379843, आईसी595241, तीन स्थानों पर प्राकृतिक परिस्थितियों में प्रतिरोधी थे। शीथ रॉट के लिए, ARC की किस्में जैसे 9002, 9004, 9038, 9044, 9052, 9058, 9064, 9067, 9070, 9074, 9076, 9086, 9102, 9118, 9119 और 9136 प्रतिरोधी पाई गई। ब्लास्ट प्रतिरोधी और संवेदनशील सुगंधित चावल की देसी किस्मों में जीन अभिव्यक्ति विश्लेषण से पता चला कि, संवेदनशील किस्मों की तुलना में प्रतिरोधी किस्मों में पेरोक्सीडेज, फेनिलएलनिन अमोनिया लाइगैस, पॉलीफेनोल ऑक्सीडेज, सुपरऑक्साइड डिसम्यूटेज और कैटालेज सहित प्रमुख डिफेनाग-संबंधित एंजाइमों की गतिविधि में उल्लेखनीय वृद्धि देखी गई। एक द्वी-जननीय मानचित्रण आबादी से बकाने रोग के विरुद्ध गुणसूत्र 6 पर एक नया QTL, qBK5.1 (जीन आईडी लोकस Os05g0518800) की पहचान की गई है। ओडिशा की इक्कीस स्थानीय किस्में जीवाणु-जनित पत्ती झुलसा रोग के प्रति प्रतिरोधी पाई गई। फाल्गुनी, सीआर. धान 203, सीआर. धान 209, सब्भागिधान और कलिंगा-II जैसी किस्में चावल की जड़ में गांठ पैदा करने वाले नेमाटोड के प्रति मध्यम रूप से प्रतिरोधी थीं। माइटोकॉन्ड्रियल COX2 जीन पर आधारित आनुवंशिक विविधता विश्लेषण से पता चला कि पीले तने के छेदक (YSB) की आबादी में विभिन्न देशों के साथ-साथ भारत के भीतर भी पर्याप्त आनुवंशिक भिन्नता पाई जाती है।

पोटेशियम सिलिकेट उपचार से परीक्षण की गई सभी चावल की किस्मों में फिनोल और लिग्निन की मात्रा में वृद्धि हुई और रक्षा संबंधी एंजाइमों की गतिविधि भी बढ़ी। वाईएसबी और बीपीएच दोनों के विरुद्ध पोटेशियम सिलिकेट के प्रयोग के बाद संवेदनशील किस्म में रक्षा संबंधी जीन अभिव्यक्ति में वृद्धि देखी गई, जो बढ़ी हुई प्रेरित प्रतिरोधक क्षमता को दर्शाती है। पोटेशियम सिलिकेट से उपचारित पौधों में विकर्षक यौगिकों की उपस्थिति बढ़ी हुई पाई गई, साथ ही अल्प-श्रेणी के आकर्षण और ग्लाइपोजिशन-उत्तेजक यौगिकों का स्तर भी परिवर्तित हुआ। वाष्पशील प्रोफाइल में इन परिवर्तनों ने वाईएसबी मादाओं के मेजबान-चयन व्यवहार को बाधित करने में योगदान दिया होगा। एएसडी डेटा का उपयोग करके चावल की पत्तियों के हाइपरस्पेक्ट्रल विश्लेषण ने व्युत्पन्न विश्लेषण, संवेदनशीलता विश्लेषण, निरंतरता निष्कासन और विशेषता चयन एल्गोरिदम के संयोजन के माध्यम से चावल के भूरे धब्बे (आरबीएस) रोग का शीघ्र पता लगाने के लिए संवेदनशील स्पेक्ट्रल क्षेत्रों और इष्टतम बैंडों की सफलतापूर्वक पहचान की। स्ट्रेप्टोमाइसिस कोरुलिएटस, S14 के संपूर्ण जीनोम से पता चला है कि इसमें 9,191 अनुमानित प्रोटीन-कोडिंग जीन, 68 टीआरएनए जीन और 6 आईआरएनए जीन शामिल हैं, जिसमें 71.03% की उच्च जी-सी सामग्री है। पी-साइमीन जैसे वीओसी, एन-पेंटाडेकेनॉल, हेप्टाडेकेन, एन-ट्राइडेकन-1-ओल, डोडेकेनल और टेट्राडेकेन जीवाणु पत्ती झुलसा रोग प्रतिरोधी किस्मों में अधिक मात्रा में पाए गए। एलएएमपी तकनीक का उपयोग करके अंकुर और मिट्टी से स्क्लेरोटियम रोल्फसी की तीव्र और सरलीकृत पहचान विकसित की गई है। चावल के झुलसा रोग के प्रबंधन के लिए स्ट्रेप्टोमाइसिस-आधारित बायोफॉर्मूलेशन का क्षेत्र मूल्यांकन रोग में कमी के साथ आशाजनक पाया गया। मेलाटोनिन के साथ बीज प्राइमिंग चावल के रूट नॉट नेमाटोड के खिलाफ प्रभावी पाया गया और इससे रक्षा एंजाइम गतिविधियों में वृद्धि हुई। कीटनाशकों के माइको-उपचार के लिए बायोमिक्सचर से लिग्निन-अपघटनकारी कवक उपभेदों को अलग किया गया और सभी पृथकों ने 1 से 10 पीपीएम तक की सांद्रता में बिस्पाइरिबैग-सोडियम (बीएस), सरबेंडाज़िम (सीएआर) और इमिडाक्लोप्रिड (आईएमआई) के प्रति सहनशीलता प्रदर्शित की। एसिफेट की उपघातक सांद्रता ने विकास की अवधि को कम किया और प्रजनन क्षमता को बढ़ाया, जबकि उच्च सांद्रता ने प्रजनन क्षमता को कम किया और जीवनकाल को घटाया।

एक बहुआयामी अजैविक तनाव-सहिष्णु (एनजी) चावल जीनोप्लाज्म प्रबिष्टि को एनईपीजीआर में एक अद्वितीय आनुवंशिक स्टॉक के रूप में पंजीकृत किया गया था। साठ निचलीभूमि मैदानी चावल जीनोटाइपों का मूल्यांकन लंबे समय तक जलमग्नता और स्थिर बाढ़ की स्थिति में किया गया। तीन सप्ताह तक जलमग्नता सहन करने वाले जीनोटाइपों में SUBI और SNORKEL दोनों एलील मौजूद थे, जबकि केवल SNORKEL एलील वाले जीनोटाइपों ने स्थिर बाढ़ की स्थिति में कम उपज के साथ बेहतर प्रदर्शन किया। यह देखा गया कि लबण खारे पानी की बाढ़ का संयुक्त तनाव व्यक्तिगत तनावों की तुलना में अधिक हानिकारक था। बाढ़ सहन करने वाले जीनोटाइपों ने आम तौर पर संयुक्त तनाव में बेहतर प्रदर्शन किया, जबकि लबण सहन करने वाले जीनोटाइप लबण पानी की बाढ़ के तनाव को सहन करने में कमजोर थे। पोटेशियम प्रतिधारण और बाढ़ सहनशीलता चावल में संयुक्त तनाव सहनशीलता के प्रमुख निर्धारक थे। यह पाया गया कि जड़ एक्रेसीज़ना चावल की जड़ों में सोडियम भंडारण के लिए एक सिंक के रूप में कार्य कर सकती है और इस प्रकार नमक सहनशीलता में सहायता कर सकती है। मेलाटोनिन (100 μM) के प्रयोग से अंकुरों में वृद्धि पाई गई। चरणबद्ध सूखा सहिष्णुता का परीक्षण किया गया। सजीवप्रजक अंकुरण के लिए पचास जीनोटाइप का मूल्यांकन किया गया, जिनमें से पाँच जीनोटाइप को सहिष्णु पाया गया। पिछले अध्ययनों से संकेत मिलता है कि निम्न PEP Km और कम प्रतिक्रिया अवरोध C4 PEPC में प्रमुख विकासवादी परिवर्तन थे। प्राइम एडिटिंग टूल्स का उपयोग करके, C3-जैसे से C4-जैसे कार्यक्षमता वाले PEPC प्राप्त किए गए। संपादित PEPC किस्मों ने जंगली प्रकार की तुलना में मैलेट संवेदनशीलता में कमी, उच्च उत्प्रेरक गतिविधि, क्लोरोफिल मात्रा में वृद्धि, उच्च प्रकाश संश्लेषण दर और बेहतर प्रकाश उपयोग दक्षता प्रदर्शित की। 100 से अधिक जीनोटाइप का मूल्यांकन बायोनास उत्पादन क्षमता और शुद्ध एसिनुलेशन दर के लिए किया गया, जिनमें से दो को उच्च उपज और प्रकाश संश्लेषण दक्षता के लिए चुना गया। उच्च प्रतिरोधी स्टार्च (RS) और कम ग्लाइसेमिक इंडेक्स (GI) वाले चावल के जीनोटाइप का मूल्यांकन स्टार्च पाचन क्षमता में एमाइलोज और एमाइलोपेक्टिन संरचना की भूमिका को समझने के लिए किया गया। 110 जीनोटाइपों में, GI, RS और एमाइलोज की मात्रा में महत्वपूर्ण भिन्नता देखी गई। तीन विपरीत जीनोटाइपों के आणविक विश्लेषण से पता चला कि कम-GI जीनोटाइप IG 23 में पुलोलानेज में एक प्रमोटर गतिविधि होती है, जो इसकी अभिव्यक्ति को बढ़ाती है और एमाइलोपेक्टिन श्रृंखलाओं की लंबाई, उच्च स्टार्च क्रिस्टलीयता और बढ़े हुए RS को बढ़ावा देती है। चावल के दाने के प्रसंस्करण की विभिन्न विधियों के प्रभावों का परीक्षण किया गया और पाया गया कि चावल के दानों में विभिन्न हाइड्रोथर्मल प्रसंस्करण स्थितियों के तहत प्रोलासिन (एक कम पचने योग्य प्रोटीन अंश) की मात्रा में उल्लेखनीय वृद्धि हुई। चावल के दाने में प्रोटीन और विभिन्न अमीनो एसिड की मात्रा का गैर-विनाशकारी अनुमान 90% से अधिक सटीकता वाले पूर्वानुमान मॉडल के साथ मानकीकृत किया गया।

रंजित चावल की किस्मों की फाइटोकेमिकल संरचना और एंटीऑक्सीडेंट गतिविधि का अध्ययन किया गया। दो देसी किस्मों को पोषण बढ़ाने में कारगर पाया गया। रंजित चावल से एंथोसायनिन निकालने की विधि को मानकीकृत किया गया, और खाना पकाने की प्रक्रिया के दौरान निकाले गए एंथोसायनिन वर्णक को मिलाने से पके हुए चावल के पोषण संबंधी मापदंडों में काफी सुधार हुआ। चावल की भूसी की स्थिरीकरण क्षमता और तेल की गुणवत्ता पर नमी की मात्रा के प्रभाव का परीक्षण किया गया, और यह पाया गया कि जब चावल की भूसी में सामान्य नमी की मात्रा बनी रहती है तो माइक्रोवेव स्थिरीकरण अधिक प्रभावी होता है।

इस प्रभाग ने भारत भर में चावल उत्पादकों की आय, स्थिरता और लचीलेपन को बढ़ाने के लिए क्षमता निर्माण, प्रौद्योगिकी प्रसार और नीति-उन्मुख सामाजिक-आर्थिक अनुसंधान के एकीकृत उपाय को अपनाया। परियोजना RECAP ने चावल प्रौद्योगिकियों के प्रसार, प्रशिक्षण कार्यक्रमों और 'atQBIce' जैसे चावल मूल्य-श्रृंखला मॉडल के विकास के माध्यम से उत्पादकों की सामाजिक-आर्थिक क्षमताओं को मजबूत किया, जिससे निर्यात-उन्मुख उत्पादन और कृषि आय में वृद्धि हुई, और इस प्रकार बाजार-संबंधित विकास और मूल्यवर्धन को बढ़ावा मिला। श्रम-साध्यता मूल्यांकन परियोजना ने महिला-अनुकूल कृषि मशीनों का प्रदर्शन किया और मानव शारीरिक श्रम-साध्यता सूचकांक का उपयोग करके उनके प्रभाव का मात्रात्मक मूल्यांकन किया, जिससे आदिवासी महिलाओं में शारीरिक तनाव में उल्लेखनीय कमी और कार्य कुशलता में सुधार हुआ, जो लैंगिक रूप से समावेशी मशीनीकरण और श्रम दक्षता को बढ़ावा देता है। ज्ञान प्राप्ति, व्यवहार परिवर्तन और आजीविका परिणामों के संदर्भ में किसान प्रशिक्षण कार्यक्रमों की प्रभावशीलता का वैज्ञानिक रूप से आकलन करने के लिए एक मजबूत किर्कपैट्रिक-आधारित मूल्यांकन ढांचा विकसित किया गया, जिससे क्षमता-निर्माण हस्तक्षेपों का व्यवस्थित मूल्यांकन और निरंतर सुधार सुनिश्चित हुआ। सीआरआरआई ई-एक्सटेंशन प्लेटफॉर्म 'सीआरआरआई बार्ता' के विश्लेषण में विभिन्न फसल चरणों में वीडियो-आधारित सलाहों की प्रभावशीलता और दर्शकों की सहभागिता का मूल्यांकन किया गया, जिससे हितधारकों के बीच डिजिटल पहुंच को मजबूत किया जा सके और तकनीकी ज्ञान तक समय पर पहुंच को बढ़ाया जा सके। इन पहलों ने सामूहिक रूप से प्रौद्योगिकी प्रसार, लैंगिक समावेशिता, प्रशिक्षण प्रभावशीलता और डिजिटल पहुंच में सुधार किया, जिससे चावल से जुड़े हितधारकों की सामाजिक-आर्थिक स्थिति में सुधार हुआ और साथ ही साक्ष्य-आधारित नीति अनुसंधान के लिए एक मजबूत आधार तैयार हुआ। इसी संदर्भ में, भूजल भेद्यता आकलन परियोजना ने आईपीसीसी ढांचे और पीसीए-आधारित सूचकांक के तहत 472 जिलों का विश्लेषण किया, जिससे पता चला कि लगभग आधे जिले भूजल क्षरण के प्रति उच्च से अत्यधिक संवेदनशील हैं, विशेष रूप से पंजाब, हरियाणा और प्रमुख चावल उत्पादक राज्यों में। इससे महत्वपूर्ण स्थिरता चुनौतियों और अनुकूली जल प्रबंधन रणनीतियों की आवश्यकता पर प्रकाश डाला गया। परियोजना विंग्स के तहत, चावल उत्पादक जिलों को उत्पादकता स्तरों के आधार पर वर्गीकृत किया गया, जिससे पता चला कि 26% चावल क्षेत्र कम उत्पादकता के अंतर्गत आता है, जबकि लगभग 54% राष्ट्रीय औसत के बराबर या उससे अधिक है। यह क्षेत्रीय असमानताओं और उत्पादकता और संसाधन उपयोग दक्षता में सुधार के लिए लक्षित हस्तक्षेपों की गुंजाइश को उजागर करता है। बरगड़ जिले के लिए मौसम संबंधी कारकों का उपयोग करते हुए, चावल की उपज का पूर्वानुमान लगाने वाली एक परियोजना ने सांख्यिकीय और मशीन लर्निंग मॉडल विकसित और मान्य किए, जिसमें LASSO और Elastic Net उपज पूर्वानुमान के लिए सबसे सटीक मॉडल के रूप में उभरे, जिससे चावल उत्पादन प्रणालियों में वैज्ञानिक योजना और जोखिम प्रबंधन को मजबूती मिली। ओडिशा में कृषि यंत्रीकरण परियोजना ने मशीनरी वितरण, सब्सिडी की प्रभावशीलता और लैंगिक समावेशन का विश्लेषण किया, जिससे डीबीटी-सक्षम सब्सिडी वितरण के कारण बढ़ी हुई पहुंच, बेहतर स्थिति और महत्वपूर्ण लागत बचत का प्रदर्शन हुआ, जिसने दक्षता में वृद्धि और खेती को बढ़ावा देने में योगदान दिया। इन परियोजनाओं ने सामूहिक रूप से जल स्थिरता पर महत्वपूर्ण नीतिगत अंतर्दृष्टि प्रदान की।

उत्पादकता दक्षता, उपज पूर्वानुमान और मशीनीकरण के माध्यम से चावल क्षेत्र की योजना को मजबूत करना, संसाधन उपयोग दक्षता में सुधार करना और चावल आधारित उत्पादन प्रणालियों में आय और आजीविका की स्थिरता को बढ़ाना संभव हो पाता है।

इस कार्यक्रम का उद्देश्य बर्षाश्रित उपरिभूमि, निचले इलाकों और तटीय लब लबणीय पानी की पारिस्थितिकियों के लिए जलवायु-प्रतिरोधी चावल प्रौद्योगिकियों का विकास करना था। इसके लिए छोटे और सीमांत किसानों के लिए तनाव-सहिष्णु किस्मों और एकीकृत फसल प्रबंधन पद्धतियों को बढ़ावा दिया गया। सीआर धान 111 (डीआरवी07) को सीधी बुवाई के लिए जारी किया गया, और आशाजनक डीएसआर और वायवीय किस्मों की पहचान की गई। अवायवीय अंकुरण, बीज शक्ति, पोषक तत्व तनाव, ठंड सहनशीलता और रोग प्रतिरोधक क्षमता पर किए गए आनुवंशिक अध्ययनों ने जलवायु-प्रतिरोधी प्रजनन प्रयासों में सहयोग प्रदान किया। भूरी खाद, नैनो यूरिया, एकीकृत खरपतवार प्रबंधन और देशी जैविक नियंत्रण एजेंटों सहित कृषि विज्ञान और कीट प्रबंधन उपायों का मूल्यांकन सीआरयूआरआरएस, हजारीबाग में 2024-25 और खरीफ 2025 के दौरान किया गया। वहीं, आरआरएलआरआरएस, गेरुआ ने जर्मप्लाज्म संरक्षण, बाढ़-सहिष्णु किस्मों के मूल्यांकन और बड़े पैमाने पर बीज उत्पादन के माध्यम से (अनाज-आधारित, निचले इलाकों में) उत्पादन को मजबूत किया, जिसमें सीआर. धान 801 और सीआर. धान 302 ने जलमग्नता में अच्छा प्रदर्शन किया। तटीय पारिस्थितिकी तंत्र में, श्रीकाकुलम स्थित क्षेत्रीय तटीय चावल अनुसंधान केंद्र ने गुणवत्तापूर्ण ब्रीडर, मैक्लियस और टीएल बीज उत्पादित किए, और किस्मों के मूल्यांकन से स्थानीय चेक के समान प्रदर्शन पाया गया। बेहतर नाइट्रोजन प्रबंधन ने सीधी बुवाई वाले चावल में उत्पादकता बढ़ाई, जबकि उन्नत कीट पूर्वानुमान मॉडल और पेटेंटेड नॉक्टिलेंस उपकरण ने प्रभावी कीट निगरानी में सहायता की। आंध्र प्रदेश में किसानों के खेतों में आईपीएम प्रथाओं के सत्यापन से पैदावार में और सुधार हुआ और कीटों का प्रकोप कम हुआ, जो एकीकृत, जलवायु-अनुकूल चावल उत्पादन रणनीतियों की समग्र सफलता को दर्शाता है।

MAJOR RESEARCH AREAS

01

Germplasm Exploration & Conservation
Super Rice
Hybrid Rice
Bio-fortified Rice
Climate Smart Varieties

02

Input Management
Resource Conservation Technologies
Farm Mechanization
Climate Resilience
Harnessing Microbial Potentials
Integrated Farming Systems

03

Integrated Pest Management
Integrated Disease Management
Stored Grain Pests
Pesticide Formulation
Pesticide Residue Management

04

Stress Tolerant Rice
Low Glycemic Rice
Grain Quality
C_4 Rice

05

Development and Testing of New Extension Models
Socio-economic Studies
Rice Value Chain
Technology Dissemination
Training and Advisory Services

06

Climate Resilient Technologies
Rainfed Upland
Rainfed Lowland
Coastal Ecology

CRRI AT A GLANCE

08	NEW RICE VARIETIES RELEASED
16	TECHNOLOGIES COMMERCIALIZED AND 3 PATENT GRANTED
23	MEMORANDUM OF UNDERSTANDING (MOU) SIGNED
121	RESEARCH AND REVIEW PAPERS PUBLISHED
36	INSTITUTE BULLETINS RELEASED
464	SOCIAL MEDIA POST AND 131 MEDIA HIGHLIGHTS
10	NEW RICE VARIETIES DEMONSTRATED IN FARMERS FILED
4220	PERSONNEL INCLUDING FARMERS VISITED THE INSTITUTE
182	TRAININGS CONDUCTED & 7552 PERSONS ATTENDED
55	AGROMET ADVISORY BULLETINS RELEASED
24	AGRO ADVISORY SERVICES & 26 INSTITUTE VIDEOS RELEASED
2712	FIELD DEMONSTRATIONS CONDUCTED

INTRODUCTION

ICAR-Central Rice Research Institute (ICAR-CRRI), was established by the Government of India in 1946 at Cuttack, as an aftermath of the great Bengal famine in 1943, to initiate a consolidated approach to rice research in India. The administrative control of the Institute was subsequently transferred to the Indian Council of Agricultural Research (ICAR) in 1966. The institute has three research stations, at Hazaribag, in Jharkhand, at Gerua in Assam, and at Naira in Andhra Pradesh. The CRRI regional station, Hazaribag was established to tackle the problems of rainfed uplands, and the CRRI regional substation, Gerua for problems in rainfed lowlands and flood-prone ecologies. Two Krishi Vigyan Kendras (KVKs) also function under CRRI, one at Santhpur in Cuttack district of Odisha and the other at Jainagar in Koderma district of Jharkhand. The research policies are guided by the recommendations of the Research Advisory Committee (RAC), Quinquennial Review Team (QRT) and the Institute Research Council (IRC). The CRRI also has an Institute Management Committee (IMC) to support implementation of its plans and programmes.

Vision

To ensure sustainable food and nutritional security and equitable prosperity of our Nation through rice science.

Goal

To ensure food and nutritional security of the present and future generations of the rice producers and consumers.

Mission

To develop and disseminate eco-friendly technologies to enhance productivity, profitability and sustainability of rice cultivation.

Mandate

Conduct basic, applied and adaptive research on crop improvement and resource management for increasing and stabilizing rice productivity in different rice ecosystems with special emphasis on rainfed ecosystems and the related abiotic stresses.

Generation of appropriate technology through applied research for increasing and sustaining productivity and income from rice and rice-based cropping/ farming systems in all the ecosystems in view of decline in per capita availability of land.

Collection, evaluation, conservation and exchange of rice germplasm and distribution of improved plant materials to different national and regional research centres.

Development of technology for integrated pest, disease and nutrient management for various farming situations.

Characterization of rice environment in the country and evaluation of physical, biological, socio-economic and institutional constraints to rice production under different agro-ecological conditions and farmers' situations and develop remedial measures for their amelioration.

Maintain database on rice ecology, ecosystems, farming situations and comprehensive rice statistics for the country as a whole in relation to their potential productivity and profitability.

Impart training to rice research workers, trainers and subject matter/extension specialists on improved rice production and rice-based cropping and farming systems.

Collect and maintain information on all aspects of rice and rice-based cropping and farming systems in the country.

Linkages

The CRRI has linkages with several national and international organizations such as the Council for Scientific and Industrial Research (CSIR), Indian Space Research Organization (ISRO), SAUs, State Departments of Agriculture, NGOs, Banking (NABARD) and the institutes of the Consultative G roup for International Agricultural Research (CGIAR), such as the International Rice Research Institute (IRRI), Philippines and International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India.

Location

The institute is located at Cuttack about 35 km from Bhubaneswar airport and 7 km from the Cuttack railway station on the Cuttack-Paradeep State Highway. The institute lies approximately between 850 55'48" E to 850 56'48" longitudes and 200 26'35" N to 200 27'35" N latitudes with the general elevation of the farm being 24m above the MSL. The annual rainfall at Cuttack is 1200 mm to 1500 mm, received mostly during June to October (kharif or wet season) from the southwest monsoon. Minimal rainfall is received from November to May (rabi or dry season).

PROGRAMME
01

Genetic Improvement of Rice

The agricultural sector is confronted with a multitude of complex and interrelated challenges. In response to the emerging challenges, the Crop Improvement Division continuously intensifies its research, seed production, and varietal development programmes. The extensive research and development undertaken by the Division are reflected as varietal development, hybrids released, development and deployment of modern tools during 2025. These advancements are strategically focused on enhancing climate resilience, addressing malnutrition through biofortification, improving productivity and profitability in rice and rice-based ecosystems. The Division's activities are efficiently coordinated by nineteen scientists, supported by twenty four technical staff members, who are currently implementing 11 institutional research projects and 40 externally funded projects.

1 NO POVERTY
2 ZERO HUNGER
3 GOOD HEALTH AND WELL-BEING
12 RESPONSIBLE CONSUMPTION AND PRODUCTION
13 CLIMATE ACTION
15 LIFE ON LAND
16 PEACE, JUSTICE AND STRONG INSTITUTIONS
17 PARTNERSHIPS FOR THE GOALS

Managing rice genetic resources for sustainable utilization

Characterisation and documentation of rice germplasm of Andhra Pradesh, Kerala and Tamil Nadu region (P Sanghamitra, BC Marndi and Manoj Patra)

A set of 204 rice germplasm accessions of Andhra Pradesh, Kerala and Tamil Nadu region conserved in CRRI gene bank were characterized based on 19 qualitative and 9 quantitative traits. Maximum variability (5) was observed for kernel colour and hull colour. Highest variability (CV) was observed for yield (24.84%) followed by leaf length (21.46%). AC 6036 was identified with highest 100-grain weight (3.6 g) (Table 1.1) whereas AC 318 was found with highest yield (22.8 g/plant). The germplasm of Andhra Pradesh region showed distinctiveness with longer leaf (67.07cm), tall plant height (164.81cm) with late maturing type (160 days). However, higher yield was observed in genotypes of Tamil Nadu region (10.15 g) (Fig. 1.1).

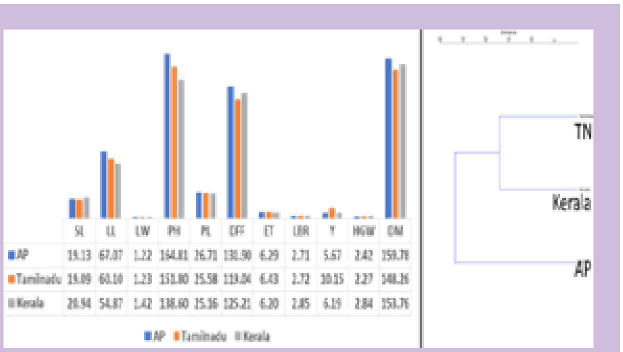


Fig. 1.1. Variability in quantitative traits

Development of database of rice germplasm (P Sanghamitra, S Samantaray, BC Marndi and Manoj Patra)

A database of about 50,000 rice germplasm accessions conserved in Module I and Module II of CRRI gene bank consisting of AC, IC, EC collections, ARC collections, JBS collections, wild rice, farmers' varieties, released varieties, NHN materials, N22 mutant lines, genotypes for biotic and abiotic stresses was prepared and is now available online in the ICAR-CRRI website. These germplasm were documented with available passport and characterized data.

Germplasm supply (P Sanghamitra, BC Marndi and Manoj Patra)

A total of 464 germplasm accessions were supplied to researchers within the institute (295) and other research institutes (169). A revenue of Rs.35,800 was generated by sharing the germplasm through signing of MTA with the indenters for its utilization in research purpose.

Table 1.1. Variability in quantitative traits.

Trait	Mean	Range	CV (%)
Plant height (cm)	149.34	69.0–196.3 (AC 39379–AC 2677)	18.86
Leaf length (cm)	59.42	27.0-86.3 (AC 1627–AC 630)	21.46
Leaf width (cm)	1.20	0.86– 1.56 (AC 39378–AC 321)	11.37
Panicle length (cm)	25.23	17.0–34.3 (AC 39379–AC 39410)	12.46
No. of Tillers	6	2.5-11.0 (AC 39387–AC 39378)	18.90
Days to maturity	153.4	133–187 (AC 39561–AC 371)	16.7
L/B	2.65	1.7–3.86 (AC 39393 –AC 2868)	8.47
100-Grain weight (g)	2.41	1.1-3.6 (AC 39542-AC 6036)	11.25
Yield/plant (g)	7.49	0.76–22.8 (AC 39369–AC 318)	24.84

Maintenance breeding, quality seed production and seed technology research for enhancing rice yield

Seed production and its maintenance (BC Marndi, RP Sah and Anilkumar C)

The nucleus seed of 134 varieties released from the institute were multiplied following the standard progeny row method. Genetic purity was ensured by following multiple expert monitoring visits, along with rigorous rouging and removal of off-type plants. True-to-type panicles were collected for advancing nucleus seed and breeder seed production. During 2024-25, 17.89 quintals of nucleus seed from 134 varieties were produced for further multiplication. To meet the breeder seed demand of DAC and other agencies, 471.0 quintals of breeder seed from 76 varieties were produced at ICAR-CRRI farm, Cuttack (Fig. 1.2).

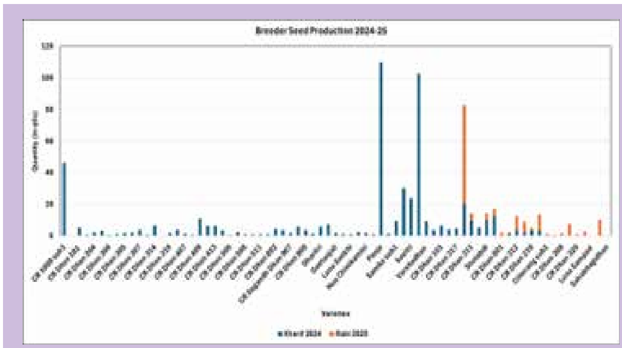


Fig. 1.2. Breeder seed production during the year

Participatory seed production (BC Marndi, RP Sah and Anilkumar C)

Truthfully labeled (TL) seed production was undertaken to meet farmers' demand. MoUs were signed with three farmer groups: Maa Banadurga Farmers Club, Orshaka, Kendrapada; Mahatma Gandhi Krushak Club, Bhandilo, Kendrapada; and Nischintakoili Farmer Producer Company Ltd., Nischintakoili, Cuttack. A total of 489.95 quintals of TL seeds of 11 popular varieties were produced (Fig. 1.3) through participatory seed production approach. The seed was subsequently procured back by the institute and made available to other farmers for purchase as TL seeds from the Institute.

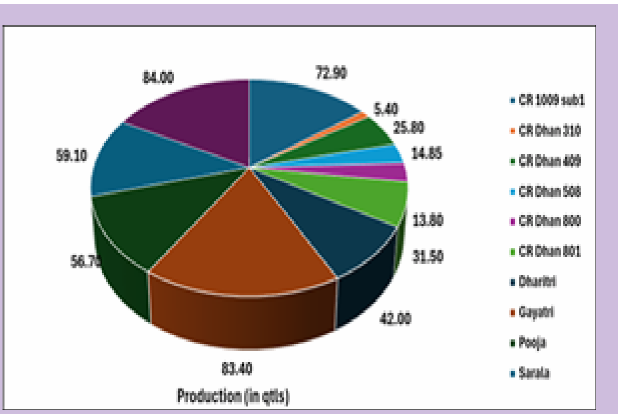


Fig. 1.3. TL Seed Production during the year

Understanding deep seeding emergence mechanisms in rice for higher seedling establishment under DSR (RP Sah and BC Marndi)

The present study investigated the genetic and physiological factors controlling seedling emergence in rice under deep-seeding conditions, a major constraint in direct-seeded rice (DSR) systems. Evaluation of 192 genotypes sown at 6 cm depth revealed substantial variation in emerging ability and early seedling traits. Correlation analysis (Fig. 1.4) showed a strong, positive association between mesocotyl length and seedling emergence, highlighting mesocotyl elongation as a key adaptive trait for deep sowing. Mesocotyl length was also positively correlated with seedling vigor traits, including shoot length, biomass accumulation, and root growth, indicating enhanced early establishment. In addition, seed trait such as test weight was positively associated with mesocotyl length and seedling biomass, suggesting that larger seed reserves support better emergence under deep-seeding conditions. Overall, genotypes with longer mesocotyls and superior seedling vigor exhibit improved emergence and represent valuable breeding resources for enhancing DSR establishment.

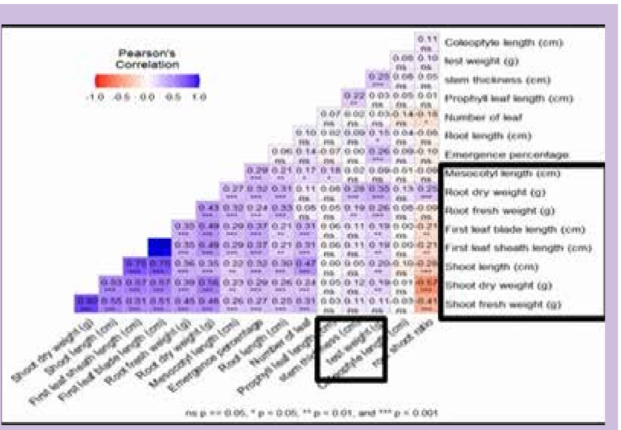


Fig. 1.4. Correlation matrix of seedling vigour traits under DSR

Pre-breeding for broadening the genetic base of rice by utilizing wild species of *Oryza*

Expansion of the A-genome core markers into a subset for genus *Oryza* (M Chakraborti and MK Kar)

Out of 23.5K STMS markers evaluated for cross-amplification in *O. punctata* (BB genome), 813 were predicted to be transferable, but only 240 were common with the *O. sativa* complex (A genome). Similarly, out of 360 markers predicted as cross-amplifiable to *O. coarctata* (KKLL genome), only 81 were transferable to the A-genome. Overall, just 42 markers were common to the AA, BB, and KKLL genomes and were distributed across eleven rice chromosomes (Fig. 1.5), with 78.57% being genic SSRs. Except for two markers, all amplified as predicted after sequence curation. Validation across 37 accessions from 21 *Oryza* species using 27 selected markers revealed 2–7 alleles per locus (123 total alleles), effectively discriminating species complexes and outlier taxa in agreement with established taxonomy (Fig. 1.6).

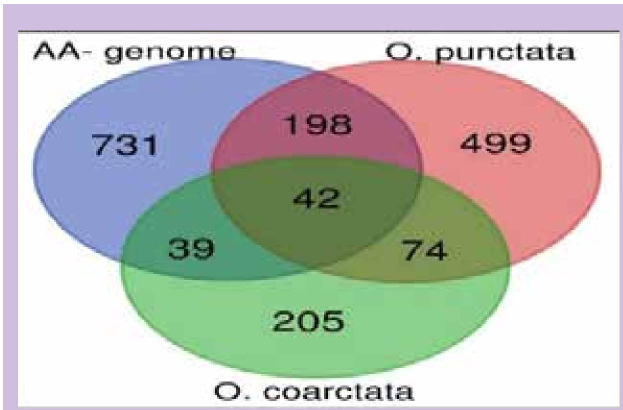


Fig. 1.5. Venn diagram depicting number of common markers identified among eight species of *O. sativa* complex (A-genome), *O. punctata* and *O. coarctata*

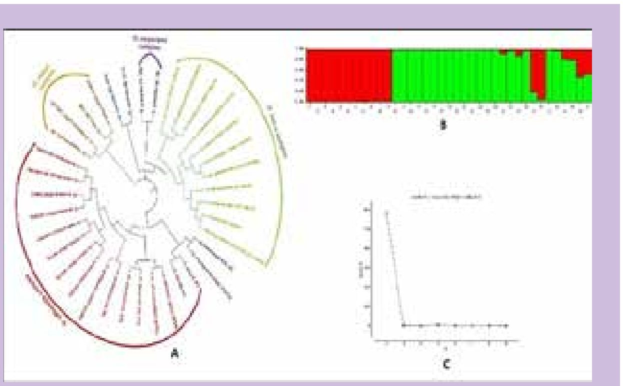


Fig. 1.6. Clustering pattern and population structure of 37 accessions belonging to 21 species of *Oryza* representing different species complexes and outliers. **A**. Dendrogram depicting genetic relatedness based on 123 alleles from 27 polymorphic markers. *O. meyeriana* complex is represented by only *O. granulata* due to lack of any authentic taxonomic key to establish *O. meyeriana* and *O. granulata* as distinct species; **B.** Population structure and allele sharing pattern among the 37 genotypes. The numerical sequence of the genotypes is as per sequence in Panel-3; **C**. Delta K value of the predicted population structure against K- values in X-axis

Study of interaction among *Sub1A*, *SNORKEL*, and *SD1* genes (M Chakraborti, K Chakraborty, KA Molla and MK Kar)

This study examined allelic interactions among *Sub1A*, *SNORKEL1*, *SNORKEL2* and *sd1* genes controlling submergence tolerance in rice. A population of 489 recombinant inbred lines (RILs) derived from cross between Swarna, Swarna-Sub1, and a submergence-tolerant *Oryza nivara*–derived line (NPS-95) was genotyped using allele-specific markers, revealing twelve gene combinations. QTL analysis in Swarna-Sub1/NPS-95 population identified a minor-effect QTL on chromosome 9 associated with survival and elongation under 14 days of submergence **(**Fig. 1.7 & 1.8**)**. Lines carrying *Sub1A-2* with *SNORKEL1* and *SNORKEL2* showed survival comparable to Swarna-Sub1, while *Sub1A-2* alone conferred moderate tolerance. Under prolonged submergence, survival was restricted to genotypes with *Sub1A-1*, with the highest survival observed when combined with *SNORKEL1*, *SNORKEL2*, and *sd1*, indicating synergistic effects. Near-isogenic lines of Swarna-*Sub1* carrying the *SD1* allele exhibited increased elongation without compromising survival under 14 days of submergence stress. Overall, survival was largely independent of gene dosage, whereas elongation was highly dependent. These findings provide insights into the genetic regulation of submergence tolerance and support breeding strategies for climate-resilient rice under increasing flood stress.

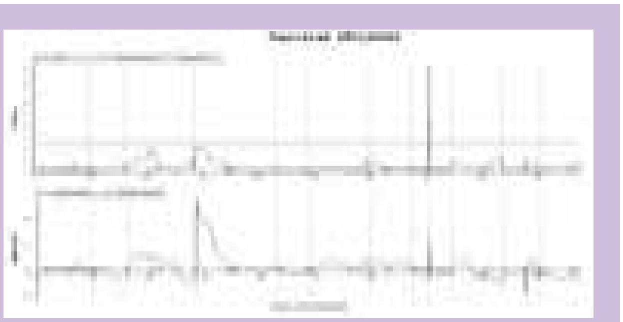


Fig. 1.7. Graphical depiction of LOD-score and additive effect values for survival percentage (15 days after desubmergence) under 14 days of submergence stress across 12 chromosomes identified through inclusive composite interval mapping. Peaks in the LOD curve indicative of putative QTL positions, while the additive effect line reflects the direction and magnitude of allelic effects contributed by each parent for survival percentage in Swarna-Sub1/NPS-95 RIL population

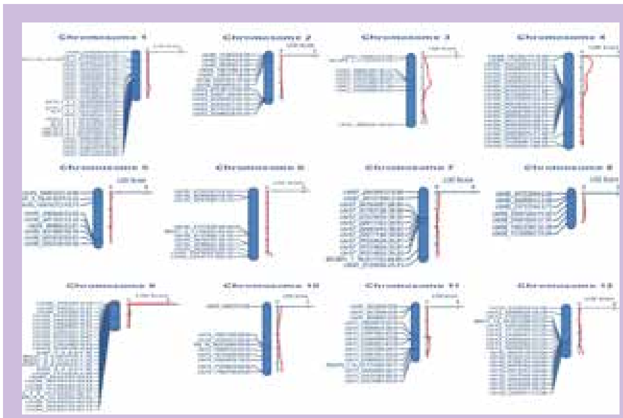


Fig. 1.8. QTL mapped for survival percentage (15 days after desubmergence) after arcsine transformation in the Swarna-Sub1/NPS-95 RIL population. Significant QTL was detected on Chromosome 9 between chr09_5008706 (left) marker and *Sub1_1* (right) marker, with LOD score of 9.3

Screening of CSSLs of CR Dhan 307/ *O. rufipogon* (AC 100444) against sheath blight disease (MK Kar and S Lenka)

Eighty CSSLs of CR Dhan 307/ *O. rufipogon* (AC 100444) were screened against sheath blight disease. Among them, 6 entries were moderately resistant, 9 entries were moderately susceptible, 41 entries were susceptible and 24 entries were highly susceptible.

Identification of herbicide tolerant variety, CR Dhan 812 (MK Kar and M Chakraborti)

The herbicide-tolerant rice variety **CR Dhan 812** (CR 4430-1-3-2-1; IET 32123) **(**Fig.1.9**)** was notified for cultivation in Odisha, Jahrkhand West Bengal, Bihar, Eastern Uttar Pradesh, Assam, and Tripura. CR Dhan 812 offers an effective solution for managing weedy rice, a major constraint in direct-seeded rice (DSR) systems. On-farm trials under mechanized DSR in weedy rice infested fields of Ghazipur, Gorakhpur, and Deoria districts of Uttar Pradesh demonstrated complete control of weedy rice, preventing the 50–65% yield losses previously experienced by farmers.

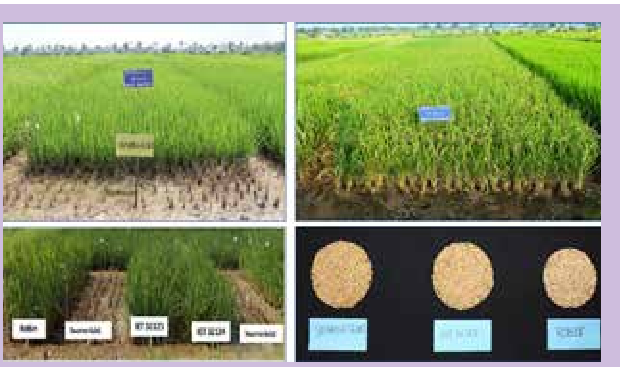


Fig. 1.9. Field performance of herbicide tolerant lines

Performance of wide cross derivatives in AICRP Trials-2024 (LK Bose and MK Kar)

IET 33202 (CR 4209-228-1-55-77-2) from the cross-combination CR Dhan 307/*O. rufipogan* (AC-100005) has been promoted to AVT1-R-DS-M for rainfed condition for AICRPR-2025 trial. IET 33257 (CR 4205-226-52-50-7-1) from the cross-combination CR Dhan 307/*O. longistaminata* (AC-110404) has been promoted to AVT1-R-DS-L for rainfed condition for AICRPR -2025 trial.

Performance of Breeding lines in AICRP Trials -2024 (MK Kar, LK Bose and M Chakraborti)

Two NILs of Swarna, **IET 32123** (CR 4430-1-3-2-1) and **IET 32124** (CR 4430-13-19-1-1) with submergence and herbicide (Imazethapyr) tolerance were found promising in AVT-2- RSL, NIL-SUB and NIL-HT trials of AICRP. IET 32123 (CR 4430-1-3-2-1) was identified for release as CR Dhan 812.Two NILs of Pooja, **IET 32130** (CR 4431-117-3-2-1) and **IET 32131** (CR 4431-63-2-1-1) with herbicide (Imazethapyr) tolerance were found promising in AVT-2- RSL and NIL-HT trials of AICRP.BPH tolerant NIL of Pooja, **IET 33264** (CR 4696-2-15-32-82) was promoted to AVT-2- RSL based on its performance in AVT-1-RSL and NSN trial of AICRP.

Developing genetic solutions for enhancing input use efficiency in rice for rainfed and irrigated rice ecologies

Breeding programme for aerobic condition, early maturity, and DSR condition (J Meher)

A total of 68 elite rice lines, identified based on yield BLUPs and DSR traits, are set to be utilized in future breeding programs and a new elite crossing program was initiated, resulting in 11 F_1 cross combinations. During Line Stage Testing (LST), 398 lines were evaluated for yield potential under DSR conditions. In addition, 250 lines were evaluated under combined low nitrogen and phosphorus conditions in aerobic systems at seedling stage.

Mapping QTLs for Early Vigor and Yield Traits in Rice Under Direct-Seeded Conditions (RP Sah)

A panel of 170 genotypes were evaluated for early vigor traits at 14 and 28 days after sowing under DSR. A total 137 marker–trait associations (MTAs) across 112 SNPs, with 1405 annotated genes was retrieved from the MSU database. Similarly, nine yield-related traits resulted in 234 SNPs, were identified.

AICRIP promotion and nomination (J Meher and Reshmi Raj KR)

Out of the nominated entries, six entries have been promoted to AVT-2 for evaluation: CR 4075-1341-3-3-2-2-1-4-3 (ETP, IET 30637), CR 4077-1357-5-4-2-1-1 (IME, IET 30713), CR 4397-4-6-27 (LPT, IET 31107), CR 4457-IR 129477-4026-249-15-1-4 (Aerobic, IET 31741), CR 4466-126-WB-1 (LPT, IET 31968), CR 4467-RGA-100 (LPT, IET 31976). Three entries have been promoted to AVT-1 for evaluation: CR 6322-RGA-59 (Aerobic, IET 32616), CR 4396-3-16-1-2 (LPT, IET 32860), CR 4383-RGA-70 (LPT, IET 32861). A total of 16 new nominations were submitted for different trials.

Genetic diversity in rice varieties for tolerance to low phosphorus stress at seedling stage (Reshmi Raj KR)

Phosphorus (P) deficiency is a major constraint in rice production, particularly in P-depleted soils. To identify P-efficient donors at the seedling stage, 130 rice genotypes were evaluated under field and hydroponic conditions across three P levels (0, 50, and 100% of recommended dose) (Fig. 1.10). Significant genetic

Fig. 1.10. Growth performances of rice genotypes under varying phosphorous treatment levels in hydroponics condition

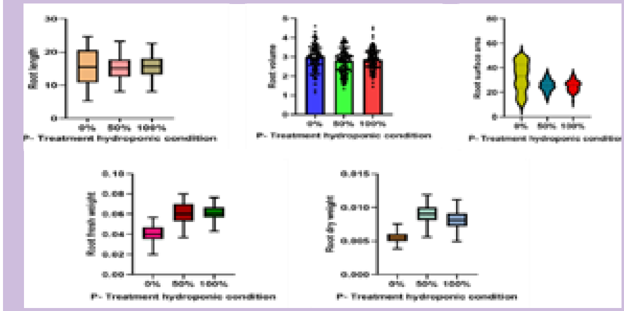


Fig. 1.11. Box plots showing the effect of phosphorus levels (0%, 50%, 100%) on different root traits

variation was observed for root and shoot traits under P stress, with root length, root surface area, root volume, and shoot biomass showing pronounced differences (Fig. 1.11). Genotypes such as CR Dhan 328, CR Sugandh Dhan 3, CR Dhan 911, VL Dhan 81, CR Dhan 202, and NDR 359 consistently outperformed the susceptible check IR64. Molecular analysis using Pup1-linked markers clustered these genotypes with the donor Kasalath, indicating shared low-P tolerance alleles. Root length and root surface area accounted for over 60% of phenotypic variation under P deficiency. These results identify promising donors for breeding P-efficient rice varieties for sustainable production in P-limited environment.

Breeding for Aroma and Grain Quality in Rice

Development of aromatic genotypes with short/ medium/ long slender grains (S Sarkar, T Adak, N Basak, GAK Kumar, MK Kar, M Chakraborti, J Meher, P Sanghamitra, TB Bagchi, AK Mukherjee and B Gowda)

Three breeding lines, CR 4610, CR 4588 and CR 4587 developed through pedigree breeding have been nominated for evaluation of performance under IVT-ASG trial of AICRIP-2025. Non-lodging, semi-dwarf plants with strong culm, Gobindabhog grain type and aroma has been identified in BC$_3$F$_3$ generation derived from a three-way cross and are under multiplication during *kharif* 2025. For the development of semi dwarf Nua-Kalajeera resistant to bacterial blight, blast and BPH tolerance, 14 IC$_2$F$_1$ plants carrying multiple genes under transfer were identified through gene specific SSR markers and were back crossed with Nua-Kalajeera during *kharif 2024*. Through GGT analysis using 1K SNP of the 102 IC$_2$F$_1$ population identified plants with maximum recovery of recipient genome with the added genes under transfer (Fig. 1.12).

Fig. 1.12. a: Tall plant of Gobindabhog landrace b: Semi-dwarf BC$_3$F$_3$ plants of Gobindabhog **c:** Tall plant of Nua-Kalajeera, grain type and paddy d: GGT analysis using 1K SNP of the IC$_2$F$_1$ population of Nua-Kalajeera for selection of genotypes

Breeding for biofortification (K Chattopadhyay, TB Bagchi, T Adak, P Sanghamitra, N Basak, Shivashankari M, M Chakraborti, S Sarkar and AK Mukherjee)

Through Field RGA (speed breeding) twenty breeding populations (around 2000 plants/population) in F2-F4 having diverse donors for zinc and protein content was advanced. Three generations in a year was achieved using dense sowing and fertilizer management. Ten elite breeding lines with high zinc or protein content such as CRAC-3998- 129-1, CRAC-3998-77-1, CR-4201-7-1-B, CR-4200-16-1-B, CR 4513-3-B, CR 4228-3-247-1, CR-4233-3-2-B, CR4562-19-17-7-13-7-91-1, CR4566-26-7-8-34-19-14-7-1, CR4616-27-9-7-19-1-3-7-28-9 were nominated in AICRP Biofortification programme.

Improvement of biofortified lines for stress tolerance

Introgression of major QTLs for biotic (BB) and abiotic (drought, submergence) tolerance in high yielding biofortified varieties (Swarnanjali, CR Dhan 310/other elite lines) are in progress. Around 44 breeding lines (F4-F5) derived from cross of Swarnanjali and its derivatives with BB tolerance were phenotyped for submergence tolerance. Thirteen lines were detected with more than 70% survivability. A few notable lines were CR 4510-BC-1-4-Su-1-B, CR-4531-2-2-Su-1-B, CR-4556-3-1-Su-B, CR 4556-2-2-Su-1, CR 4532-4-B-Su-2-1, CR 4532-4-B-Su-2-4.

Calibration of NIR for proximate estimation of essential amino acid (EAA) and phenotyping of mapping population

HPLC data from 150 rice genotypes with wide variation in essential amino acids (EAAs) were used to develop NIRS calibration and prediction models, achieving high accuracy ($R^2 = 0.91–0.97$) with optimal chemometrics (2,8,8,1). Using these models, ~300 BC$_1$F$_4$ lines derived from CR Dhan 311/Bindli//CR Dhan 311 were evaluated during *kharif* 2023 and 2024 at ICAR-CRRI, Cuttack. Dehusked rice samples showed significant and normally distributed variation in EAA content (mg g^{-1}), ranging from 0.19–0.28 (His), 0.40–0.55 (Arg), 0.26–0.43 (Thr), 0.19–0.29 (Lys), 0.30–0.39 (Val), 0.23–0.34 (Ile), and 0.41–0.55 (Leu).

Upscaling of biofortified varieties

Six MoUs were signed for seed production and popularization of three biofortified rice varieties (CR Dhan 310, CR Dhan 311, CR Dhan 411) with four seed companies. Breeder seed indent was around 20q for biofortified rice varieties. Around 50 q TL seed was produced in 2024-25 which was distributed and demonstrated through farmers' field trials.

Lodging resistant Semi-dwarf black rice derivative of Chakhao with high antioxidant, CR4450-48-26-13-14-19(IET 32901) and CR4450-65-36-8-17 (IET 32906) were nominated for IVT-Coloured Rice Trial. The lines CR4550-48-1-50, CR-4450-48-2-53-3 with high values for total anthocyanin content, CR4550-48-1-98 with high total flavonoid content and Gamma-Oryzanol and CR4550-48-1-2 with high total phenol content were

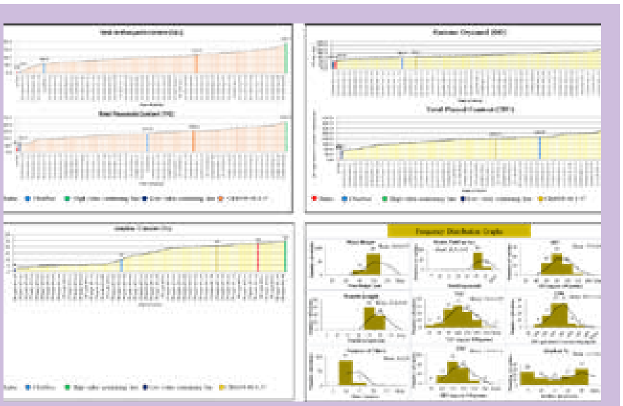


Fig. 1.13. Variation displayed by population derived from *Chakaho Amubi* **(AC9044) ×** Ratna

Fig. 1.14. CR Dhan 417 in dough stage

identified for registration and development of mapping population **(**Fig. 1.13**).**

Marker assisted genetic improvement of Chakhao derived semi dwarf black rice for resistance to BB, blast and BPH have been undertaken. Twenty-nine Doubled Haploid plants with multiple genes were developed from selected IC_1F_1 plants. Intercrosses among these lines have also been undertaken for attainment of homozygosity and gene pyramiding using MAS. Two new nominations have been submitted for trial under AICRP, IVT- Coloured Rice Trial-2025.

Breeding for specialty rice, pigmentation, slender grains and sensory qualities (S Sarkar, P Sanghamitra, A Anandan J Meher, M Chakraborti, K Chattopadhyay, TB Bagchi, SK Dash, GAK Kumar, N Basak, T Adak, Shivashankari M, AK Mukherjee and Guru Prasanna Pandi G)

Breeding line IET 32719 was promoted to AVT1-MS under medium slender grain type category. Two new nominations: CR4615 (RPBIO226/IHRY-MS-130) and CR4570 (Ratna/Heera) developed through pedigree breeding were submitted for evaluation under IVT- MS trial under AICRP-2025.

Gene mapping and precision breeding for enhancing climate resilience in lowland varieties

Enhancing resilience for submergence, drought, BB and BPH in shallow lowland varieties (SK Dash, L Behera, AK Mukherjee, MK Lal and N Barik)

CR Dhan 417 (Fig. 1.14) was released and notified for cultivation in the states *viz.,* Assam, Tripura, Andhra Pradesh, and Karnataka. It is basically a variety with medium slender grains and perform superior in shallow lowlands with duration of ~147 days. It is a semi-dwarf, lodging-tolerant variety (108.4 cm) with long slender grains and high productivity (64.6 q ha^{-1}; up to 9.4 t ha^{-1}). It exhibits high resistance to stem borer, leaf folder, moderate resistance to gall midge, and moderate tolerance to leaf and neck blast.

Yield improvement under shallow lowland conditions is challenged by both abiotic and biotic stresses. Five advanced fixed selections CR 6457-1, CR 6457-2-5, CR 3838-2-2-1-1-4, CR 2538-42-17-32-3, and IRGC 71545-1 showed 6.2–41.6% higher yield than the check.

To develop a climate-resilient replacement for the widely grown variety Swarna under rainfed shallow lowland conditions, key abiotic (drought and submergence) and biotic stress resistance genes were introgressed into the Swarna background. Donor lines included Swarna-Sub1 (*Sub1*), IRBB60 (*Xa21, xa13, xa5* for BLB), CR 306 (*qBph4.3*), CR Dhan 801 (*Sub1, qDTY1.1, qDTY2.1, qDTY3.1*), and CR Dhan 317 (*Bph31*). Following backcrossing and BC2F5 foreground selection using SSR and SNP markers, recombinant lines with multiple gene/QTL combinations were identified, including some carrying 6–7 target loci. As segregation persisted due to multiple crosses, rigorous single-plant selection and evaluation in larger plots were undertaken to assess yield performance, phenotypic acceptability, and the cumulative effect of introgressed genes.

There are several selections *viz.,* PW 767-1, PW-773, PW-388. PW-150, PW-484, SW- 36, PR 359-1, and PR -189 were having higher grain yield w.r.t popular variety Swarna (4-47.3%). Among them PW 767-1, PW-773, PW-150, PW-484, SW- 36 and SW-225 had better survival percentage, whereas PW 767-1, PW-773, PW-150, PW-484 and SW-225 (Table 1.2) were endowed with higher BB resistance and better survival under 14 days submergence and could be nominated for national testing after phenotyping for BPH .

CR Dhan 810 (IET 30409) developed from Gayatri (popular rice variety for lowland) introgressed with QTLs for submergence resistance *Sub-1* released for Odisha, W.B. and Assam. Similarly, CR Dhan 811 (IET 30410) is a MAS derived NIL (Sarla*3 / IR49830-7) introgressed with QTL *Sub-1,* for submergence resistance in Sarala (popular rice variety for lowland with

Table.1.2. Performance of Swarna NILs introgressed with multiple stress resistance genes/QTLs.

Genotypes	Av. Yield (t/ha)	% superiority over Swarna	BB Score	Av. survival %	QTL/Genes
PW-767-1	6.185	47.33206	2.33	95.45	7(*qDTY1.1, qDTY2.1, qDTY3.1, BPH31, XA5+XA21+SUB1*)
PW-773 (Dw White)	6.035	43.75893	4.33	72.73	6 (*qDTY1.1, qDTY3.1, BPH31, XA5, XA21, SUB1*)
PW-388	5.14.5	22.55836	3	0	6(*qDTY1.1, qDTY2.1, qDTY3.1, BPH31, xa5, XA21*)
PW-150	4.86.5	15.88852	2.33	90.91	7 (*qDTY1.1, qDTY2.1, qDTY3.1, BPH31, XA5, XA21, SUB1*)
PW-484	4.76	13.38733	2.33	95.45	7 (*qDTY1.1, qDTY2.1, qDTY3.1, BPH31, XA5, XA21, SUB1*)
SW-36	4.67	11.24345	5.67	72.73	6 (*qDTY1.1, qDTY2.1, qDTY3.1, PH31, XA5, SUB1*)
PR-359-1	4.45.5	6.121963	3	22.73	7 (*qDTY1.1, qDTY2.1, qDTY3.1, BPH31, XA5+XA21+SUB1*)
PR-189	4.435	5.645545	5	27.27	7 (*qDTY1.1, qDTY2.1, qDTY3.1, BPH31, XA5+XA21+SUB1*)
SWARNA	4.198	-	9.0	4.545	-

MS grain introgressed with *Sub-1* gene for submergence tolerance) released for Odisha and W.B. In 2025-26, breeder seed indent of 7.35 q for CR Dhan 810 and 2.15 q of CR Dhan 811 was indented which showed its popularity.

Pyramiding of QTLs/genes for deeper rooting (*Dro 1*) and phosphorus deficiency tolerance (uptake) (*Pup1*) in the popular rice variety 'Maudamani' (L Behera and SK Dash)

Pyramiding of QTLs/genes for deeper rooting (*Dro 1*) and phosphorus deficiency tolerance (uptake) (*Pup1*) in the popular rice variety 'Maudamani' has been done through MAS breeding approach. In BC2F4 phenotyping and genotyping results recorded few potential genotypes *viz*., AP-6-11-1-6-R3 (*Dro1, Dro3, Pup1),* AP-6-16-2-38-R1 (*Dro1, Dro3, Pup1,* AP-6-11-4-2-R3 (*Dro1, Dro3, Pup1),* AP-6-16-2-11-R1 (*Dro1, Dro3, Pup1),* AP-6-16-2-11-R1 (*Dro1, Dro3, Pup1)and* AP-6-16-2-8-R1 (*Dro1, Dro3, Pup1)* having *Dro1, Dro3, Pup1 qtls* endowed with high yield at par with recurrent parent along with superior root and phosphorus use efficiency (Table 1.3).

In lowland semi deep ecology the selection in segregating populations of Varshadhan Sub-1 in advance generation has resulted in promising lines in the background of Varshadhan Sub-1 based on panicle size (6.85g to

Table 1.3. Performance of pyramided 'Maudamani' lines at reproductive stage.

Pyramided lines / Parent	DFF (Days)	Plant height (cm)	No. of tillers	Panicle length (cm)	Panicle weight (g)	No. of Grains / Pan	No. of Chaffs / Pan	1000 Grain Weight (g)	L/B	Grain Yield (t ha^{-1})
Maudamani (Recipient)	108	105	7.17	24.63	6.65	245.5	15.33	23.08	2.42	7.12
AP-6-11-1-6-R3 (*Dro1, Dro3, Pup1)*	112	106	8.33	26.31	6.95	265.54	26.67	23.07	2.64	7.43
AP-6-16-2-38-R1 (*Dro1, Dro3, Pup1)*	113	109	7.83	25.91	6.83	261.50	20.33	22.38	2.97	7.33
AP-6-11-4-2-R3 (*Dro1, Dro3, Pup1)*	113	111	8.33	24.63	6.79	255.94	21.83	22.47	2.51	7.15
AP-6-16-2-11-R1 (*Dro1, Dro3, Pup1)*	113	110	7.83	24.38	6.53	220.56	24.17	24.1	2.70	6.95
AP-6-16-2-8-R1 (*Dro1, Dro3, Pup1)*	112	111	7.17	25.64	6.69	249.63	20.17	22.08	2.74	7.26

Fig. 1.15. Variation in panicle size in selected segregating populations of Tropical japonica

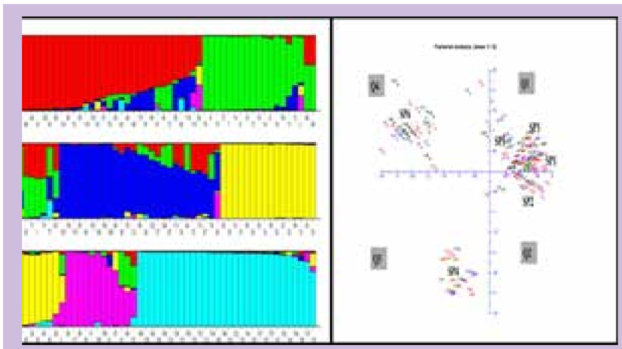


Fig. 1.17. Distribution and clustering pattern of 150 rice genotypes based on SSRs

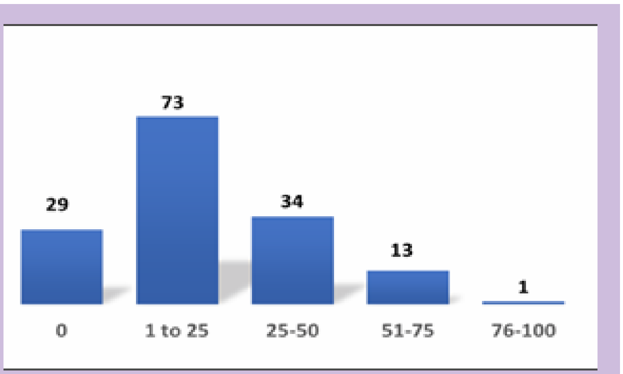


Fig. **1.16** Anaerobic germination in lowland Genotypes

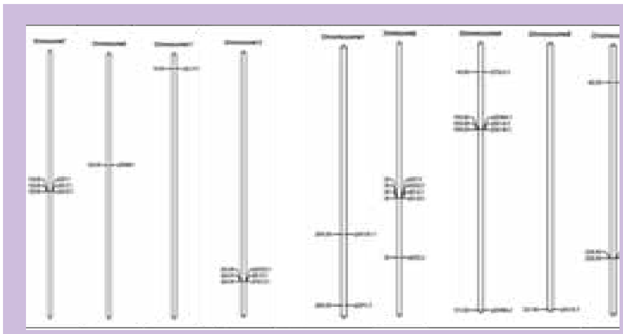


Fig. 1.18. QTL locations on the chromosomes for germination percentage, speed of germination, shoot length, root length, and drought tolerance index under moisture stress

9.34g). Similarly, the selection in segregating populations of tropical japonica and its derivatives varied from 7 to 11 g with 390-450 grains **(**Fig. 1.15**).**

Variety proposals suitable for shallow lowland ecology: CR Dhan 513 (Mahadev) (SK Dash, L Behera and N Barik)

One new proposal CR Dhan 513 (Mahadev) is submitted for identification and release of variety in semi deep ecology. This has higher yield potential to the tune of 5.6 t ha^{-1} along with red grains and non-lodging plant type and good kneeing ability.

Genome wide association study for locating novel genes/QTLs controlling seed vigour and seed viability (P Sanghamitra, L Behera and SK Dash)

About 150 genotypes were tested for anaerobic germination where one genotype was reported with 76.6% germination, whereas 13 genotypes were reported with 51-75% germination (Fig.1.16). Some of the genotypes with less anaerobic germination are endowed with AG1_1, AG3_1 and AG3_2 indicates the presence of some other genes for higher values *viz.*, MD-35.

In another study, 150 rice germplasm lines selected from 300 diverse accessions from the CRRI Gene Bank were evaluated for seed longevity traits under varying temperature and moisture conditions. Significant variation was observed for germination percentage, shoot and root length, total seedling length, seedling dry weight, and seed vigor index. Genotypic diversity was assessed using 145 polymorphic SSR markers, and parameters such as polymorphic information content, gene diversity, and heterozygosity were estimated using PowerMarker v3.25. Population structure analysis classified the genotypes into six genetic groups, with lines showing ≥80% membership assigned to distinct subgroups and others to an admixture group (Fig. 1.17**).**

Table 1.4. Trait association of 24 genes detected with higher PV value and responsible for different component traits of seed storage.

TRAIT	No. of QTLs	QTL	CHR. NO.	POSITION (cM)
Germination Percentage	3	qGP1.1	1	289
		qGP3.1	3	171
		qGP7.1	7	159
Speed of Germination	4	qSOG3.1	3	171
		qSOG3.2	3	237
		qSOG6.1	6	238
		qSOG12.1	12	262
Shoot Length	1	qSL11.1	11	15
Root Length	1	qRL12.1	12	262
Total Seedling Length	2	qTSL4.1	4	44
		qTSL12.1	12	262
Seedling Dry Wt	3	qSDW4.1	4	109
		qSDW4.2	4	313
		qSDW8.1	8	126
Seed Vigour Index-I	5	qSV-I1.1	1	209
		qSV-I3.1	3	171
		qSV-I4.1	4	109
		qSV-I5.1	5	327
		qSV-I6.1	6	238
Seed Vigour Index-II	5	qSV-I7.1	7	159
		qSV-II3.1	1	171
		qSV-II4.1	4	109
		qSV-II6.1	6	40
		qSV-II7.1	7	159

A total of 549 polymorphic alleles were detected, confirming high genetic diversity, and marker–trait associations (Fig 1.18) were identified for seed longevity–related traits (Table 1.4).

Genetic enhancement for multiple stress tolerance in rice for coastal ecosystem (K. Chattopadhyay, BC Marndi, K. Chakraborty, LK Bose, A. Poonam, KA Molla, Kiran Gandhi, AK Mukherjee, SD Mohapatra, Devanna BN and AK Nayak)

Evaluation of rice germplasm for salinity tolerance

During *kharif* 2024, a total of 174 germplasm selected from a 2000 panel were evaluated for their salinity tolerance at the seedling stage. FL 478 and IR 29 were used as tolerant and susceptible checks, respectively. A salinity stress (EC) of 12dSm-1 was imposed and scoring was done 30 days after sowing. Based on SES scores, 38 entries were classified as tolerant (score 3), 93 as moderately tolerant (score 5), 38 as susceptible (score 7), and 5 as highly susceptible (score 9).

Development of elite lines suitable for coastal ecology

Five lines have been promoted in coastal salinity tolerant varietal trial (CSTVT) conducted by AICRPR during *kharif* 2024. IET 32822 (CR-2814-1-S-1-6-B-5-B-39-B) derived from Naveen/ FL 478 with 3910 kg ha^{-1} grain yield and IET 32813 (CR-4086-5-B-3-2) derived from CR2814-1-S-1-6-3-2B-1/Binadhan 10 cross with 3658 kg ha^{-1} were promoted to Zone III. IET 32807 (CRAC-4423-111) doubled haploid of F1s (Savitri x Pokkali) yielded 3510 kg ha^{-1} and promoted to AVT-1 in zone-III and on overall basis. IET 31878 (CR4290-281-14-3-1- 1-1-1) derived from SR 14-5-1 / Luna Sankhi with 5003 kg ha^{-1} grain yield and IET 31067 (CR 4283-274-6-2-1) derived from CR Dhan 310/ Getu with 5129 kg ha^{-1} grain yield were promoted to AVT-2 in Zone-III and Zone-VI, respectively. Another 12 elite lines in medium and late duration were identified promising in station trials and in coastal saline areas were nominated for AICRIP trials in 2025.

Breeding lines identified with multiple stress tolerance

Breeding lines such as CR 3483-1-M-4-B-SU-1-5-S-1-B and CR 3477-1-M-1-B-SU-78-S-2-B were detected with multiple stress tolerance (salinity and osmotic stress) in the AICRIP-Physiology trial. Besides, two saline tolerant lines, CR 4215-2-5-2-M-4-SU-2-S-1, CR 4111-1-2-1-B-SU-1-SU-B were identified with submergence tolerant through evaluation at submergence screening facility.

Evaluation of Breeding lines under salinity stress (EC=12 dSm-1) during *kharif* 2024

Around 240 breeding lines (F_2–F_4), along with checks FL 478 (tolerant) and IR29 (susceptible), were evaluated for salinity tolerance at the seedling stage. Fifty lines were identified as tolerant (SES score 3) and 146 as moderately tolerant (SES score 5). Among these, CR 4182-4-2, CR 4525-BC-1-38-1, CR 4523-BC-1-23-1, and CR 4186-2-1-2-2 showed over 93% survivability with an SES score of 3. Approximately 11,000 tolerant and moderately tolerant seedlings (scores 3 and 5) were rescued and transplanted for generation advancement.

Evaluation of salinity tolerant 'Mutant Shatabdi' lines

Mutant lines of cv. Shatabdi; CR 6509-400Gy-6-Sal-3-5-B, CR 6509-300Gy-1-Sal-1, CR 6509-300Gy-1-Sal-5-1, CR 6509-500Gy-1-Sal-4-2-B, and CR 6509-300Gy-11-Sal-4-3-B were identified as salinity tolerant both at seedling and reproductive stages, while retaining the grain type and agro-morphological traits of Shatabdi. In a replicated yield trial under normal conditions during *rabi* 2024–25 at ICAR-CRRI, Cuttack. CR 6509-400Gy-6-Sal-3-5-B, CR 6509-500Gy-1-Sal-4-2-B, and CR 6509-300Gy-11-Sal-4-3-B (Fig.1.19) recorded significantly higher yields (4325–4576 kg ha^{-1}) than Shatabdi (3700–4140 kg ha^{-1}). These lines were nominated for multilocational testing under AICRPR in *kharif* 2025.

QTLs for reproductive stage salinity tolerance in rice

Using backcross-derived (IR64/Pokkali) and RIL (Savitri/AC39416a) populations, salinity tolerance at the reproductive stage was mapped using SSR, 50K SNP, and 44K SNP marker systems, identifying 9, 22, and 9 additive-effect QTLs, respectively. Several common QTLs—*qSSI-STE-2-1*, *qSSI-STE-4-1, qPL_NS-6-1, qGrain-S-4-1, qSTE-NS-3-1, qGrain-NS-4-2, qGWT_S-4-1, qDEG_S-3-1, and qK_S-1-1*—were associated with key traits including spikelet sterility,

Fig. 1.19. Field view of salinity tolerant mutant of Shatabdi, CR 6509-300Gy-11-Sal-4-3-B

panicle length, grain number, spikelet degeneration, grain weight, and flag-leaf K^+ concentration. Potassium transporter genes (*LOC_Os06g45940.1, LOC_Os02g31910.1, LOC_Os04g32920.2*) were identified as putative candidates for further validation.

Hybrid rice for enhancing yield, quality and sustainability

(RL Verma, JL Katara, Reshmi Raj KR, S Sarkar, Priyamedha, S Samantaray, Parameswaran C, SK Dash, Devanna BN, M Chakraborti, AK Mukherjee, SD Mohapatra, BC Marndi and MK Kar)

Maintenance of source nursery

A source nursery with 1261 diverse genotypes was constituted, maintained, and characterized; of these, 37 lines that harboured Rf (*Rf3* and *Rf4*) genes were utilized in the crossing program.

Development of CMS, restorer and hybrid combinations

A total of 862 test crosses from 12 CMS lines and 167 pollen parents (with >5.0 GEBVs) were evaluated, leading to the identification of 18 heterotic hybrids (3 long, 5 mediums, 2 medium-early, and 8 medium-slender), 13 maintainers, and 41 good restorers. The medium-duration CMS; CRMS61A (Kalinga-I) (BCN283-24) exhibited 42% outcrossing. Furthermore, 83 sterile backcrosses (BC2-BC12) with improved seed producibility and sustainability (BLB, BPH, wide compatibility, and outcrossing) were advanced.

Hybrid release/new promising hybrid combinations

The medium-duration hybrid CR Sankar Dhan 706 (IET 30613), with long-bold grains, was released and notified for cultivation in Odisha, Bihar, West Bengal, Jharkhand, and Uttar Pradesh **(**Fig.1.20**)**. Another medium-duration hybrid, CR Sankar Dhan 705 (IET 29752), with long-slender grains, high HRR (67.7%), moderate protein (7.36%), Zn (16.2 ppm), and high Fe (10.0 ppm), was released by SVRC, Odisha. Hybrids CRHR-166 (AVT-1 Late) and CRHR-175 completed three years of AICRPR testing. CRHR-181 was evaluated in AVT-1-M in Zone VI, while CRHR-192 (IET 33078; 7663 kg ha^{-1}) was promoted to AVT-1-IM in Zone III. In Bihar state trials, CRHR-150 and CRHR-105 completed three years of testing, CRHR-154, CRHR-156, and CRHR-173 two years, and CRHR-175, CRHR-181, and CRHR-187 one year. Under adaptive trials in Odisha, five hybrids (CRHR-173, CRHR-175, CRHR-181, CRHR-185, and CRHR-187) showed yield superiority over checks **(**Fig. 1.21**)**. Under DSR at CRRI, five hybrids (CRHR-102, CRHR-181, CRHR-187, CRHR-191, and CRHR-192) were superior. Of 27 new hybrids revalidated in 2024–25, 16 showed consistent yield advantage (6.22–23.58% heterosis) over hybrid checks

Trait development/genetic diversification of parents and hybrids

The restorer Improved IR42266-29-3R and maintainer Improved CRMS 32B were introgressed with BPH31. Introgression of WC genes into *ixj* ABL SR 11-3-1 (donor: Khawo-Hawm) was completed, while CR 1033 (donor SR1-5-1) was advanced to BC_2F_4. Introgression of HT (*AHAS*), *BPH31*, and *Xa38/Xa21* into elite restorers (Pusa 33-30-3R, CR 22-102-5-1, CR 22-16-5-1-1, CR 22-103-1, and CRL123R) reached BC_2F_2. Improved CRMS31B and CRMS32B carrying 4BB resistance, *Sub1*, and *Saltol* are under CMS conversion. Introgression of the long-stigma trait from *O. longistaminata* into CRMS31B and CRMS32B progressed to BC_3F_9, with 12 fixed long-stigma lines under CMS conversion (BC_6F_1) and 21 lines advanced to BC_3F_1.

Development of heterotic pool

A total of 308 genetically diverse lines (91 maintainers and 218 restorers) were phenotyped and genotyped using 342 hypervariable SSR markers. The data are now being utilized for the development of heterotic groups.

Restorer and maintainer breeding

A total of 3280 single-plant progenies (F_3 to F_{14}) from 138 crosses (AxR, RxR and BxB) were evaluated, with 48 selected for use in HR breeding. Six random mating populations (RMPs), consisting of four maintainers and two restorers, were advanced to the 12th RMP generation. Besides, two inter-subspecific MAGIC populations (B and R, each comprising with 10 parental genotypes) were advanced to the IC3F6.

Genomic selection and speed breeding

Total 112 breeding populations (F3 to F8) were advanced under field RGA. In Parental Selection Trial-5, 120 entries, including 30 ABLs from CRRI (F6-7generation, 11 families), were phenotyped across four locations; amongst, 17 ABLs with yields over 6.0 t ha^{-1} and high BLUP were selected for hybrid development. In the station trial for *kharif 2025*, 1033 ABLs of R and B derivatives were evaluated along with checks, of those 138 lines yielding more than 6.0 t ha^{-1}.

Seed production of parents/hybrids

Total 1008.5 kg of TL seeds of 28 hybrids were produced, along with 149.0 kg of breeder seeds from 14 CMS lines and nucleus seeds from 6 hybrids. Agro-practices for seed production of 14 new hybrids were refined. Additionally, 25 paired crosses for each CMS line CRMS 31A, CRMS 32A, PMS17A, IR 42266-29-3R, CRL 22R, CRL123R, and CR 546 with CMS were generated and evaluated for the constitution of nucleus seeds of the respective parental lines.

DNA fingerprinting of parent/hybrid

Fingerprints of the hybrids CR Dhan 706, CRHR 166, CRHR 175 and CRMS 60A were generated using 36 hypervariable SSR markers. Through GWAS analysis of 182 lines, a QTL hotspot (09_4136552) was identified, influencing the number of secondary branches (NSB), grain filling (NFG), and yield (GYP).

Fig. 1.20. Field view of rice hybrid, CR Sankar Dhan 706

Fig. 1.21. Performance of new hybrids in adoptive trials in Odisha

Evaluation of AICRIP trials

Altogether, 04 hybrid rice AICRPR trials, IHRT-E (19 entries), IHRT-ME (48 entries), IHRT-M (34 entries), and IHRT-MS (10 entries) were evaluated, and data have been submitted to the Coordinator.

MoUs/Consultancy services

A total of 16 licenses for three hybrids; CR Dhan 702, CR Dhan 703 and CR Dhan 704 were granted to M/s Daftari Seed, M/s Nirmal Seeds Pvt. Ltd, M/s Niali Farmer Producer Company Limited, M/s Mahanga Farmer Producer Company Limited, M/s Baramba Farmer Producer Company Limited, and M/s Tangi Farmer Producer Company Limited for commercial seed production.

Development of New Generation Rice for enhancing yield potential in favourable ecology

Identification and release of variety CR Dhan 604

(SK Dash, L Behera and J Meher)

The new variety CR Dhan 604 (Fig. 1.22) was identified and released for Odisha after three years of AICRIP testing (2022–2024), where it consistently outperformed checks. It recorded a mean yield of 6913 kg ha^{-1}, showing 23%, 21%, and 26% higher yield over the national (IR64), regional (Gautam), and local checks, respectively. CR Dhan 604 flowers in 100–105 days and matures in 130–140 days. It has long-slender grains, making it highly suitable for the Odisha market and attractive to farmers, millers, and consumers. The

Fig. **1.22** Field view of CR Dhan 604, panicles and grains

Fig. 1.23. CR 3074-1-1-1-1, a potential advance culture with superiority of yield performance in rich and marginal environment

variety is resistant to leaf blast, neck blast, false smut, stem borer and moderately resistant to sheath rot, sheath blight, bacterial blight, leaf folder, gall midge and BPH.

A total of nine NGR entries were promoted to advance varietal trials, out of which i.e. CR 3856-44-22-2-1-11-4-1-1 was promoted to AVT1 while CR3938-1-2-1-4-1-2 , CR 4459-3-1-1-1-1, CR4379-4-3-1-1-12 , CR 6316-14-1-1-1-1, CR4379-12-1-1-1-1, CR 4474-7-5-4-3-1, CR 3844-38-2-2-3-1 and CR 3984-2-1-1-2 were promoted to AVT2 in AICRIP trial. Pre-breeding lines of *O. rufipogon* has been used in varietal development programme and a total of four disomic lines i.e. CR 4209-228-3, CR 4205-229-15-1, CR 4209-228-1-55-77-2 and CR 4205-226-52-50-7-1 have been promoted in AICRIP trial from IVT to AVT1. Out of the entries CR 6316-14-1-1-1-1 (IET 32394 in IVT IME) recorded potential yield of 11.381 t ha^{-1} at Puducherry followed by CR 3856-44-22-2-1-11-4-1-1 with 9.048 t ha^{-1} (AVT1 IM). Similarly, advanced varietal trial for optimum environment recorded highest grain yield of 8.575 t ha^{-1} (C4057-6-1-1-1) , followed by 8.52 t ha^{-1} (C3074-1-1-1-1) and 8.495 t ha^{-1} (C4612-3-1-1-1) and 8.23 t ha^{-1} (C4055-3-1-1-2) with yield superiority of 33.17 to 38.75% over the best check CR Dhan 307. Similarly, in an advance varietal for marginal environment, C4197-4-1-3 and C3074-1-1-1-1-3 (Fig. 1.23) recorded the productivity of 7.332 t ha^{-1} followed by 5.528 t ha^{-1} with yield superiority of 64.7% and 24.2%, respectively.

Targeted trait improvement in available NGR cultures (SK Dash, L Behera and AK Mukherjee)

Marker trait association studies for heavy panicle genotypes have been studied. One NGR with heavy panicles with introgression of BB, Sheath Blight, BPH resistance was released as CR Dhan 316. The validation of gene was done for sheath blight, BB and BPH using marker RM11935, RM11968, RM11945 (for sheath blight), *XA5, XA13, XA21*(for BB) and, *BPH 31*(PA26 & RM2334 (for BPH), respectively. A total of 23 plants were found to be positive for all the targeted genes. An average of 89-92% of genome recovery was found in BC$_3$F$_1$ stage, and was allowed for selfing to generate BC$_3$F$_2$ seeds (*rabi* 2025). A total of 19 BC$_3$F$_2$ plants were found to be homozygous for all the targeted genes. The genotypes have been evaluated during 2024 and has been repeated in 2025 as well.

Molecular dissection of NGR traits (SK Dash, RP Sah, Anilkumar C, L Behera and Parameswaran C)

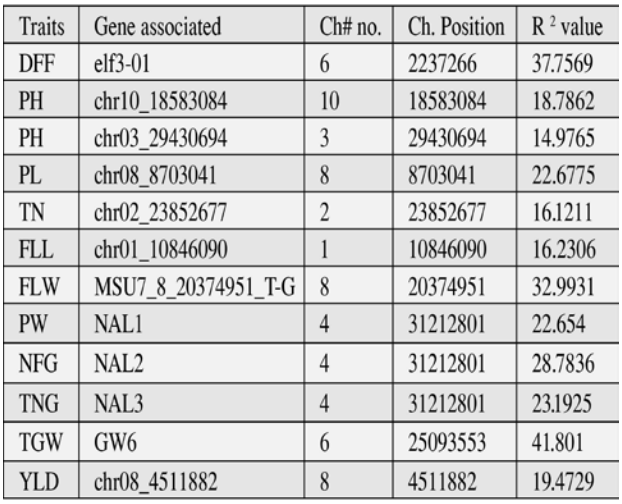
Upon genotyping and analysis of 200 cultures with significantly higher yield and NGR traits, it was found that these were positive for *GS3, Ghd7-2-02, elf3-01, NAL, TGW6, Spike, ToND 1 and GRF-4* indicating heading date, panicle traits, grain traits and N-use efficiency related traits are majorly contributing towards high yield. These 92 genotypes were selected on the basis of heavy panicle which included NGR, HYV and other materials to study harvest index on the productivity of NGR in breaking yield ceiling. Genome wide association study is in progress using 1K RiCA genotyping. Initial analysis could identify the following QTLS which may be further confirmed for molecular breeding (Table 1.5). The result shows plant height (PH), panicle length (PL), tiller number (TL), flag leaf length (LL), leaf width (LW) and panicle weight (PW), Total no. of grains (TNG), 1000-grain weight (TGW) and grain yield (YLD) have phenotypic variance of more than 10 and hence the QTLs identified could be of significant value.

Commercialization of NGR variety, CR Dhan 314 (SK Dash)

Commercialization of NGR variety CR Dhan 314 (Fig.1.24) has been done through signing of MoU with M/s Mangal Murti Seeds Pvt. Ltd. (Odisha) &

Fig. 1.24. CR Dhan 314 in farmer's Field

Table 1.5 Chromosomal position of genes associated with studied traits.



Traits	Gene associated	Ch# no.	Ch. Position	R ^{2} value
DFF	elf3-01	6	2237266	37.7569
PH	chr10_18583084	10	18583084	18.7862
PH	chr03_29430694	3	29430694	14.9765
PL	chr08_8703041	8	8703041	22.6775
TN	chr02_23852677	2	23852677	16.1211
FLL	chr01_10846090	1	10846090	16.2306
FLW	MSU7_8_20374951_T-G	8	20374951	32.9931
PW	NAL1	4	31212801	22.654
NFG	NAL2	4	31212801	28.7836
TNG	NAL3	4	31212801	23.1925
TGW	GW6	6	25093553	41.801
YLD	chr08_4511882	8	4511882	19.4729

M/s Ambedkar Nagar Agro Krishi Vikas Producer Company Ltd. (U.P.). Similarly, CR Dhan 108 has been commercialized through M/s Basant Agro Tech (India) Ltd., Kaulkhed, Akola, Maharashtra.

Utilization of genome editing, *in vitro* mutagenesis, transgenics and doubled haploid technologies for rice improvement

Anther culture device (Patent No. 574471, granted 25 November 2025) (S Samantaray, Parameswaran C, Devanna BN, JL Katara and RL Verma)

The "Vacuum-Based Anther Culture Device and Method of Doubled Haploid Production" (Patent No. 574471, granted 25 November 2025) is a compact, multi-functional device which enables rapid and efficient doubled haploid production in rice, accelerating the development of homozygous breeding lines. Its sterile, autoclavable design minimizes contamination, ensuring higher tissue culture and regeneration success. High-throughput anther collection (500 - 600 anthers per minute) markedly improves efficiency over manual methods, while the collector/media container also supports anther collection for crossing and pollination in breeding programs.

Rice varieties released through Androgenic-based DH technology (S Samantaray and RL Verma)

A total of 5 DH varieties were released across different ecologies through SVRC-Odisha (2025): CR Dhan 215 (Indumati) with salinity and anaerobic germination tolerance for coastal and aerobic areas; CR Dhan 325 (Salila) and CR Dhan 334 (Satyadev), both medium-duration doubled haploid varieties suited for irrigated ecosystems; CR Dhan 335 (Alok), a premium quality variety adapted to DSR, irrigated, and rainfed shallow lowlands and CR Dhan 912 (Ashutosh Mehek) is a high-yielding, non-basmati aromatic variety with premium grain quality for the irrigated ecosystem. Out of which 4 DH varieties got notified: CR Dhan 215, CR Dhan 325, CR Dhan 335 and CR Dhan 912.

A DH line CRAC-3998- 41-2, with a low GI (55.0) has been nominated in SVRC-Odisha. A total of 3 DH lines were identified showing tolerance to abiotic stress and submergence (AICRIP Physiology,2024): CRAC-4423-10 (salinity and submergence); CRAC 4424-122 (salinity) and CRAC 4423-49 (osmotic).

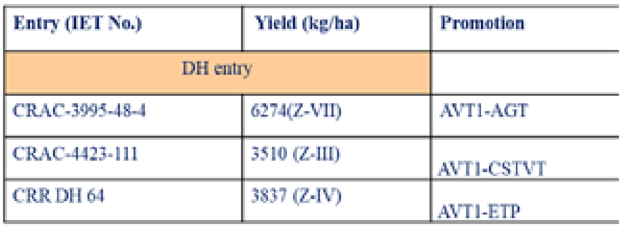
Nomination of promising DH lines to AICRIP -2025 (S Samantaray, RL Verma, Parameswaran C and Devanna BN)

A total of 22 DH lines were nominated for various trials under the AICRP *kharif* 2025 (**Table 1.6**). These trials span a diverse range of categories, including IVT-MS, IVT-IM, IVT-ETP, IVT-CR, IVT-Biofort, IVT-Aerobic, IVT-CSTVT, IVT-Late showcasing the versatility of the DH lines for different agro-climatic zones and traits. Notably, CRAC-3995-48-4 derived from parentage BS6444G, have advanced from IVT-AGT to AVT1-AGT in Zone VII. Similarly, CRR DH64, developed from the cross Savitri × Pokkali, has been promoted from IVT-ETP to AVT1-ETP in Zone IV along with CRAC-4423-111 (developed from Savitri × Pokkali), has been promoted from IVT-CSTVT to AVT1-CSTVT **(Table 1.7).**

Table 1.6. List of DHs nominated to AICRIP 2025.

AICRIP Trials	DHs	Parentage	Dff	Yield(t ha^{-1})
IVT-MS	CRAC-3998-118-4	27P63	88	6.67
IVT-MS	CRAC-3998-39-7	27P63	85	4.82
IVT-MS	CRAC-3998-169-2	27P63	98	5.12
IVT-ETP	CRAC-3998-62-2	27P63	90	5.28
IVT-ETP	CRAC-3998-105-3	27P63	88	5.35
IVT-CR	CRAC-6465-3	A42xN22	105	3.91
IVT-CR	CRAC-6465-6	A42xN22	98	4.12
IVT-Biofort	CRAC-3998-129-1	27P63	95	4.21
IVT-Biofort	CRAC-3998-77-1	27P63	90	4.13
IVT-IM	CRAC-3998-106-2	27P63	107	6.57
IVT-IM	CRAC-6467-40-2	CRHR 150	104	4.69
IVT-IM	CRAC-6467-45-1	CRHR 150	102	5.01
IVT-Late	CRAC-6465-72	A42xN22	111	5.92
IVT-Late	CRAC-6467-41-4	CRHR 150	110	4.42
IVT-Late	CRAC-6467-40-1	CRHR 150	108	4.53
IVT-CSTVT	CRAC-4423-17-1	Savitri x Pokkali	97	5.12
IVT- CSTVT	CRAC-4424-122	8433DT	98	4.65
IVT- Aerobic	CRAC-4423-49	Savitri x Pokkali	95	5.32
IVT- Aerobic	CRAC-4424-31-1	8433DT	94	5.31
IVT- Aerobic	CRAC-4424-171	8433DT	102	5.11
IVT-MS	CRAC-4424-9	8433DT	97	5.14
IVT-IM	CRAC-4424-23	8433DT	100	4.81

Table 1.7. List of DHs promoted in AICRIP 2025.



Entry (IET No.)	Yield (kg/ha)	Promotion
DH entry		
CRAC-3995-48-4	6274(Z-VII)	AVT1-AGT
CRAC-4423-111	3510 (Z-III)	AVT1-CSTVT
CRR DH 64	3837 (Z-IV)	AVT1-ETP

DH lines registered in NBPGR (S Samantaray, RL Verma, Parameswaran C and Devanna BN)

Two promising DH lines CR 4423-14 (INGR 25044): osmotic dehydration tolerance at seedling stage with higher shoot dry weight under severe osmotic stress (2%) and CR4423-17(INGR 25005) with multiple abiotic stress tolerance such as osmotic, drought, salinity and with high anaerobic germination, got registered in NBPGR. during 2025.

Identification of yield and yield-related QTLs in DH population of B x R lines of rice hybrid CR Dhan 704 (Anilkumar C, S Samantaray and RL Verma)

Yield and yield-related QTLs were identified in a DH population of B x R lines of rice hybrid CR Dhan 704 developed through androgenesis. A total of 104 SSR markers were employed across 110 DHs with identification of several QTLs governing grain yield and components. q$GPP_{10.1}$ (grains per panicle) was found to be a stable QTL (**Table 1.8**) explaining ~13% phenotypic variation across both *kharif* and *rabi* seasons.

Efficiency of DH technology in introgression of BB and drought genes/QTLs into an elite rice variety, Daftari-1008 (S Samantaray, RL Verma, Parameswaran C and Devanna BN)

The potentiality of the androgenic protocol was proven by producing a significant number of DHs by amalgamating BB genes (*Xa21+xa5+xa13*) and drought qtls (*qdty2.1+qdty3.1*) into elite rice variety "Daftari-1008" and generate traits (BB+ drought) pyramided DH population with both the donors, CR Dhan 800 and CR Dhan 801.Out of 22 DHs carrying any four gene/QTLs combinations, five DHs exhibited stable BB resistance with lesion lengths of 3.38–21.23% while four DHs showed mean yield reduction of drought screened DHs (12.27–49.6%) as compared to irrigated conditions. Further, a total of six DHs recorded 6.31–14.60% higher yield than Daftari-1008, and lastly two DHs were identified for resistant to BB, tolerance to drought and high yielding.

In vitro mutagenesis (S Samantaray, Parameswaran C)

Mutant lines derived from the aromatic rice landraces Acharmati and Tulasikanthi were developed through EMS-based mutagenesis *in vitro* mutagenesis and systematically characterized. Height reduction of mutants ranged between 19.76-39.14% and 7.38%-38.25% in EMS derived mutants (M_1) of Acharmati and Tulasikanthi, respectively (Fig. 1.25).

Fig. 1.25. A: Mutants of Acharmati (M1), B: mutants of Tulasikanthi (M1)

Fig. 1.26. Maintenance of edited lines with wild type (WT) control. (A) Edited lines showing ~40 cm height reduction compared to WT control. (B) T1 lines growing in the climate controlled green house with the control

CRISPR-Cas9-mediated *OsSD1* knockout confers semi-dwarfism in aromatic rice landrace Nua-Kalajeera (KA Molla)

Aromatic landraces like Nua-Kalajeera are prized for their quality but are limited by tall height and lodging. This study used CRISPR-Cas9 to edit the *OsSD1* gene, developing semi-dwarf, lodging-resistant Nua-Kalajeera lines. Three hypotheses were tested in this study; (1) establishing an efficient *in vitro* regeneration protocol, (2) validating *OsSD1*-targeting gRNAs using

Table 1.8. Details of main QTLs identified through inclusive composite interval mapping (ICIM) for yield-related traits in DHs derived from B x R lines of CR Dhan 704.

Trait	Ch # No.	QTL Name	Position(cM)	Left Marker	Right Marker	LOD	PVE %	Add
PT	8	*qPT 8.1*	86.78	RM23005	RM23377	3.52	11.60	1.12
PL	5	*qPL 5.1*	3.16	RM592	RM17923	3.56	11.03	0.57
PL	7	*qPL 7.1*	44.25	RM21764	RM22164	3.10	10.29	-0.54
GPP	10	*qGPP 10.1*	8.04	RM25146	RM244	3.04	12.01	10.30
SF	2	*qSF 2.1*	96.12	RM13605	RM318	3.92	11.58	-1.90
SF	8	*qSF 8.1*	69.78	RM22899	RM23005	3.82	13.29	-2.08
PH	7	*qPH 7.1*	4.25	RM20913	RM21136	3.58	11.46	-1.99

a protoplast-based assay, and (3) generating stable semi-dwarf mutants without yield compromise. A high-efficiency regeneration protocol was standardized with a regeneration rate of ~72%. A rapid protoplast transfection system achieved up to 81% efficiency, confirming gRNA activity via PCR and sequencing. CRISPR-Cas9 editing could produce stable T_0 lines with large deletions (382 bp, 621 bp) in *OsSD1*. Edited plants showed significant height reduction (~40 cm), increased tiller number, and no adverse effects on fertility, panicle length, or photosynthesis (Fig. 1.26). HPLC-MS revealed up to 57.2% lower GA_3 levels; histological analysis showed 26.3% reduced internodal cell length. T_1 lines are growing in the green house for further validation. This study presents a precise genome-editing platform for aromatic rice improvement, yielding semi-dwarf Nua-Kalajeera lines suitable for sustainable cultivation under changing climates.

Genome editing toolbox developed using AI-designed Cas9 (KA Molla)

Artificial Intelligence has opened numerous unique doors in every field, facilitating further improvement and development. Molecular biologists and biotechnologists not only adapted themselves to this AI era but also used AI to design various proteins. We utilized an AI-generated nuclease and made it compatible with the plant system. Plant Ai Designed (PAiD) editor has been harnessed to introduce knockout, base editing and prime editing in rice (Fig. 1.27). For knockout, we used both single and dual guides. We developed Adenine and Cytosine base editors. Prime editor has also been prepared using PAiD. For each type of editing tool, we used the wild-type counterpart i.e. SpCas9 for better comparison. The whole process includes sequential steps of vector construction, guide cloning, sequence confirmation by Sanger Sequencing, transfection in rice protoplast, isolation of DNA from protoplast, target amplification, editing confirmation by NGS and finally statistical analysis to get the complete editing profile. In most of the cases, our PAiD system showed comparable editing efficiency with SpCas9 based editor. We have also generated mutant lines using PAiD.

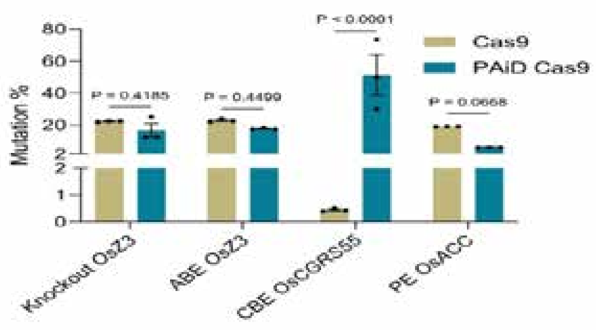


Fig. 1.27. Efficiency of PAiD assisted knockout, base editing and prime editing at different targets. Among many targets for each editing tools, only the highest performing one is presented here

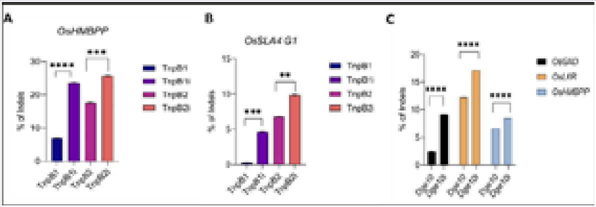


Fig. 1.28. Deep sequencing data presented in the form of bar graph showing percentage of indels derived using TnpB nuclease and intronized TnpB nuclease targeting (A) OsHMBPP and (B) OsSla4 G1 genes in rice protoplast in pK-TnpB1, pK-TnpB2, pK-TnpB1i, pK-TnpB2i background. (C) Percentage of indels derived using Dge10-TnpB nuclease and intronized Dge10-TnpB nuclease targeting three genes (OsGAD, OsLKR, OsHMBPP) in rice protoplasts in pK-Dge10B2 and pK-Dge10B2i background

Intronization of TnpB endonuclease to improve its efficiency in plant genome editing (KA Molla)

Genome editing has reshaped the landscape of plant science, with CRISPR-Cas systems being at the forefront. However, there are some newly emerged tools like TnpB, which provide unique advantages due to their small size and programmable activity. TnpB proteins are small RNA-guided endonucleases encoded by IS200/IS605 transposons and believed to be the evolutionary ancestors of Cas12 nucleases. TnpB uses a guide RNA (reRNA) derived from the transposon's right-end element to recognize and cleave DNA targets. Like Cas9, which depends on a PAM (protospacer adjacent motif), TnpB relies on an upstream TAM (transposon-associated motif) for site specificity. TnpB-variants have demonstrated RNA-guided DNA cleavage activity in bacteria, human cells and plants. However, their efficiency remains sub-optimal in many eukaryotic loci. To address this problem, present research focuses on enhancing the efficiency of TnpB-based genome editing tools. Literature studies revealed that intronization, incorporating introns into coding sequences, significantly boosts gene expression. In this study, intronized versions of 2 endonucleases of TnpB family (ISDra2 and ISDge10) were developed and compared with the conventional versions using PEG-mediated transfection of rice protoplast. NGS analysis revealed that the intronized version achieved nearly twice the editing efficiency of the conventional construct, highlighting its potential as a powerful tool for crop improvement (Fig. 1.28).

Development of Novel Genomic Resources for Rice Improvement

The blast-resistant rice genotype DHR-9, carrying the *Pi42* locus, was whole-genome sequenced to generate genomic resources for genome-editing applications. A bi-parental population of 220 recombinant inbred lines (RILs) was genotyped using the 1K RiCA SNP panel and phenotyped for bakanae disease to reconfirm the resistance QTL *qBK5.1* from the donor parent Thavalakannan. Genetic variability for straw fodder quality was assessed in 449 rice varieties released between 1921 and 2020, identifying 79 varieties with high straw protein (>7%), 77 with low lignin (<3.3%), 119 with low silica (<13.3%), and 59 with high in vitro organic matter digestibility (IVOMD >45.6%), with several varieties combining superior fodder quality and acceptable straw yield, making them suitable donors for dual-purpose breeding. Haplotype analysis of six drought-responsive genes—*OsCYP72A32, OsNCX5.2, OsSPX2, OsSTA104, OsRING313*, and *Os3BGlu6* under drought stress identified superior haplotypes in four drought-tolerant genotypes (NCS 901 A, H 15-23-DA, LOHAMBITRO, and MEJANES 2). PCR-based analysis using brown planthopper (BPH) resistance candidate gene-specific primers for RPM1, leucine-rich repeat family protein, and ZOS4-01-C2H2 zinc finger protein revealed clear polymorphisms between resistant (Salkathi and CR-3006-8-2) and susceptible (TN1 and Naveen) parents, supporting their potential role in BPH resistance mechanisms in Salkathi.

Whole-genome re-sequencing and marker development for key resistance loci (Devanna BN, Parameswaran C and L Behera)

The blast-resistant rice genotype DHR-9, harbouring the *Pi42* locus, was whole-genome sequenced using the Illumina platform. High-quality reads were aligned to the Nipponbare reference genome to assemble DHR-9–specific scaffolds. The scaffold corresponding to the *Pi42* locus was extracted and characterized, generating a valuable sequence resource for resistance gene analysis and genome-editing applications (Fig. 1.29).

Identification and mapping of QTLs and genes associated with biotic stress resistance, abiotic stress tolerance, and straw quality

Mapping genomic regions for Bakanae disease resistance (Anilkumar C, RP Sah, Raghu S and L Behera)

A bi-parental population of 220 recombinant inbred lines (RILs) was genotyped using the 1K RiCA SNP panel. Phenotyping for bakanae disease resistance is in progress to reconfirm the reported *qBK5.1* QTL from the donor parent Thavalakannan.

Assessment of straw fodder quality in rice varieties released before and after the Green Revolution (RP Sah, L Behera and A Kumar)

A total of 449 rice varieties released between 1921 and 2020 were evaluated for straw protein, fibre, lignin, silica, in vitro organic matter digestibility (IVOMD), and straw yield. Wide genetic variability was observed across traits (Fig. 1.30), with digestibility and silica content contributing most to phenotypic variation. Lower lignin content was associated with improved digestibility, and post–Green Revolution varieties maintained fodder quality alongside higher grain yield. The screening identified 79 varieties with high straw protein (>7%), 77 with low lignin (<3.3%), 119 with low silica (<13.3%), and 59 with high IVOMD (>45.6%). High straw protein was recorded in Nagarjuna, Pavizam, and Ratnagiri-5, while Daya, Asha MO-5, and Jalaprava showed superior IVOMD. Straw yield was highest in Jalamani, CO-27, and Sonamani, whereas CO-34, CO-07, and Tanmayee exhibited the lowest lignin content, and CO-07, Jalaprava, and Samalei recorded the lowest silica levels. Varieties such as Jalamani, Tanmayee, Ratnagiri-1, Karjat-4, Ghanteswari, Nagarjuna, and IR-28 combined superior fodder quality with acceptable straw yield and were identified as promising donors for dual-purpose rice breeding. Regression analysis indicated that fodder quality traits have remained largely unchanged over time, while grain yield has improved due to targeted breeding (Fig. 1.31).

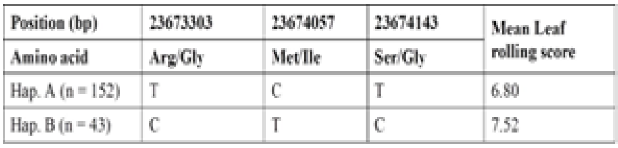
Gene prospecting and epigenetic analysis for abiotic stress tolerance (Parameswaran C, J Meher, Devanna BN, and L Behera)

Haplotype analysis of six drought-responsive genes, *OsCYP72A32* (Table 1.9, Fig. 1.32), *OsNCX5.2, OsSPX2, OsSTA104, OsRING313,* and *Os3BGlu6,* under drought stress identified superior haplotypes in four drought-tolerant genotypes, NCS 901 A, H 15-23-DA, LOHAMBITRO, and MEJANES 2 (Fig 1.33). High genetic advance for relative water content, plant height, and leaf number highlighted their usefulness as selection criteria for drought-tolerance breeding.

Functional validation of candidate genes for biotic stress resistance (M Chakraborti, G Pandi G, MK Kar, L Behera and Devanna BN)

Gene-specific primers were designed for candidate genes underlying brown planthopper (BPH) resistance QTLs, including disease resistance protein *RPM1*, leucine-rich repeat family protein, *ZOS4-01-C2H2* zinc

Table 1.9. Non-synonymous SNPs in the *OsCYP72A32 (Os01g0602400)* gene significantly associated with leaf rolling score and amino acid variations..



Position (bp)	23673303	23674057	23674143	Mean Leaf rolling score
Amino acid	Arg/Gly	Met/Ile	Ser/Gly	
Hap. A (n = 152)	T	C	T	6.80
Hap. B (n = 43)	C	T	C	7.52

finger protein (*qBPH4.3*), and serine/threonine-protein kinase (*qBph4.4*), using whole-genome sequence data from resistant (Salkathi) and susceptible (TN1) genotypes. PCR amplification using resistant (Salkathi and CR-3006-8-2) and susceptible (TN1 and Naveen) parents revealed clear polymorphisms for one primer pair each from RPM1, leucine-rich repeat family protein, and *ZOS4-01-C2H2* zinc finger protein (Fig. 1.34). These markers will be validated in mapping populations to confirm their association with BPH resistance

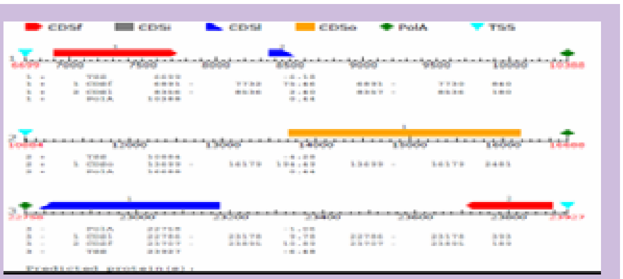


Fig. 1.29. Prediction of genes in the Pi-42 locus specific scaffold extracted from rice genotype Nipponbare and corresponding region in 'DHR-9'

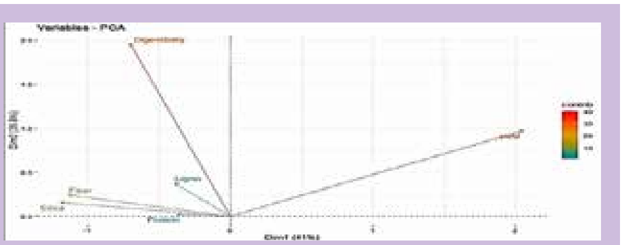


Fig. 1.30. Contribution of fodder quality traits to total diversity among 449 varieties

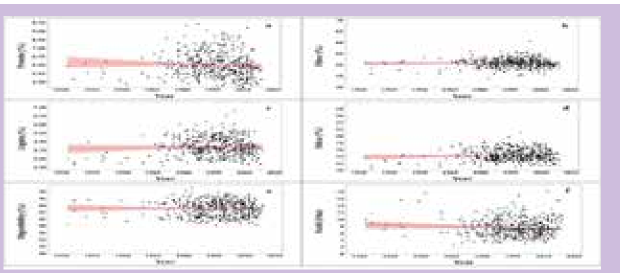


Fig. 1.31. Regression plots showing trend of key traits over years

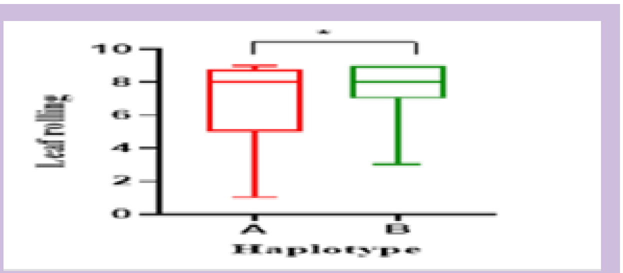


Fig. 1.32. Variation in mean values of leaf rolling score indicated haplotypes of OsCYP72A32 (*p < 0.05)

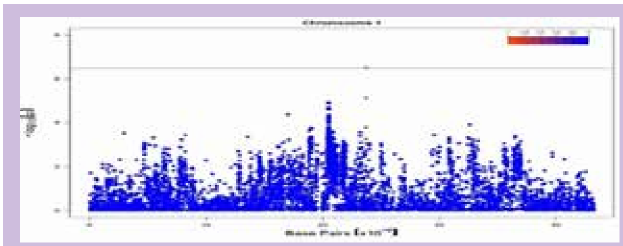


Fig. 1.33. Linkage Disequilibrium map of chromosome 1

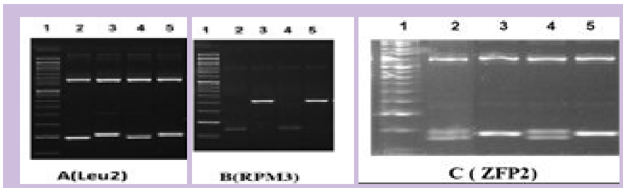
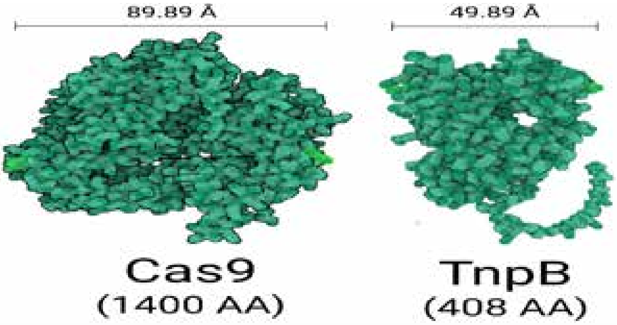


Fig. 1.34. PCR amplification with primers specific to (a) Leucine rich repeat family protein, (b) disease resistance protein RPM1, (c) ZOS4-01 - C2H2 zinc finger protein, 1- 50 bp DNA ladder, 2-Salkathi, 3- TN1, 4- CR-3006-8-2, 5-Naveen

Conclusion

The Genetic Improvement of Rice Programme has made significant progress in developing high-yielding, climate-resilient, and nutritionally enriched rice varieties through the integration of conventional breeding and advanced genomic tools. The use of marker-assisted selection, gene pyramiding, doubled haploid technology, rapid generation advancement, and genome editing has accelerated the development of superior genotypes with resistance to major biotic and abiotic stresses. Extensive germplasm characterization and the identification of trait-specific donors have strengthened the genetic base for future breeding programmes. The release and promotion of improved varieties and hybrids, along with enhanced seed production and dissemination, have contributed to increasing productivity and ensuring seed availability. Emphasis on biofortification, direct-seeded rice systems, and resource-use efficiency further supports nutritional security and sustainable agriculture. Overall, the programme is well-positioned to address emerging challenges in rice production and to deliver innovative, farmer-centric solutions for improving livelihoods and ensuring food and nutritional security.



New plant genome editing tool based on TnpB

PROGRAMME
02

Enhancing Productivity, Sustainability and Resilience of Rice Based Production System

Improvement in productivity, profitability, efficient use of resources, climate resilience are the major requirement in sustainable rice production. An integrated program has been conceptualized to produce and promote innovations for rice-based systems. It focuses on development in precise nutrient and water use through the application of digital technology and nanotechnology, site-specific cropping practice for pest and weed management, environment friendly rice residue management techniques, design, develop and refinement of small farm equipment, microbe-based techniques for nutrient management. It also includes impact evaluation of land-use changes, as well as the promotion of climate smart technologies, to improve resilience in stress-prone regions.

Enhancing nutrient use efficiency in rice through advance agronomy using smart sensors, models and nano fertilizers

Calibration and validation of GreenSeeker for in-season nitrogen application in rice (Sangita Mohanty and Rahul Tripathi)

A field experiment was conducted during the wet season of 2024 using long-duration rice varieties Pooja and Swarna to evaluate a previously developed NDVI-based nitrogen topdressing strategy. The experiment followed a split-plot design with varieties as main plots and nitrogen management treatments as sub-plots, replicated thrice. Four nitrogen treatments comprised of two GreenSeeker (GS)-based strategies, the recommended dose of nitrogen (RDF) applied in three equal splits, and an absolute control, with N-rich plots (120 kg N ha^{-1}) maintained for all varieties. NDVI measurements taken at maximum tillering and panicle initiation were used to estimate In-Season Estimate of Yield (INSEY) and guide the first and second topdressing applications, which varied from 20.7 to 30.1 kg N ha^{-1}. Grain and straw yields and yield attributes were recorded at harvest. Grain yield under GS-based N management ranged from 4.57 to 5.12 t ha^{-1}, while agronomic nitrogen use efficiency varied from 21.2 to 24.3 kg kg^{-1}. For both the varieties, yields under GS-based N application were statistically *at par* with those under the recommended N dose.

Nitrogen metabolism in 52 years old long-term fertility paddy soil (Upendra Kumar)

De-novo whole metagenome sequencing was conducted in 6 contrasting treatments (absolute control, N, NPK, FYM, FYM+N and FYM+ NPK) from paddy soil of 52-year-old Long-Term Fertilizer Experiments (LTFE). Nitrogen metabolism pathway was analyzed using the Kyoto Encyclopedia Genes and Genomes (KEGG) pathway. The results indicated that Glutamate synthetase (Gln A) protein was enriched in all LTFE treatments, suggesting that ammonium is mainly assimilated through glutamate metabolism under these treatments. Interestingly, Arginine biosynthesis pathway (ArcC and CynT) was also present in FYM and FYM+N treatments, in addition to Glutamate synthetase. ArcC plays a role in a carbon-nitrogen coupling pathway, highlighting its importance in balancing the metabolic needs of organisms for both carbon and nitrogen, while CynT plays an important role in nitrogen fixation. The presence of both pathways in FYM and FYM+N treatments suggests that the addition of FYM might enhance the alternative pathway. Nitrite reductase (cytochrome c-552) (NrfAH), responsible for Dissimilatory Nitrate Reduction to Ammonium (DNRA) activity, was enriched in all LTFE treatments except control and NPK. Nitrous oxide reductase (NorBC) was present in control which is responsible for denitrification activity that converts nitric oxide to nitrous oxide whereas in NPK, nitrate reductase (NarGHI) was enriched, which is responsible for the conversion of nitrate to nitrite and denitrification. Notably, ammonia monooxygenase (AmoCAB) was enriched in FYM and FYM+N treatments, catalyzing the oxidation of ammonium to hydroxylamine (nitrification pathway). Nitrification (AmoCAB), denitrification (NirK) and DNRA (NrfAH) proteins were enriched together in FYM and FYM+N treatments.

Evaluation of organic nutrient management for soil carbon and nitrogen (C-N) dynamics in rice-based systems (Debarati Bhaduri)

A trial on organic nutrient management (ONM) in rice-based system was implemented for long-term organic input-based treatments, comprising of FYM, rice straw, rice straw compost, green manure (*in-situ*), biofertilizer (Endo-N) both alone and in combinations. The performance of aromatic rice varieties (Geetanjali, Nuakalajeera, Poornabhog) was evaluated in *kharif* and *rabi* seasons. So far, cv. Poornabhog performed better with a grain yield of 4.65 t ha^{-1} under the treatments like FYM + Green manure and biofertilizer + rice straw compost. Further, carbon and nitrogen mineralization (dC_{min}/dt and dN_{min}/dt) pattern through 90-days incubation experiments was conducted, followed by first-order model fitting, the potentially mineralizable C and N (C_0, N_0), carbon and nitrogen rate constants (k_C, k_N) receiving different ONM treatments were enumerated, revealing the highest C_0 (42.3 mg g^{-1}) and N_0 (119.3 mg g^{-1}) observed at FYM + Green manure. (Fig. 2.1)

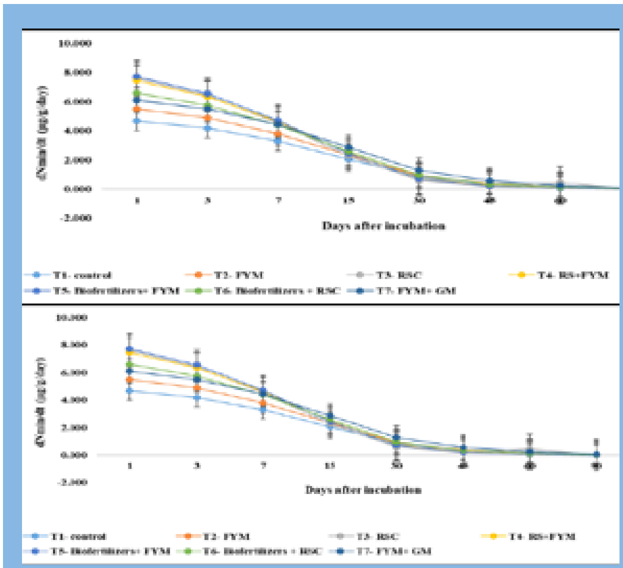


Fig. 2.1. C-mineralization rate (dC_{min}/dt) and N-mineralization (dN_{min}/dt) under different ONM treatments

Long-term organic nutrient management on carbon and nitrogen dynamics in rice-fallow systems (Dibyendu Chatterjee)

The long-term effect of organic fertilization on C and N dynamics was studied. Various C fractions such as recalcitrant C, less labile C, labile C and very labile C ranged from 24.98-51.97%, 12.64-38.85%, 18.86-43.28% and 1.19-2.21%, respectively. The potentially mineralizable C varied from 255–603 mg kg^{-1} day^{-1}. Carbon mineralization rate constant ranged from 0.081–0.111 day^{-1}. Potentially mineralizable C (C_0) and C mineralization rate constant (k_C) were highest in FYM + *Azolla* (FYAZ) application (Table 2.1). The C_0k_C factor and mineralization half-time ranged between 26.53 - 68.52 and 6.13 - 8.53 days, respectively. The lowest mineralization half-time was observed in FYAZ (6.13 days). Among 8 different treatments, the available nitrogen was observed highest under FYM + *Azolla* (397.23 kg ha^{-1}). Both C and N mineralization follow first order kinetics [$N_t = N_0(1 - e^{-kt})$].

Table 2.1. Potentially mineralizable carbon, C mineralization rate constant, half time, C_0k_C, standard error of equation and R^2 as influenced by various treatments.

Treatment	Potentially mineralizable carbon (C_0) (mg kg^{-1} day^{-1})	Carbon mineralization rate constant (k_c)(day^{-1})	C_0k_C	Mineralization half time (days)	Standard Error of equation (SE)	Coefficient of determination (R^2)
C	255.42^{f}	0.104^{ab}	26.53^{f}	6.67^{cd}	11.04	0.958
FYM	551.64^{b}	0.109^{ab}	60.27^{b}	6.36^{cd}	14.84	0.98
GM	342.04^{e}	0.081^{d}	27.82^{f}	8.53^{a}	12.97	0.973
FYGM	508.62^{c}	0.091^{cd}	46.06^{d}	7.65^{b}	15.70	0.979
FYAZ	603.68^{a}	0.114^{ab}	68.52^{a}	6.13^{d}	21.2	0.964
RSFGM	518.42^{c}	0.101^{bc}	52.34^{c}	6.87^{cd}	16.24	0.97
AZGM	394.06^{d}	0.1^{bc}	39.51^{e}	6.92^{c}	11.85	0.976
RSHGM	569.06^{b}	0.11^{ab}	62.53^{b}	6.32^{cd}	18.71	0.972
F value	320.58	8.859	137.54	12.75		
$P < \pm 0.05$	< 0.001	< 0.001	<0.001	< .001		

Long-term organic nutrient management on weed flora in rice-fallow systems (Dibyendu Chatterjee and Sushmita Munda)

The long-term effect of organic fertilization on weed flora and weed seed bank was studied. Observations like weed density, dry matter and species diversity were taken. The highest weed seed dry matter (g m^{-2}) was recorded in straw (2.5 t ha^{-1}) + green manure treatment and among the all weed species, *Echinochloa colona* contributed the most.

Mechanism of assimilation and differential gene expression under nano-urea application on rice (Dibyendu Chatterjee and Sangita Mohanty)

An experiment was conducted to study the mechanism of assimilation and differential gene expression by application of nano-urea (NU) on rice. The highest grain yield was recorded in RDF + 2 spray of nano urea, representing a 4.8% increase over 100% recommended dose of nitrogen (RDN). Yield decline of 17.7% was observed in 50% of RDN+ 2 sprays NU (compared to 100% RDN. Applying 75% of RDN (66% at basal + 17% at active tillering + 17% at panicle initiation) with two foliar spray nano-urea @ 4 mL L^{-1} of water saves 25% N with a yield penalty of 2.4% compared to 100% RDN. Both fertilizer and nano-urea treatments increased the expression of genes related to protein synthesis, signaling, and metabolism. However, the number of genes involved in these pathways was approximately 26% higher in nano urea than in NCU treatments.

National level zonation of rice ecologies, site specific planning and development of cropping and farming system models

Studies the micro-climate interactions among the enterprise components under integrated system (Annie Poonam)

An experiment was conducted during *kharif* 2024 to study the growth and yield of rice + fish under four treatments, *viz.*, control, 100% organic, 50% organic + 50% recommended fertilizer dose (RFD) and 100% inorganic (RFD @ 60: 30: 30 kg NPKha^{-1}). Long duration rice variety CR Dhan 409 (160 days) was integrated with fish (Rohu, Catla, Tilapia and Silver carp*)* in the ratio of 30: 30: 20: 20 weighing 40 - 60 g. The maximum harvest size of Rohu, Catla and Tilapia was observed under the treatment of 50% organic + 50% RFD, while the maximum harvest size of Silver carp was observed under the treatment of 100% organic. Chlorophyll a, b and total chlorophyll was observed to be higher in 50% organic + 50% RFD (Table 2.2). The highest rice equivalent yield (REY) of 11.1 t ha^{-1} was observed in 100% organic treatment. However, the highest rice grain yield was observed in 100% inorganic. On the contrary, the highest fish yield was observed in 100% organic. The highest average Zooplankton no./l and Zoobenthos (g/m^2) was observed in 100% organic (54.6 ± 3.32 mg m^{-3}) treatment.

Table 2.2. Leaf chlorophyll content (mg/g) of rice at maximum tillering stage and PI stage.

Treatments	Maximum tillering stage			Panicle initiation stage			System Rice Equivalent yield (t ha^{-1})
	chlorophyll a	chlorophyll b	total chlorophyll	chlorophyll a	chlorophyll b	total chlorophyll	
Control	3.81	3.43	20.35	2.79	2.75	20.32	5.4
100% Organic	6.46	4.19	20.38	4.17	2.72	20.32	11.1
50 % Organic + 50% RFD	8.18	5.63	20.45	6.92	4.12	20.38	10.6
100 % Inorganic (RFD)	7.20	4.99	20.42	5.68	3.34	20.35	10.9

Sustainability and profitability of different production systems under various rice-based cropping systems (B Raghavendra Goud and Dibyendu Chatterjee)

An experiment was initiated during *rabi* 2022-23 to study the sustainability and profitability of organic and natural farming systems in rice-rice, rice-green gram, and rice-groundnut cropping systems using a split plot design. Under organic farming system, varying doses of FYM were applied as per requirement of different crops. Seeds were treated with biofertilizers and *Trichoderma*. Under natural farming system, seeds were treated with *beejamrita, jeevamrita* applied as foliar spray @ 500 L ha^{-1} at 15 d interval and straw mulching (*Achhadana*) between crop rows was practiced. *Neemastra, Bramhastra* and *Agniastra* were applied to the crops for management of pests and diseases. Biodiversity in the field was promoted by growing plantation crops like coconut, arecanut, arhar and mustard on bunds in both systems and erecting straw bundles to improve the spider population in natural farming. During *rabi* 2023-24, significantly higher Rice Equivalent Yield (REY) was observed with organic farming (4.03 t ha^{-1}) over natural farming (3.67 t ha^{-1}) (Table 2.3). With respect to cropping systems, significantly higher REY was observed with groundnut (6.20 t ha^{-1}) followed by green gram (3.03 t ha^{-1}) and rice (2.30 t ha^{-1}). During *kharif* 2024-25, rice yield in organic farming (5.73 t ha^{-1}) was comparable with natural farming (5.31 t ha^{-1}). Rice-groundnut system had the highest rice yield (5.69 t ha^{-1}), significantly greater than rice-rice (5.33 t ha^{-1}). Rice-green gram system (5.54 t ha^{-1}) was comparable to both. Significantly higher system productivity was observed with organic farming (9.76 t ha^{-1}) over natural farming (8.98 t ha^{-1}). Rice-groundnut cropping system had the highest system productivity (11.89 t ha^{-1}) followed by Rice-green gram (8.57 t ha^{-1}) and rice-rice (7.64 t ha^{-1}). Organic farming demonstrated superior soil health over natural farming, yielding higher bacterial counts and significantly greater available nitrogen (215.8 vs. 183.5 kg ha^{-1}) and potassium (200.5 vs. 171.0 kg ha^{-1}), while phosphorus levels remained comparable. System-specific results showed that rice-rice cropping system in organic farming had the highest soil available nitrogen (235.8 kg ha^{-1}), whereas rice-green gram system had the higher soil available nitrogen under natural farming (194.7 kg ha^{-1}). Additionally, the rice-groundnut system optimized soil macrofauna, recording the highest earthworm density and biomass.

Table 2.3. System productivity in different production systems under various rice-based cropping systems during *rabi* 2023-24.

Treatments	Yield of *rabi* crops (t ha^{-1})	REY of *rabi* crops (t ha^{-1}) (1)	Rice yield during *kharif* (t ha^{-1}) (2)	System productivity (t ha^{-1}) (1+2)
Organic R-GG	2.23	6.46	5.92	12.38
Organic R-R	0.81	3.21	5.73	8.94
Natural R-GN	2.35	2.41	5.54	7.95
Natural R-GG	2.06	5.95	5.46	11.41
Natural R-R	0.74	2.86	5.34	8.20
Organic	2.17	2.19	5.13	7.32
Natural	-	4.03^{a}	5.73^{a}	9.76^{a}
R-GN	-	3.67^{b}	5.31^{a}	8.98^{b}
R-GG	-	6.20^{a}	5.69^{a}	11.89^{a}
R-R	-	3.03^{b}	5.54a^{b}	8.57^{b}
CD of PS	-	2.30^{c}	5.33^{b}	7.64^{c}
CD of CS	-	0.10	0.43	0.49
CD of PS x CS	-	0.25	0.23	0.21

Vulnerability analysis and assessment of climate smart agricultural technologies for enhancing resilience in stress prone rice ecologies

Climate change impact estimation using climate indices for Bolangir and Dhenkanal districts of Odisha at mid-century (2050) (RCP 4.5) (Manish Debnath)

Table 2.4. Changes in different climate indices values in 2050 over base period.

Indices	Change in magnitude for Bolangir District	Change in magnitude for Dhenkanal District	Effects
TR20 (Tropical nights)	↑ from 222 to 255 days	↑ from 243 to 276 days	Rising night time temperatures and potential heat stress.
TXx (Max Tmax)	↑ from 43.5°C to 44°C	↑ from 39.8°C to 40°C	Slight increase in peak day time temperatures; marginal but adds to heat extremes.
TNx (Max Tmin)	↑ from 28.9°C to 29°C	~Same: 28 to 28°C	Night time heat extremes intensify.
TXn (Min Tmax)	↑ from 23.8°C to 27.5°C	↑ from 23.4°C to 27°C	Significant rise in the lowest daily maximums, meaning even cooler days are getting hotter.
TNn (Min Tmin)	↑ from 8.8°C to 12.3°C	↑ from 10.3°C to 14°C	Considerable warming of the coldest nights
RX1day (Max 1-day rain)	↑ from 28mm to 32.4mm	↑ from 30.5mm to 34.5mm	More intense single-day rainfall events; higher flood risk.
R20 (Very heavy rain days ≥20mm)	↑ from 2.7 to 4 days	↑ from 4 to 5 days	More very heavy rainfall events; higher potential for localized flooding.

In the present study different climate indices were estimated for the Bolangir and Dhenkanal districts of Odisha using bias corrected block level future climate data of the two districts for the base period and for the mid-century (2050) under RCP 4.5. IITM-RCM model-based temperature data were bias corrected and the model ensemble PCP data without bias correction used for climate indices calculations using RClimDex software. The overall finding indicated a warming climate with nights projected to become warmer with higher minimum temperatures, indicating a shift towards a more consistently hot environment, with Dhenkanal likely to experience more warming nights than Bolangir by 2050 under the RCP 4.5 scenario (Table 2.4). Heat stress is expected to intensify due to a higher frequency of tropical nights and elevated minimum temperatures. Although total rainfall may not increase substantially, the intensity of single-day and extreme rainfall events is projected to rise. At the same time, dry spells are expected to lengthen slightly, accompanied by shorter wet spells, which could impose stress on agriculture, especially in rain-fed systems. Furthermore, the reduction in cold nights points to a loss of seasonal variability.

Controls of climate smart agricultural practices in vulnerable region (Dibyendu Chatterjee and M Shahid)

The objective of the study was to determine the socioeconomic factors influencing the adoption and implementation of climate-smart agricultural practices in drought-prone vulnerable regions. The opinions of 25 independent experts were collected. Rainwater harvesting (RH) had the highest cumulative score among the treatments. Subsequently, information was collected from 83 farmers across 12 villages and 3 blocks in Jharsuguda and Dhenkanal districts of Odisha. Data on various drivers influencing the adoption of climate smart agricultural practices were collected, including family, social, land and financial factors and by following standard protocols probit models were developed. The specific adoption rate ranged from 16 to 95% for 10 best climate smart agricultural technologies recommended by the experts. Poor farmers' low acceptability of furrow irrigated bed planting (FIBP) and laser levelling (LL) may be attributed to higher investment requirements and the challenges of working beyond their comfort zone, given the risk associated with adoption of new technology. Social factors such as education, rice equivalent yield, access to credit, farm income ratio, distance from important agency, access to government scheme, dependency ratio showed association with the adoption and implementation of climate-smart agricultural practices in drought-prone vulnerable region.

A study involving 308 farmers from 20 villages across 5 blocks of Kendrapada, Bhadrak, and Jagatsinghpur districts in Odisha examined factors influencing the adoption of climate-smart agricultural (CSA) practices in flood-prone ecology. The adoption rate for most CSA technologies was low (≤ 10%), except for rainwater harvesting, drainage management, improved crop varieties, and crop insurance. Factors positively influencing adoption included social factors like education and family literacy, as well as farm and economic factors such as cropping intensity, landholding size and farm income ratio. Participation in training programs, mass media exposure and access to government schemes also positively impacted adoption. Conversely, distance from important agencies and family sizes had a negative association, while access to credit showed a variable impact on adoption of CSA practices.

Changing dynamics of soil potassium under rice-based resource conservation technologies (Debarati Bhaduri)

Significant variation in different K fractions under seven different treatments was observed both in direct seeded (DSR) and transplanted rice (TPR) system in a long-term (ten years) of field experimentation. Under both the systems, green manuring along with application of 75% RDF-N significantly improve the labile and exchangeable K in the soil (130.2 and 122.5 for K_L; 111.1 and 102 mg kg^{-1} for K_{ex}, respectively), which had direct influence in K-availability. However, soil applied with 100% RDF-N under DSR and green manuring with 75% RDF-N under TPR showed significantly higher water-soluble content (20.2 and 20.6 mg kg^{-1}, respectively) compared to other treatments. Practice of brown manuring with application of 75% RDF-N under DSR and mechanical transplanting with 100% RDF-N applied using LCC under TPR significantly increased the total K content (26517 and 26014 mg kg^{-1}, respectively) in soil. Zero-tillage treatments had significant influence towards labile K (K_L) and non-exchangeable K (K_{nx}) in both DSR and TPR conditions (Table 2.5). Further from Q/I study, it was revealed that, under DSR, almost all treatments were deficient of K (ΔG_0), however, the mean values under TPR condition were lower and indicated less overall deficiency of K. Under TPR, the treatment green manuring +75% RDF-N had the higher K_s.

Table 2.5. Quantity/intensity (Q/I) parameters of soil K under different treatments under transplanted and direct seeded rice.

Transplanted Rice

Treatments	$ARe^{K}\times10^{4}$	$-\Delta K_0$ (cmol$_c$ kg^{-1})	Ks (cmol$_c$ kg^{-1})	PBC^{K} (cmol$_c$ kg^{-1})	ΔG0 (Cal mol^{-1})
T1: Conventional Transplanting + No N	27.7	0.175	0.049^{c}	63.02^{abc}	-3485
T2: Conventional Transplanting +100% RDF-N	32.5	0.166	0.102^{ab}	51.50^{c}	-3391
T3: Crop Residue Incorporation +75% RDF-N	26.5	0.150	0.113^{ab}	56.63^{bc}	-3513
T4: Green Manuring (GM) +75% RDF-N	24.2	0.143	0.123^{a}	58.53^{bc}	-3577
T5: Zero Tillage Transplanting +100% RDF-N	30.1	0.192	0.084^{abc}	63.71^{ab}	-3436
T6: Mechanical Transplanting + 100 % RDF-N	27.3	0.201	0.067^{b}	73.29^{a}	-3495
T7: T6 + CLCC	28.0	0.164	0.109^{ab}	59.02^{bc}	-3480
SEm (±)	1.55	0.01	0.015	3.88	36.84
CD5%	NS	NS	0.047	11.95	NS
CV%	9.57	14.98	28.67	11.04	-1.83

Direct Seeded Rice

Treatments	$ARe^{K}\times10^{4}$	$-\Delta K_0$ (cmol$_c$ kg^{-1})	Ks (cmol$_c$ kg^{-1})	PBC^{K} (cmol$_c$ kg^{-1})	ΔG0 (Cal mol^{-1})
T1: Conventional Direct sowing (DS) + No N	25.51^{bc}	0.138	0.059^{e}	54.06	-3534^{ab}
T2: Conventional Direct sowing (DS) +100% RDF-N	30.44^{a}	0.134	0.094^{d}	44.49	-3430^{c}
T3: Brown Manuring (BM) +75% RDF-N	23.22^{c}	0.104	0.139^{a}	44.98	-3592^{a}
T4: Green Manuring (GM) +75% RDF-N	26.28^{b}	0.126	0.117^{bc}	48.03	-3516^{b}
T5: Paired Row Rice +GM+ 75% RDF-N	25.17^{bc}	0.128	0.123^{ab}	51.03	-3542^{ab}
T6: Wet-DS (Drum Seeder)+ 100 % RDF-N	27.00^{b}	0.133	0.117^{bc}	49.27	-3501^{b}
T7: Zero Tillage +100 % RDF-N	25.36^{bc}	0.138	0.098^{cd}	54.40	-3538^{ab}
Sem (±)	0.87	0.008	0.01	3.12	19.98
CD5%	2.67	NS	0.02	NS	61.55
CV%	5.74	10.329	10.36	10.92	-0.98

Determining permissible soil arsenic levels for safe rice production under varying irrigation water quality (Rubina Khanam)

To determine the permissible levels of soil arsenic (As) for safe rice production under As contaminated conditions, rice (*var. IR-64*) was cultivated in two consecutive seasons (*kharif* 2024 and *rabi* 2024-25) with soil As levels of 0, 5, 10, 15, 20, and 25 mg kg^{-1} and irrigated either with non-contaminated water or contaminated water containing 1000 mg L^{-1} As. The results indicated that As uptake and translocation varied significantly with both soil As concentration and water quality. Under non-contaminated irrigation water, root As content ranged from 4.3 to 14.1 mg kg^{-1}, shoot As ranged from 0.99 to 2.88 mg kg^{-1}, and grain As ranged 0.09 to 1.19 mg kg^{-1} in contrast to root As 8.4-22.7 mg kg^{-1}, shoot As 1.19-4.18 mg kg^{-1}, and grain As 0.47-1.44 mg kg^{-1}, under contaminated irrigation water (WHO permissible limit 1 mg kg^{-1}) (Fig. 2.2). Fe plaque deposition was found relatively lower (1032-1916 mg kg^{-1}) under contaminated irrigation as compared to 1193 to 1922 mg kg^{-1} under non-contaminated irrigation. These results clearly showed that the presence of As in irrigation water enhanced root uptake and increased translocation of As into the shoots and grains.

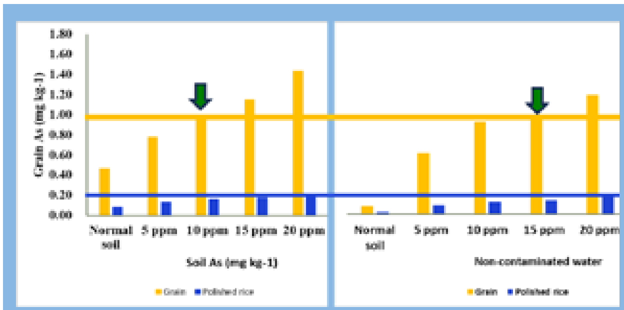


Fig. 2.2. Concentration of As in grain under different As level in soil and irrigation water

Developing agronomy for new generation rice and rice-based cropping systems

Agro-ecological intensification of rice-based cropping systems through introduction of new generation rice, CR Dhan 314 and CR Dhan 312 (B Raghavendra Goud, BB Panda and Sushmita Munda)

The study compared two production systems (conventional and conservation agriculture) in the main plots, two rice varieties (CR Dhan 314 and CR Dhan 312) in the sub-plots, and three *rabi*-season intensification strategies (sole maize, maize + cowpea, and maize + groundnut) in the sub-sub-plots. These intensification treatments were imposed during the *rabi* season following the *kharif* rice harvest to assess their residual impact on system performance. During the *kharif* 2024-25 season, the rice variety CR Dhan

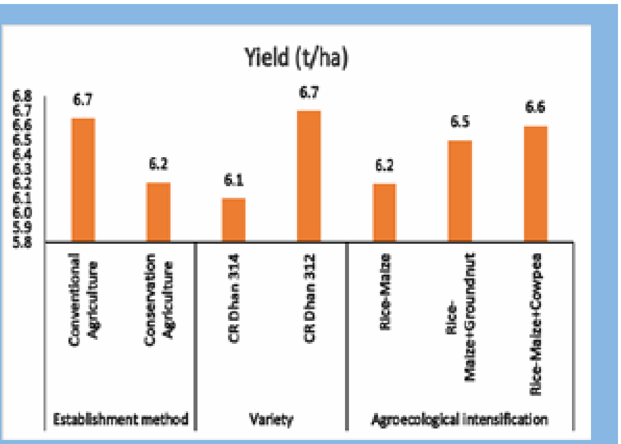


Fig. 2.3. Effect of crop establishment methods, rice varieties, and *rabi* intensification strategies on *kharif* **rice** productivity (2024-25)

312 significantly out-yielded CR Dhan 314, achieving a yield of 6.7 t ha^{-1} compared to 6.1 t ha^{-1} (Fig. 2.3). While conventional agriculture produced a higher rice yield of 6.7 t ha^{-1} relative to the 6.2 t ha^{-1} under conservation agriculture, the inclusion of legumes in the *rabi* season significantly enhanced subsequent yields. Specifically, intercropping maize with groundnut or cowpea during *rabi* season increased the following *kharif* rice yields by 6.45% and 4.84%, respectively, compared to yield after a sole maize crop.

Effect of integrated nitrogen, phosphorus and weed management on productivity of DSR (Shyam CS and BB Panda)

A field experiment was conducted during *kharif* 2024-25 at RCRRS, Srikakulam, under direct-seeded rice conditions. Treatments comprised of nitrogen application in three splits (10, 30, and 70 days after emergence (DAE) or two splits (30 and 70 DAE), combined with either basal or 30 DAE phosphorus application, along with different herbicide-based weed management practices. The highest grain yield (5.22 t ha^{-1}) obtained in three-split nitrogen application and basal phosphorus under weed-free conditions, which is *at par* with weed-free treatment with two-split nitrogen application and phosphorus (5.01 t ha^{-1}) applied at 30 DAE. The treatment, consisting of three-split nitrogen application with basal phosphorus and pendimethalin (pre-emergence) followed by metsulfuron-methyl 10% +chlorimuron-ethyl 10% (post-emergence), also produced yield (4.98 t ha^{-1}) statistically comparable to the weed-free treatments.

Development of cost-effective integrated crop management module in rainfed upland rice (dry-DSR) (Soumya Saha)

A study was conducted at CRURRS, Hazaribag during *kharif* 2024-25 to evaluate different integrated crop management (ICM) modules under rainfed upland dry direct-seeded rice (DSR) using variety *Anjali* (95 days) with no irrigation (RDF 60:30:30 kg $N:P_2O_5:K_2O$ ha^{-1}). Among the tested modules, seed treatment with *Trichoderma*, application of PSB + 50% RDP along with weed management by brown manuring + need-based mechanical weeding emerged as the best treatment in terms of grain yield, net returns, and B:C ratio (2.19 t ha^{-1}, Rs. 16254 and 1.40, respectively). The findings advocate for integrated, low-chemical-input strategies like seed treatment using bio-control agents, integrated nutrient management, and ecological weed control in dry-DSR systems.

Evaluation of advanced and fixed NGR breeding lines (SK Dash)

The new generation rice variety CR Dhan 417 (IET 30961) has demonstrated high yield potential and robust adaptability across Zone IV and Zone VII under shallow lowland production conditions. During the *kharif* 2024-25 trials, the variety exhibited a mean grain yield of 6.21 t ha^{-1} under optimum input (100% NPK), consistently outperforming the national check WGL 14 (5.63 t ha^{-1}) and the regional check Ketekijoha (4.40 t ha^{-1}). Notably, CR Dhan 417 also showed impressive resilience under low-input conditions (50% NPK), maintaining a stable yield of 5.17 t ha^{-1}. The variety responded significantly to nutrient management, recording a 20.1% yield increase when transitioning from low to optimum fertilizer doses. Location-wise data further highlighted its superior performance in regions like Raipur and Maruteru, where it achieved peak yields of 8.01 t ha^{-1} and 7.99 t ha^{-1}, respectively. The consistent performance of NGR across eight locations confirmed its suitability as a high-yielding, nutrient-responsive variety for intensive rice-based cropping systems.

Ecosystem services quantification and analysing the nexus of climate change-land use change-food security in rice production systems

Effects of projected changes in climate change on rice yield under projected scenario for mid century (Rahul Tripathi)

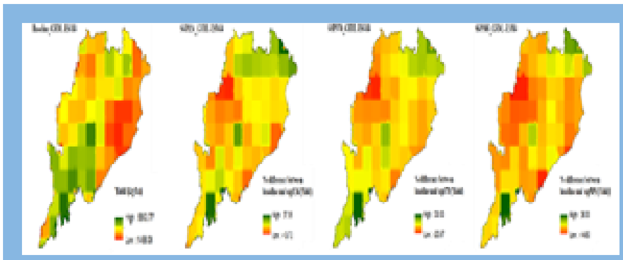


Fig. 2.4. DSSAT Model simulated rice yield using GFDL-ESM4 under different scenarios

The study evaluated the impacts of projected mid-century climate change (2035–2064) on rice yield and phenology relative to a historical baseline (1986–2013) using DSSAT crop modelling, driven by CMIP6 projections under three Shared Socioeconomic Pathways: SSP126, SSP370, and SSP585 (Fig. 2.4). Using GCMs including GFDL-ESM4 and UKESM1-0-LL, the results indicated a consistent and significant reduction in rice yield across all projected scenarios compared to the baseline, with the highest decline observed under SSP370. Specifically, modelled reductions under SSP370 dropped as low as -20.67% (GFDL-ESM4 model) and -44.79% (UKESM1-0-LL model), while even the low-emissions SSP126 scenario projected potential yield losses down to -24.07% (UKESM1-0-LL). This impact correlates strongly with temperature changes: a spatial increase in both maximum (TMAX) and minimum (TMIN) temperatures were observed across scenarios, with SSP370 projecting the greatest TMAX increase above baseline. Furthermore, models consistently projected a reduction in Days to Anthesis (ADAT) across all scenarios, suggesting accelerated crop development.

Analysis of state wise rainfall and temperature variation during 2050 and 2080 under climate change using IITM-RCM based climate data for RCP 4.5 (Manish Debnath)

Under the present activity the climate data for 33 Indian states and Union Territories during 2050 and 2080 under RCP 4.5 were analyzed. Rainfall and temperature data were bias corrected using CMhyd tool. Analysis of the bias corrected model ensemble data for rainfall and both maximum and minimum temperature (data indicated a spacio-temporal variation during the study period. Increase in maximum temperature by 1.4-2.2^{0} C during 2050 and 1.9-2.9^{0} C during 2080 is expected across Indian states. Whereas, an increase of minimum temperature by 1.2-2.0^{0} C during 2050 and 1.6-2.5^{0} C during 2080 is expected (Fig. 2.5). During 2050, about 13 states of India are expected to receive increased rainfall while 17 states are expected to receive reduced rainfall than the base period. During 2080 mostly all the states will receive higher rainfall except 9 states of India receiving reduced rainfall.

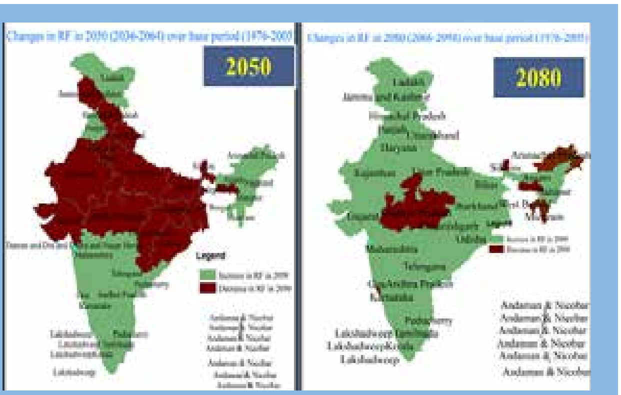


Fig. 2.5. Rainfall Variation during 2050 and 2080 over Base period

Quantification of the ecosystem services from rice and rice based production systems (Rahul Tripathi)

A meta-analysis of rice cultivation methods across six Indian agro-climatic zones shows substantial variation in energy use and greenhouse gas (GHG) emissions depending on establishment practices. Manual transplanting consistently recorded the highest energy consumption, ranging from about 7,350 to 13,500 MJ ha^{-1}, and high GHG emissions (867–1,496 kg CO_2 eq ha^{-1}), largely due to greater labour, machinery use, and fertilizer inputs. In contrast, zero tillage emerged as the most energy- and carbon-efficient option, with energy requirements reduced to about 5,500–7,400 MJ ha^{-1} and GHG emissions lowered to 711–967 kg CO_2 eq ha^{-1} across zones. Dry direct-seeded rice (DSR) and mechanical transplanting showed intermediate performance, with dry DSR generally consuming 4,665–10,036 MJ ha^{-1} and emitting 610–1,273 kg CO_2 eq ha^{-1} (Fig. 2.6). Zone-wise, the North East zone consistently exhibited the lowest GHG emissions across all methods, while the North and South zones showed higher energy use and emissions, reflecting greater labour (>300 h ha^{-1}) and nutrient application rates. Therefore, a significant potential for reducing energy demand and GHG footprints in rice systems through shifts from conventional manual transplanting

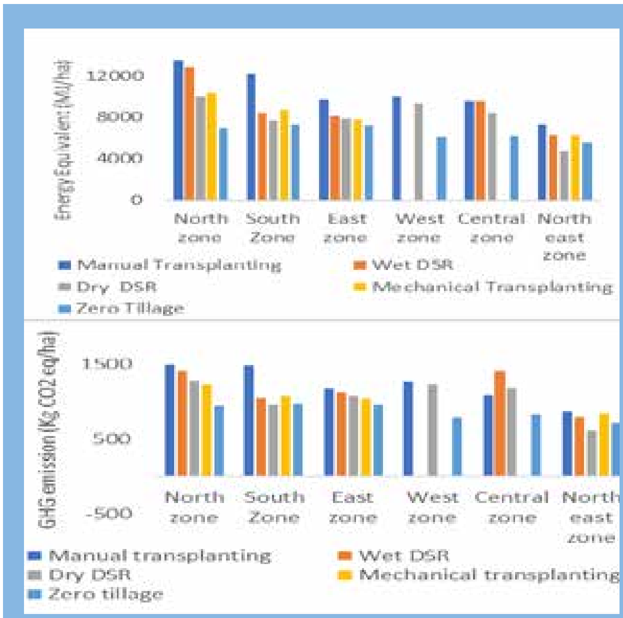


Fig. 2.6. Energy and Greenhouse gas emission equivalent under different crop establishment practices in different zones of India

to conservation-oriented practices such as zero tillage and DSR is envisioned.

Analyzing GHG emissions from food production and consumption across India (Supriya Priyadarsani)

The present study quantified state-wise GHG emissions across the agri-food life cycle in India by analysing both on-farm and off-farm activities. Consumption data of 2022–23 for 12 major food groups comprising 405 food items across 30 Indian states were obtained from the National Sample Survey Office (NSSO) and Life Cycle Assessment (LCA) methodologies were applied to estimate emissions from production, processing, transportation and consumption stages (Fig. 2.7). Results showed that livestock products contributed disproportionately to total emissions (89.81%) relative to crop-based foods (10.19%), primarily due to enteric fermentation and feed production. Among crops, rice exhibited the highest production-related emissions (2.26%), followed by oilseeds (2.20%), while wheat contributed the least (0.55%). Production-based per capita emissions were highest in Haryana (2079.4), Telangana (1934.5), Andhra Pradesh (1873.4), and Punjab (1844.7 kg CO_2e yr^{-1}), while the consumption-based emissions were highest in Nagaland (1387.4), Sikkim (1304.1), Ladakh (1085.1) and Arunachal Pradesh (1055.4 kg CO_2e yr^{-1}), driven by higher meat and rice consumption. Emissions from inter-state food transport to Union Territories ranged from 0.886 to 1.734 kg CO_2e kg^{-1} of product, reflecting strong external food dependence. The findings signify the importance of dietary shifts, improved agricultural practices, and food-waste reduction in achieving low-carbon food system transitions in developing economies.

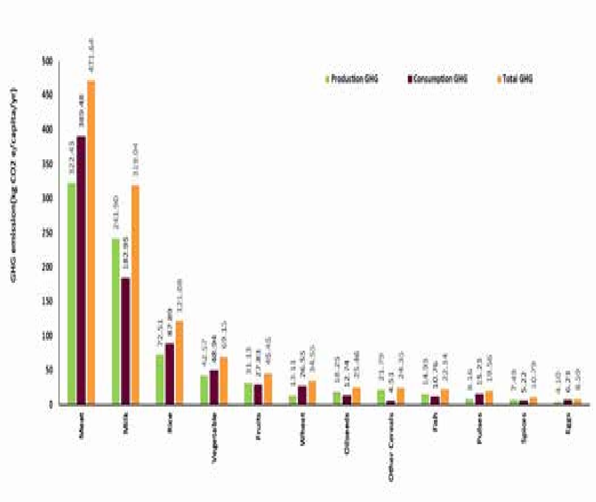


Fig. 2.7. Aggregated annual GHG emission from production and consumption of 12 food groups

Environment friendly management of rice straw and value addition for income generation to rice-farmers

In situ decomposition of rice straw (Pratap Bhattacharyya, P Panneerselvam and Sushmita Munda)

The problem of straw burning was addressed by advocating an efficient lignin-degrading solid microbial formulation, which was developed and field tested both *ex-situ* composting and *in-situ* straw decomposition. The field experiment was conducted to explore *in-situ* management options at ICAR-CRRI experimental fields (B13, 14 ab Block) during the dry (*rabi*) season 2024-25 with five treatments *viz.,* immediate incorporation of rice straw after harvesting (IIRS); zero tillage + glyphosate spray (ZT); spreading of rice straw mimicking the situation of using combined harvester (SRS); (zero tillage with glyphosate spray) + microbial intervention (ZT+MI) and spreading of rice straw + microbial intervention (SRS+MI) with four replications (Fig. 2.8). Methane emissions were highest in IIRS, followed by SRS, SRS+MI, ZT+MI, and ZT (Fig. 2.8). The CH_4 and N_2O emissions were increased from 3 to 18 days of treatment imposition and then decreased gradually up to 38 days. Higher GHGs were recorded during crop growth stages compared to the decomposition period. IIRS produced the highest crop yield (5.61 kg ha^{-1}), compared to other treatments.

Ex situ composting of rice straw (P Panneerselvam and Pratap Bhattacharyya)

Lignin-degrading solid microbial formulation (*Bacillus cereus*: MN784664 + *Penicillium sp.*: MK855473) based 'CR-Composter' was developed for the *in-situ* decomposition as well as *ex-situ* composting of rice straw. This eco-friendly technology enhances β-glucosidase activity, which accelerates the degradation process, rapidly reduces the C:N ratio, and has less GHGs emissions (25.6% reduction in GHG emissions compared to the control) during straw

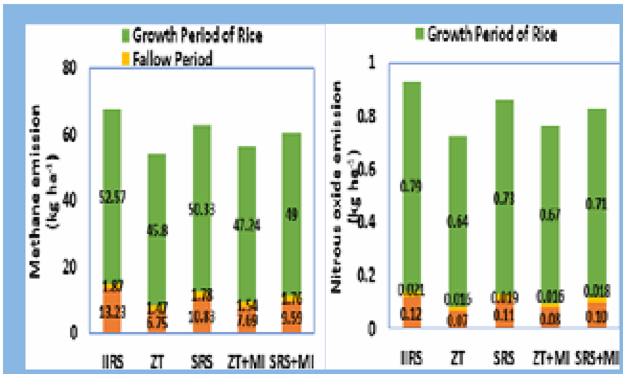
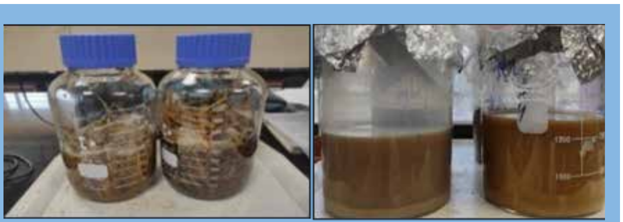


Fig. 2.8. Seasonal CH_4 and N_2O emission (both decomposition and crop growth period)

decomposition under rice-rice cropping systems in eastern India. This approach offers an eco-friendly and sustainable strategy to curb rice straw burning, supports soil health management, and mitigates greenhouse gas emissions for eastern India.

The pre-treatment techniques of rice straw for bioethanol production through microbial intervention (Pratap Bhattacharyya)

Pre-treating rice straw with 10% of lime with enzyme extraction from the microbes (*Bacillus cereus* ((MN784664) and *Penicillium* sp (MK855473) for 14 days makes it the most promising approach for enhancing bioethanol production from rice straw (19-21%), and ultrasonication with same microbial pretreatment could be an alternative for bioethanol production (17-18%), supporting renewable energy generation and income diversification for rice farmers and industry stakeholders.



Microbial Pretreatment of rice straw

Collection of pretreated bio-products from rice straw

Fermentation of the pretreated bioproduct

Fermentation of rice straw (samples)

Fig. 2.9. Pretreatment of rice straw for bioethanol recovery

Rice straw burning in Odisha: A three years' scenario (Debarati Bhaduri)

Rice straw burning events in Odisha was studied for four years during 2019-2023. It usually occurs during December to March (after *kharif* harvest) as per the analysis of data from MODIS sensor on-board Terra and Aqua satellites. During 2019-2020, frequent burning events were observed in Bargarh (230, peak in December) and Nabrangpur (270, peak in February). However, burning events expanded to more districts in subsequent year, 2020-2021: Bargarh (524), Nabrangpur (359), Balasore (247), Sambalpur (241), Kalahandi (234) during the same time (December to March). In the year 2022-2023, it was observed that total fire events in Odisha were like 516 (December), 766 (January), 357 (February), 711 (March), where in Bargarh district it was rampant in every month. Some technical and social hindrances like shortage of labours, high cost in collection of straw, unavailability of straw baling machines, lack of scientific training for better handling of paddy straw, poor market linkage to sell straw as cattle feed and poor extension agent-farmer interaction make it more prone to straw burning, as inferred from published literatures.

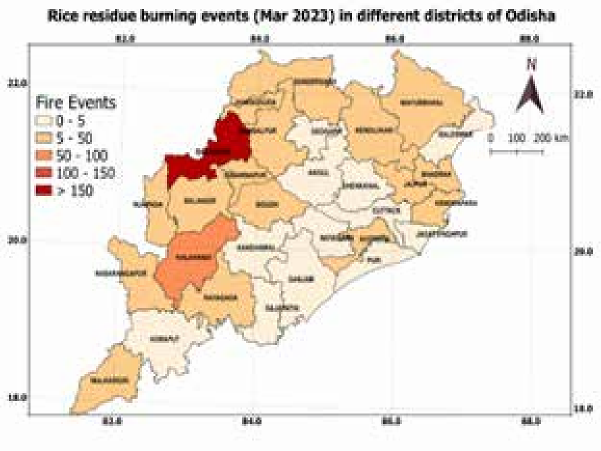


Fig. 2.10. GIS map of rice residue burning events in different districts of Odisha in March, 2023

Harnessing Microbiome for enhancing rice productivity and improving soil health

Assessment of metabolic pathways in two contrasting Azolla species (Upendra Kumar)

Whole-metagenome heatmap analysis showed that *Azolla* microphylla and A. pinnata clustered together are distinct from their cyanobiont-free counterparts. Natural *Azolla* species exhibited higher carbohydrate utilization, including 2-O-α-mannosyl-D-glycerate and acetoin/butanediol metabolism, along with enrichment of carboxysome-related genes such as the RuBisCO operon regulator and β-carboxysome carbon uptake proteins. Amino acid metabolism, particularly alanine, serine, glycine, arginine, and ornithine pathways, was also elevated, whereas proline metabolism was higher in cyanobiont-free samples. Overall, this study indicated that the presence of the cyanobiont enhances carbon fixation and amino acid metabolic pathways in *A. microphylla* and *A. pinnata***,** which showed the distinct and functionally enriched metabolic profiles compared to their cyanobiont-free counterparts.

Dissimilatory nitrate reduction to ammonium (DNRA) pathway in diverse rice agro- ecosystems (Upendra Kumar)

The present study used nrfA-targeted metagenomics and CCA analysis to assess DNRA communities across upland, lowland, and semi-deep rice ecosystems in a sub-humid tropical region. Lowland soils were enriched with *Actinomyces radicidentis*, *Geobacter uraniireducens*, and *Thermogutta terrifontis*, while upland soils were dominated by *Anaeromyxo bacter* spp. Semi-deep systems were characterized by Deinococci and Anaerolineae, with soil extracellular enzymes enhancing DNRA activity. This finding indicated that DNRA microbial communities are strongly regulated by soil environmental conditions, with flooding-driven redox dynamics enhancing nitrogen retention through DNRA activity.

Development of an Arbuscular Mycorrhizal Fungal (AMF) package for low land rice production (P Panneerselvam)

A vermiculite-based solid mixed AMF inoculum was developed, comprising *Glomus* sp. (NRRI-CPD-AMF3), *Funneliformis* sp. (NRRI-CPD-AMF1), *Rhizophagus* sp. (NRRI-CPD-AMF6), and *Acaulospora* sp. (NRRI-CPD-AMF7), with an infective propagule density of 1.61-1.73 × 10^3 propagules. The inoculum was standardized under nursery conditions to produce mycorrhizal rice seedlings and optimized at a rate of 2.0 kg per 1000 m^2 of rice nursery beds. AMF application at the nursery stage significantly enhanced mycorrhizal root colonization (68.0-73.0%) compared to the un-inoculated control (29.0-32.0%). The mycorrhizal seedlings were evaluated under field conditions with varying levels of phosphatic fertilizers in variety Naveen. The results showed that the treatment comprising of 100% NK + 75% P with AMF produced grain yields (5.44–5.58 t ha^{-1}) at par with the 100% recommended dose of fertilizers (5.35–5.50 t ha^{-1}) during both the *kharif* and *rabi* seasons. The study clearly indicated that application of AMF at the nursery stage could be an ideal approach for lowland rice cultivation.

Strigolactone-mediated enhancement of arbuscular mycorrhizal symbiosis in lowland rice production (P Panneerselvam)

The application of synthetic strigolactones (SLs-GR 24) was optimized as a seed priming treatment at 5 µM in 100 ml per kg of seeds, which significantly improved mycorrhizal root colonization and plant growth in rice variety *Naveen* at nursery stage. When combined with 2.0 kg AMF inoculum per 1000 m^2 during the nursery stage, AMF root colonization increased significantly (81.0–83.0%) compared to conventional seedlings. Field evaluation of these mycorrhizal seedlings under 100% NK + 75% P fertilization showed a significant yield improvement over treatment with only 100% NK + 75% P. Overall, rice seed priming with SLs-GR24 combined with AMF inoculation enhanced mycorrhizal colonization at the nursery stage, and transplanting these seedlings with 100% NK + 75% P resulted in a 4.0% higher yield compared with the recommended dose of fertilizers (RDF) alone.

Scale-up, distribution, and promotion of microbial inoculants to stakeholders (P Panneerselvam and Upendra Kumar)

Mass production of CRRI-Endo N and Tech CRRI Decomposer was carried out at the Bio-fertilizer Production Unit and distributed to various stakeholders. Demonstrations of CRRI-Endo N were conducted over more than 1,000 acres, with performance monitored on 157.5 acres, showed an average yield increase of 10% along with 25% nitrogen savings. Around 2.17 tons of Tech CRRI Decomposer were produced and supplied to farmers and KVKs for agricultural waste decomposition. Additionally, 21 awareness-cum-demonstration programs were conducted in Odisha, benefiting 1,137 farmers. These initiatives received coverage in local media, including 35 news articles and videos. During 2025, a total of 2,430 stakeholders visited the CRRI Bio-fertilizer facility.

Development of weed management strategy and assessing the risk of herbicide resistance in rice weeds

Assessment of variations in morphology and seedling growth pattern in rice field weed, Echinochloa crus-galli (Sushmita Munda, Kavita Kumari and B Mondal)

A total of 57 accessions of *Echinochloa crus-galli* seeds were collected from farmers' field across various parts of the country (Punjab, Telangana, Chhattisgarh, Uttar Pradesh and Odisha) where repeated application of herbicides were reported to have failed to control this weed. The seeds of collected *E. crus-galli* accessions were put for germination test, of the 57 accessions, only 32 accessions germinated (Fig. 2.11). Analysis based on test weight of the seeds clearly distinguished the accessions collected from different states. There was a high degree of variation in the test weight of the accessions with the highest 1000-grain weight (1.87 g recorded in PN4) being about 2.08 times than the

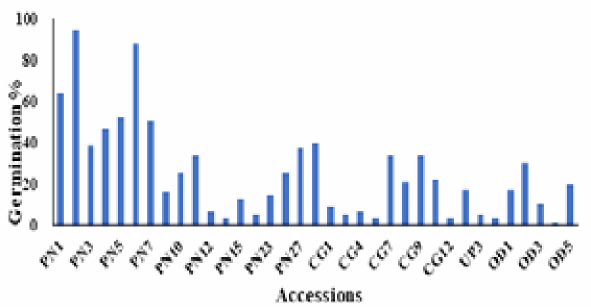


Fig. 2.11. Variation in germination pattern among the accessions

lowest 1000-grain weight (0.9 g recorded in OD3). A significant variation in germination pattern was also observed as 24 accessions germinated without any dormancy breaking treatment while 32 germinated with acid scarification. Overall, PN6, PN8, PN20, PN23, TG1 and UP8 had good growth while PN1, PN2, PN3, PN10, PN26, CG4, CG10, CG13 and OD5 had poor growth. The intra specific variations are strongly influenced by factors such as root and shoot length, biomass, grain weight and germination pattern.

Identification of resistance development against selected test herbicides (Sushmita Munda, Kavita Kumari and B Mondal)

Herbicides, *viz.,* bispyribac-sodium and penoxsulam, were evaluated against *E. crus-galli* accessions under pot culture conditions. Six dose levels (0, 25, 50, 100, 200, and 300% of the recommended dose) were imposed. Herbicide efficacy was assessed based on visual injury, plant survival, biomass reduction. GR_{50} values were estimated through probit analysis, followed by assessment of the magnitude of herbicide resistance among accessions through Resistance Index (RI). For bispyribac sodium (RD 30g a.i. ha^{-1}), 14 accessions showed moderate resistance with RI >2 (Table. 2.6). The highest GR_{50} was observed for CG15 followed by PN15 which required 25.72 and 22.78 g a.i. ha^{-1}, respectively, to achieve a 50% reduction in growth, resulting in high resistance indices of 5.22 and 4.62. Bisparybac sodium being an ALS inhibiting herbicide falls in category B i.e weeds have high risk of evolving resistance to this herbicide. However, no accession showed resistance to penoxsulam (RD 25g a.i. ha^{-1}) except CG15 (GR_{50} 12.12 g a.i. ha^{-1}) suggesting the absence of cross resistance in the collected accessions.

Comparison of conservation agriculture (CA) practices in rice-green gram cropping system with and without herbicide tolerant rice (HTR) (Sushmita Munda, Kavita Kumari and B Mondal)

Table 2.6. GR_{50} value and resistance index of the *E. crus-galli* accessions against bisparybac sodium.

Accession	Regression Equation	GR_{50} (a.i. ha^{-1})	RI	Category
PN1	y=-6.764+6.186x	12.40	2.52	Moderately Resistant
PN2	y=-5.588+5.343x	11.11	2.25	Moderately Resistant
PN3	y=-12.935+11.416x	13.59	2.76	Moderately Resistant
PN4	y=-5.654+5.312x	11.60	2.35	Moderately Resistant
PN5	y=-4.193+5.192x	6.42	1.30	Susceptible
PN6	y=-3.710+3.557x	11.04	2.24	Moderately Resistant
PN7	y=-4.124+4.153x	9.84	2.00	Susceptible
PN8	y=-3.238+4.476x	5.29	1.07	Susceptible
PN10	y=-3.326+4.199x	6.20	1.26	Susceptible
PN11	y=-3.256+3.391x	9.13	1.85	Susceptible
PN12	y=-3.555+3.855x	8.36	1.70	Susceptible
PN15	y=-3.758+2.768x	22.78	4.62	Moderately Resistant
PN20	y=-3.555+3.855x	8.36	1.70	Susceptible
PN21	y=-3.287+3.574x	8.31	1.69	Susceptible
PN23	y=-3.030+3.314x	8.21	1.67	Susceptible
PN26	y=-2.768+3.996x	4.93	1.00	Susceptible
PN27	y=-4.169+5.207x	6.32	1.28	Susceptible
TG1	y=-6.375+5.533x	14.19	2.88	Moderately Resistant
CG1	y=-3.016+4.147x	5.34	1.08	Susceptible
CG2	y=-5.564+5.117x	12.23	2.48	Moderately Resistant
CG4	y=-13.927+11.508x	16.23	3.29	Moderately Resistant
CG7	y=-4.925+5.958x	6.71	1.36	Susceptible
CG8	y=-3.205+3.626x	7.65	1.55	Susceptible
CG10	y=-3.457+4.133x	6.86	1.39	Susceptible
CG11	y=-4.702+4.479x	11.21	2.27	Moderately Resistant
CG13	y=-13.237+11.376x	14.57	2.96	Moderately Resistant
CG15	y=-4.485+3.181x	25.72	5.22	Moderately Resistant
UP3	y=-4.156+4.473x	8.49	1.72	Susceptible
UP8	1.580+2.049x	5.90	1.20	Susceptible
OD1	y=-2.982+4.145x	5.24	1.06	Susceptible
OD3	y=-4.499+4.355x	10.79	2.19	Moderately Resistant
OD5	y=-13.360+11.345x	15.06	3.05	Moderately Resistant

An experiment was conducted to compare CA practices in rice-green gram cropping system with and without herbicide tolerant rice (HTR) with the following treatment combinations in 5 replications: T1: Direct seeded rice (DSR)-C+HTR followed by (*fb*) green gram; T2: DSR-C (conventional tillage) + Non-HTR *fb* green gram; T3: Non-puddled transplanted rice (NPTPR)-ZT + HTR *fb* green gram; T4: NPTPR-ZT + Non-HTR fb green gram; T5: DSR-ZT + HTR *fb* green gram; T6: DSR-ZT + Non-HTR *fb* green gram. Near isogenic line (NIL) of Swarna *sub-1* (HTR) was compared with was Swarna *sub-1* (non-HTR) in *kharif* season. In *rabi*, Virat cultivar of green gram (IIPM 205-7) was cultivated. For green gram, conventional tillage was followed in T1 and T2, whereas, it was cultivated under ZT in treatments T3, T4, T5 and T6. Imazethapyr was applied @ 100 g a.i. ha^{-1} in HTR, 15 DAE, whereas in non-HTR, fenoxaprop-p-ethyl + ehoxysulfuron was applied @ 100 g a.i. ha^{-1} +25 g a.i. ha^{-1} at 25 DAE.

System productivity was highest (8.42 t ha^{-1}) in NPTPR-ZT + HTR *fb* green gram and it was significantly higher than conventional tillage DSR *fb* green gram (7.13 t ha^{-1}). In *kharif*, treatments with HTR recorded higher grain yield (avg. 4.62 t ha^{-1}) compared to non-HTR (4.15 t ha^{-1}) with highest yield in NPTPR-ZT + HTR *fb* green gram. Green gram yield ranged from 7.8 to 9.05 q ha+ HTR *fb* green gram with highest in conventional tillage, T1 and lowest in T6. At 30 days after herbicide application, treatments with HTR (T1, T3, T5) recorded >90% suppression of weeds. Treatments with non-HTR (T2, T4, T6) recorded only 40% suppression of weeds. The average B:C ratio of NPTR based system (1.7) was 25% higher compared to DSR-ZT based system (1.3). Conventional tillage-based system recorded B:C ratio of <1.0.

Development and Refinement of Farm implements, post-harvest and value addition technologies for small farm mechanization

Development of non-destructive solar powered bird scaring system (Prakash Jena)

Fig. 2.12. Non-destructive solar powered bird scarring system for protecting crop yield

A solar-powered, automated bird scaring device that uses ultrasonic sound stimuli to deter birds from rice fields without harming them was designed and developed at CRRI (Fig. 2.12). The machine was tested for effectiveness in reducing bird damage and it was found efficiency of > 90%. This machine provides an eco-friendly and sustainable solution to minimize crop loss due to birds, reducing the need for harmful chemical repellents and manual labour.

Development and performance evaluation of IoT-based Smart real-time irrigation scheduling system for rice (Manish Debnath)

An IoT-enabled system using soil moisture sensors, soil characteristics data to automate rice irrigation scheduling was developed. It was evaluated for the system's accuracy and water-saving efficiency in field trials. It enhances water use efficiency and crop productivity by delivering precise irrigation, reducing wastage and supporting climate-smart agriculture practices.

Optimizing rice processing for arsenic reduction and nutrient enhancement (Rubina Khanam and M. Sivashankari)

A multi-factor experiments on parboiling, milling, and cooking methods across different rice varieties to minimize arsenic content while retaining micronutrients (Zn, Fe) was conducted. The study identified safe processing combinations tailored to rice types. It ensures safer rice consumption in arsenic-prone areas without compromising nutritional quality, guiding processing protocols, consumer awareness, and policy frameworks.

Optimization of rice noodles fortified with moringa leaf powder (M. Sivashankari)

Rice noodle formulations using CR Dhan 310 (high protein) rice flour fortified with moringa leaf powder, Carboxy Methyl Cellulose (CMC), salt and water was developed and optimized (Fig. 2.13). The product was evaluated for cooking quality, texture, sensory attributes, and nutritional profile to identify the best formulation. This produces a nutritious, gluten-free rice noodle enriched with moringa's health benefits, catering to health-conscious consumers and those with gluten intolerance.

Fig. 2.13. Fortified rice noodles with morning leaf powder

Development and characterization of rice-based gluten-free multi-composite cookies (M. Sivashankari)

The cookies using high-zinc rice variety (CR Dhan 315) flour combined with bajra, sorghum, ragi, and wheat flour were formulated (Fig. 2.14). The products were analyzed for physical attributes, protein content, phytochemicals, texture and colour. These were recommended best formulations based on sensory appeal and nutrition. They offer a nutritious gluten-free bakery product enriched with micronutrients, addressing dietary needs of gluten-sensitive individuals while promoting millet and rice-based ingredients.

Fig. 2.14. Rice-based gluten-free multi-composite cookies

Development, validation, and commercialization of rice by-product based fish feed (S. Priyadarsani)

A sinking, floating fish feed was developed using rice by-products and other agricultural ingredients. It was evaluated for physical properties, nutrient content, and fish growth performance (weight gain, survival, feed conversion). Floating feed showed superior fish growth compared to the performance of commercial fish feed. It provides cost-effective, sustainable fish feed alternatives using locally available by-products, supporting small-scale fish farmers and promoting circular agriculture.

Enhancing water use efficiency in rice-based cropping system

Evaluation of varietal performance under Direct Seeded Rice (Anjani Kumar)

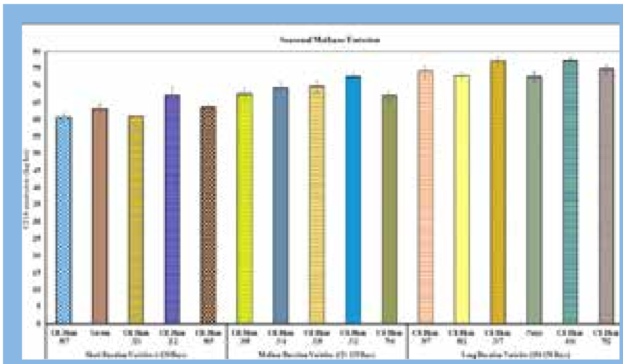


Fig. 2.15. Seasonal methane emissions of short, medium, and long-duration rice varieties under direct-seeded conditions

Assessing CH_4 emissions among rice varieties is essential for identifying genotypes that can lower methane output without affecting grain yield. For this, a field experiment was carried out at ICAR-CRRI, Cuttack to identify high-yielding, low-methane-emitting rice varieties across short (<120 days), medium (121–135 days), and late (136–150 days) duration categories under the direct-seeded rice (DSR) establishment method. The findings showed distinct variations in methane emissions both among and within the different duration groups of rice varieties. In the short-duration category (<120 days), emissions ranged from 60.6 kg ha^{-1} in CR Dhan 807 - the lowest in this group to 67.2 kg ha^{-1} in CR Dhan 212, the highest emitter (Fig. 2.15). Among the medium-duration varieties (121–135 days), overall emissions were higher, with CR Dhan 704 recording the lowest value at 67.1 kg ha^{-1} and CR Dhan 312 the highest at 72.5 kg ha^{-1}. The long-duration group (136–150 days) showed the highest emissions overall, with Pooja emitting 72.5 kg ha^{-1} at the lower end and CR Dhan 414 reaching the maximum at 77.3 kg ha^{-1}. These results highlight that choosing the right varieties can be an effective approach to lowering methane emissions and promoting climate-resilient rice production systems.

Long-term groundwater recharge flux estimation for CRRI research Farm (Manish Debnath)

The long-term groundwater recharge (2000-2024) for CRRI Research farm was estimated combining the Thornthwaite-Mather approach for evapotranspiration estimation, the Central Groundwater Board (CGWB) water balance method for groundwater recharge quantification and a newly developed runoff estimation method for paddy fiel d. (Monthly variation in estimated recharge flux during the study period is shown in Fig.

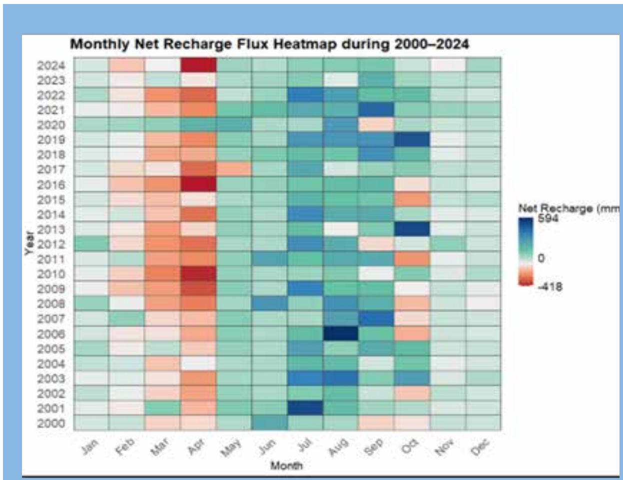


Fig. 2.16. Monthly estimated net recharge flux variation at the farm during 2000-2024

2.16.) Based on the estimation it was observed that the net change in groundwater recharge during *kharif* season ranged from +11.2 mm to +1347.4 mm. In contrast, the net change in groundwater recharge during the *rabi* season varied from –768 mm to +759 mm. On an average, the net groundwater recharge amounted to +521 mm in *kharif*, whereas a depletion of 516 mm was observed in *rabi*, mainly due to groundwater extraction from the aquifer for irrigation. Present study demonstrated that monsoon-season recharge consistently offsets dry-season depletion, with a long-term net positive storage of in the underlying aquifer.

Conclusion

The Crop Production Division has undertaken various research initiatives, leading to significant advancements in agricultural practices. Key achievements may help in transforming rice crop production through smart integration of high-tech agronomy, soil-plant microbes interaction, climate smart technology, machinery and value addition. Experiments conducted on the use of sensor-based nitrogen scheduling through GreenSeeker, along with nano-urea, have highlighted that substantial savings could be made on N, while at the same time, there are no adverse effects on yields, owing to molecular mechanisms that enhance genetic expression and improve N assimilation. Long-term experiments on fertility and organic nutrient management have established that balanced nutrient supply, especially FYM, green manures, Azolla, and microbes, improve C and N mineralization, fixation, and health, particularly nitrogen retention mechanisms such as DNRA. Rice-fish integration, legume intensification and diversified rice cropping systems resulted in increased productivity for cropping systems, fertility, biodiversity and economic benefits. Conservation agriculture, herbicide-tolerant rice and other integrated weed management strategies could address issues like labour scarcity and herbicide resistance, maintaining system productivity and high benefit-cost ratios. Climate vulnerability assessments and modelling studies provided critical foresight into mid-century climate risks. Projections indicate rising temperatures, increased heat stress, altered rainfall patterns, and shortened crop phenology, all of which threaten rice yields. In addition, there might be issues of soil and water quality associated with arsenic. However, there is a possibility of developing targeted climate-smart technologies and variety choice that can provide viable options to overcome the challenges. In addition, socioeconomic analysis showed that the adoption of the technologies would be driven strongly by education, income, credit access, institutional support and perceived risks. The quantification of ecosystem service and the use of life cycle assessments further emphasized the need to develop and use low-emitting techniques of establishment such as zero tillage and dry direct-seeded rice to reduce energy and greenhouse emissions. Rice straw management innovations, such as the use of microbes as decomposers, composting and production of ethanol, provided an alternative to residue burning with new avenues for income generation. Simultaneously, the development of other microbiome technology, like inoculums of AMF, strigolactones, Azolla, demonstrated the ability to reduce dependence on fertilizers and improve soil health. Farm mechanization, IoT-based irrigation management, post-harvest processing and the promotion of value-added rice products have largely increased the scope for a more sustainable rice cropping system. It is obvious from the varied outputs generated by the programme that for a resilient rice cropping system to emerge, multi-disciplinary interventions are required for sustainable rice cropping systems. The programme offers a very sound scientific basis and innovations for the future rice crop.

PROGRAMME

03

Biotic Stress Management in Rice

The programme focuses on advancing sustainable and effective pest management strategies for rice cultivation under different ecologies. The programme entrusted key research areas such as identifying new durable donors against major and emerging insect pests, pathogen and nematodes in different ecologies, characterization of emerging and re-emerging pests using advanced tools and techniques, elicitation of population dynamics of pests and diseases in response to climate change, and exploring the chemical-molecular mechanisms that govern interactions between rice plant, pests, and natural enemies. In addition, the division is focusing on the research on innovative pest monitoring and forecasting tools, AI-based detection systems, while also seeking to develop new management solutions that integrate both existing pesticides and natural resources. The programme is working on biological control of insect pests and diseases, pesticide residues and management in various systems. The programme also continues to implement Integrated Rice Health Management (IRHM) strategies across diverse rice-ecologies.

Identification and characterization of donors against biotic stresses

Identification of resistant donor against Brown Plant hopper (BPH) and White Backed Plant hopper (WBPH) (Guru Pirasanna Pandi G and PC Rath)

A collection of 100 genotypes were screened under artificial condition against BPH and WBPH. Out of 100, only one genotype *i.e.* IC 316446 recorded moderately resistant (SES score:3) and remaining 99 genotypes including susceptible check (TN1) were susceptible to WBPH and BPH.

Another set of 152 rice genotypes were screened against BPH and genotyped using 82 SSR markers linked to 28 resistance genes/QTLs. After three seasons, 33 resistant genotypes (SES score-1) were identified. Compared to susceptible lines, resistant genotypes showed reduced plant damage (4.60–8.90%), lower nymphal survival (11.50–24.00%), and decreased honeydew excretion (3.43–7.43 cm^2), though feeding marks were higher (22.67–32.00 per plant). Genetic analysis revealed moderate diversity (0.150) and polymorphism content (0.128). Cluster and population structure analyses grouped genotypes into three categories, validated by Principal Coordinate Analysis. Marker-trait association identified RM1313 (Bph9) and RM7 (Qbph3) as significant, with RM7 consistently linked to BPH resistance.

Identification of resistant sources against rice yellow stem borer (YSB) (Annamalai M, SD Mohapatra and PC Rath)

A total of 140 rice germplasm lines, along with TN1 and TKM-6 as susceptible and resistant checks, respectively, were screened for resistance to the rice yellow stem borer (YSB) at the vegetative stage (dead heart stage) under natural field conditions with artificial supplementation of YSB egg masses. Based on the percentage of dead heart damage and D-scale rating following the IRRI Standard Evaluation System (SES), the rice entries Salkathi, ARC-5758, ARC-5768, ARC-10973, ARC-11434, CR Dhan-801, CR Dhan 310, Moti, TKM-6, Ramkrishna, CR Dhan-310, Champa-6, Kalia Lendi, Kala Kaincha, Kala Mulia, Balangir Kala Krishna and PTB 33 exhibited consistently moderate resistance to rice yellow stem borer.

Genetic and molecular characterization of resistance to brown planthopper in rice (Guru Pirasanna Pandi G)

Previously identified 22 resistant germplasm accessions carrying diverse QTLs/genes, along with resistant (*Salkathi*), susceptible check (TN-1), and four popular varieties were evaluated using 89 markers linked to 31 QTLs/genes revealed moderate diversity (0.269) and polymorphism content (0.228). Cluster and population analyses grouped genotypes into resistant, moderately resistant, and susceptible categories. Marker-trait association identified five significant markers, with RM261 (*Bph15*) consistently linked to resistance.

Genetic Basis of *Cnaphalocrocis medinalis* (Guenee) Resistance in Rice Landraces (Prasanthi G)

Ninety-six ARC rice landraces were screened against leaf folder followed by genotypic analysis. Genetic dissection of 96 land races using 8 (eight) QTL/gene linked markers grouped into three major clusters based on genetic similarity. Cluster I, included 5 resistant (R), 19 moderately resistant (MR), and 10 susceptible (S) genotypes. Cluster II, the most resistant-dominant group with 27 landraces, exhibited 15 R (55.56%), 10 MR, and 2 S genotypes. Cluster III, the largest group with 35 landraces, encompassed 10 R, 18 S, and 7 MR genotypes. The inclusion of standard checks in Clusters II and III validated the clustering accuracy, as these checks aligned with their expected resistance categories (Fig. 3.1).

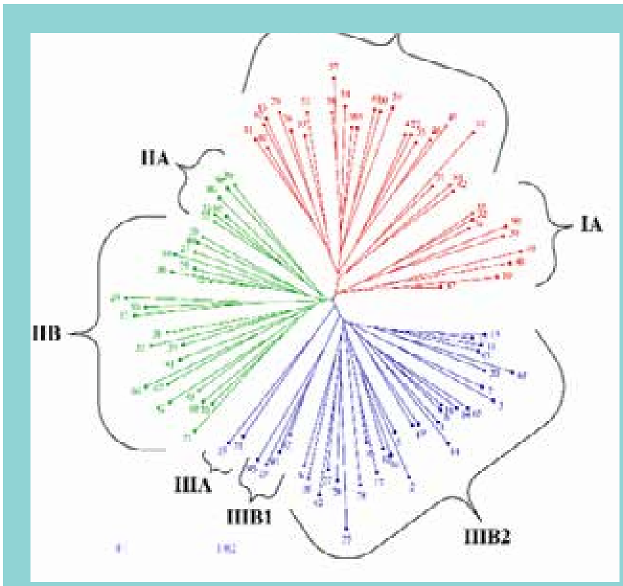


Fig. 3.1. UPGMA dendrogram showing the clustering pattern of 96 ARC based on SSR marker data

Identification of rice gall midge resistance associated loci at the genome scale using genic markers (Basana Gowda G)

A panel of 115 diverse rice accessions was phenotyped for resistance to gall midge biotype 2. After assessing genetic diversity and relatedness, a GWAS using candidate gene-derived and microsatellite markers identified 50 significant MTAs (*P<0.05*) across all chromosomes except chromosome 11. Major QTLs on chromosomes 6, 8, and 9 (linked with 66F/67R, 54F/55R, and RM107) explained the highest phenotypic variation. Allele effects clearly separated susceptible and highly resistant genotypes, confirming marker associations. Seven stress-response genes were detected within resistance QTL regions, and a putative gall midge resistance gene on chromosome 9 was linked to RM23914. These findings strengthen understanding of gall midge resistance and support marker-assisted breeding and functional validation of resistant cultivars.

Identification of rice sheath blight disease resistant donors (Srikanta Lenka)

Thirty two CRRI released varieties and 46 ARC collections were screened against sheath blight disease. Out of these, varieties like Chandrama, CR Dhan 205, CR Dhan 311, Abhishek and Assam Rice Collections (ARC) like ARC 5759, ARC 5937, ARC 6033, ARC 6097 were found as moderately resistant to sheath blight disease under artificial inoculated condition.

Screening for resistant donor to False Smut (*Ustilaginoidea virens*) pathogens (Manas Kumar Bag)

A set of 163 entries comprising of CRRI released varieties, few ARC collections, and selected NGB accessions were screened under field condition against false smut disease of rice. ARC collections namely, ARC 5769, 5776, 5842, 5937, 5940, 5975, 5982, 6005, 6006, 6609, 6628, 7009, 7035, 7085, and NGB accessions like IC466660, IC114371, IC435159, IC324679, IC379843, IC595241 were found resistant against false smut disease of rice. Out of these,12 ARC collections were evaluated repeatedly and found as resistant to false smut disease. These 12 ARC collections along with local susceptible checks were further evaluated at 6 different locations like CRRI, Cuttack; Gangavati, Karnataka; Ranchi, Jharkhand; IIRR, Hyderabad; Nawagaon, Gujarat; and CRURRS, Hazaribagh. ARC 6628 was found resistant in all 5 locations, whereas ARC 6005, 6006, 7085, and 5982 were found resistant in all except one location where they have shown moderately resistant (MR) or moderately susceptible reaction (MS).

Identification of resistant genotypes against sheath rot disease (Prabhukarthikeyan SR, Keerthana U and Manas Kumar Bag)

Sixteen ARC lines like ARC 9002, 9004, 9038, 9044, 9052, 9058, 9064, 9067, 9070, 9074, 9076, 9086, 9102, 9118, 9119, and 9136 were found resistant to sheath rot disease of rice under artificial inoculation condition (Table 3.1).

Gene expression dynamics in blast resistant *vs.* susceptible aromatic rice landraces (Keerthana U, Prabhukarthikeyan SR and Manas Kumar Bag)

The defense responses of resistant and susceptible aromatic rice landraces to rice leaf blast caused by *Magnaporthe oryzae* were studied. Four resistant genotypes (Benugopal, Manas, Karpurkali, and Kalajeera) and two susceptible genotypes (Kalikati 2 and Kalikati 1) were evaluated through biochemical and molecular analyses. The resistant genotypes, particularly Benugopal (AC 44184) and Karpurkali (AC 44155), exhibited significantly enhanced activities

Table 3.1. Sheath rot resistant genotypes

Sl. No.	Genotype	Plant height (in cm)	Tiller no.	Yield per plant (in gm)	Percent Disease Index	Disease Reaction
1	ARC 9002	159.00	13	28.23	4.44	R
2	ARC 9004	155.84	12	27.45	5.29	R
3	ARC 9038	161.50	10	19.92	7.41	R
4	ARC 9044	176.34	8	25.12	7.11	R
5	ARC 9052	148.00	8	24.39	9.33	R
6	ARC 9058	169.33	7	24.16	8.03	R
7	ARC 9064	143.34	7	23.88	8.02	R
8	ARC 9067	167.33	7	23.55	8.21	R
9	ARC 9070	153.50	9	25.72	5.56	R
10	ARC 9074	150.34	8	23.08	9.66	R
11	ARC 9076	160.50	7	23.28	7.94	R
12	ARC 9086	162.83	7	21.76	9.88	R
13	ARC 9102	155.50	8	21.48	6.67	R
14	ARC 9118	168.34	7	25.55	6.28	R
15	ARC 9119	144.00	7	20.63	9.66	R
16	ARC 9136	178.50	7	20.02	7.58	R

of key defense-related enzymes, including peroxidase, phenylalanine ammonia lyase, polyphenol oxidase, superoxide dismutase, and catalase, compared with the susceptible genotypes [*Kalikati* 2 (AC 44236) and *Kalikati* 1 (AC 44156)]. Consistent trends were also observed for β-1,3-glucanase activity and total phenolic content. To further substantiate these findings, RT-qPCR analysis was performed to quantify the expression levels of PO, PAL, PPO, SOD, and CAT genes in resistant and susceptible genotypes following inoculation with *M. oryzae* (RLB 06) at multiple time points. Marked genotype-dependent differences in defense gene expression were evident, with resistant genotypes showing pronounced upregulation of these genes relative to susceptible ones. Importantly, the transcriptional profiles of defense genes were in strong agreement with the corresponding spectrophotometric enzyme activity data, highlighting a coordinated biochemical and molecular defense response in resistant aromatic rice landraces (Fig. 3.2).

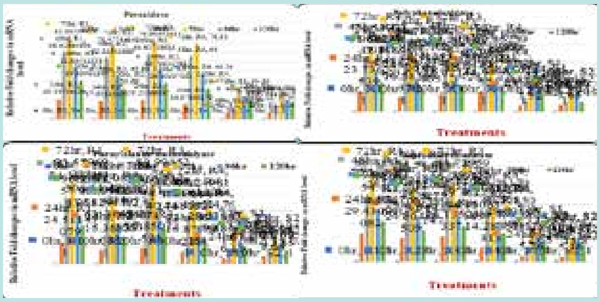


Fig. 3.2. Levels of expression of defense enzymes in response to M. oryzae in resistant and susceptible genotype of aromatic rice leaf by using qRT-PCR

Identification of a novel QTL for bakanae disease resistance in non-basmati indica rice (Raghu S, Jeevan B and Anil Kumar C)

Bi-parental mapping population was developed by crossing a highly resistant cultivated rice genotype, Thavalakannan, with a cultivated rice genotype, Pooja. Genotyping of 150 RIL lines was done using 103 markers. Four important probable candidate genes were identified in the confidence interval of the main effect QTL on chromosome 5. Among the four identified genes, three were related to gibberellic acid biosynthesis pathway, and one gene with locus ID Os05g0518800 is known for biotic stress response (Fig. 3.3). These genes can be considered for further validation and characterization against the bakanae pathogen.

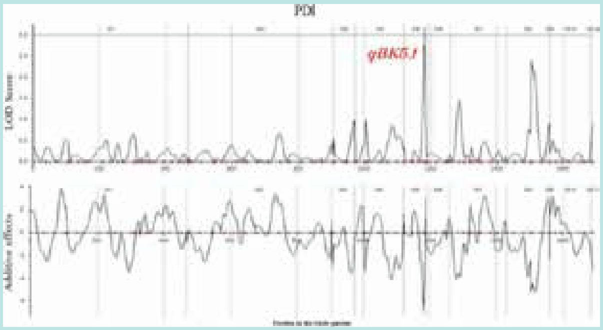


Fig. 3.3. The main effect QTL identified on chromosome 5 and additive effect of the identified QTL. Inverted peak in the additive effects represents that the QTL favors lower disease score, i.e., resistance, in the mapping population

Screening for Bacterial Blight Resistance (Arup Kumar Mukherjee)

A total of 171 lines comprised of CRRI released varieties (29), ARC Collections (63) and 79 Odisha land races were screened for their resistance to bacterial blight using artificial screening. Out of all the genotypes, 3 lines namely (*Nadalghanta*, ARC-5976, SB-28) showed highly resistant reaction with SES score 1. Four CRRI released varieties (CR Dhan 326, CR Dhan 800, CR Dhan 313, CR Dhan 412), 21 Odisha land races (*Koraput Machakanta, Champaneuli, Ganjam Ratnachudi, Maguramanji, Kaliasaru, Safari, Saraswati, Kalamugajai, Kadalikenda, Ispit, Baikani, Binabahar, Kanakchampa, Kansapurimajhijuly, Bhutia, Bhajana, Samudrabali, Jangalijata, Samulai, Gelhaiguti, Harishankar*) and 23 ARC collections showed resistant reactions.

Mass multiplication of *U. virens* (Manas Kumar Bag)

Mass multiplication of *U. virens* pathogen for artificial inoculation is required. *U. virens* isolates grow 20 times higher in rice leaf extract mixed potato sucrose broth (RLEPSB) over potato sucrose broth (PSB) (Table 3.2, Fig. 3.4).

Table 3.2. Rice leaf extract mixed potato sucrose broth (RLEPSB) over potato sucrose broth (PSB).

	RLWPCB	PSB
Fresh weight of *U. virens* (g)	3.226	0.161
Dry weight of *U. virens* (g)	0.4	0.023

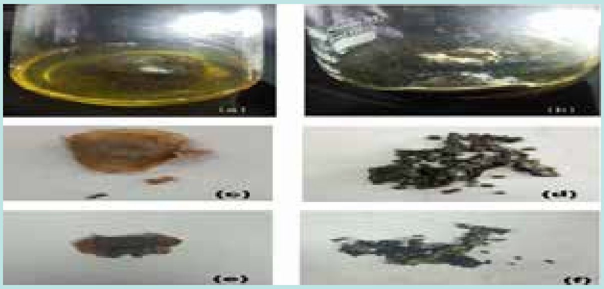


Fig. 3.4. Growth of U. virens in different broth and their mycelia growth after harvesting; (a) Growth at PSB; (b) Growth at RLEB (c) Wet mycelia in PSB (d) Wet mycelia in RLEB (e) Dry mycelia in PSB (f) Dry mycelia in RLEB

Identification and characterization of donors against rice root knot nematode (RRKN) (Rupak Jena and Gayathri B)

Out of 20 CRRI popular and aerobic varieties, Phalguni, CR 203, CR 209, Sahbhagidhan, Kalinga II were found as moderately resistant (MR) with reduced gall number, egg mass/root system and reproductive factor for RRKN. Eleven moderately resistant genotypes carried over from previous year were screened and CR 602, CR 403, CR 406, Abhishek and IR 38 were identified as MR and Ramakrishna and Panidhan expressed tolerant reaction in Rabi and Kharif, respectively. Bhasma Manika, NetaDhan and Bullo A expressed increased morphological and decreased yellowing of leaves to RRKN infection. Biochemical studies expressed that the MR varieties have increased level of chlorophyll, phenol, peroxidase, ascorbate peroxidase, malondialdehyde, catalase and hydrogen peroxide.

Ecology, diversity and interaction of plant, pest and natural enemies in rice

Genetic Diversity and Population Structure of *Cnaphalocrocis medinalis* across India and South Asia (Prasanthi G and Anil Kumar C)

The study on the genetic diversity and population structure of *Cnaphalocrocis medinalis* using mitochondrial *COI* gene sequences from 15 Indian states and other South Asian countries (A total of 100 *COI*) revealed higher haplotype diversity in Indian populations compared to other Asian regions, indicating genetic variations and potential historical bottlenecks followed by population expansions. AMOVA highlighted substantial genetic differentiation among populations for *COI* (62.51% variation). The median joining (MJ) haplotype network constructed using DNAsp and visualized in PopART for the *COI* gene sequences revealed a total of 14 distinct haplotypes (Hap_1 to Hap_14) distributed across populations from seven countries: India, Pakistan, China, South Korea, Malaysia, Philippines, and Japan. Hap_3 was identified as the most frequent haplotype, with a widespread distribution across multiple geographic locations, including India, Pakistan, and China. (Fig. 3.5).

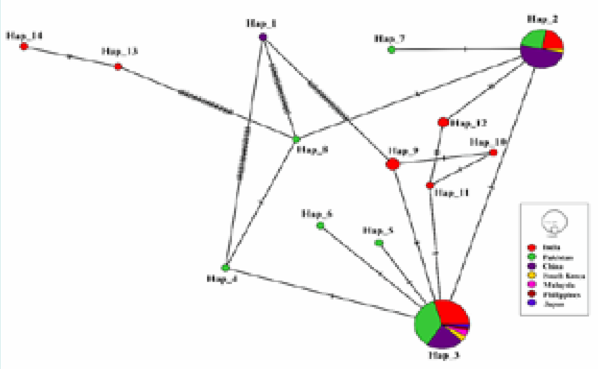


Fig. 3.5. Haplotype Network Analysis of COI Gene Sequences. The network displays relationships between 14 haplotypes (Hap_1 to Hap_14) from different populations. The circle size corresponds to the number of individuals sharing the haplotype, and the colors represent the geographic distribution of haplotypes across seven countries: India (red), Pakistan (green), China (yellow), South Korea (orange), Malaysia (pink), Philippines (purple), and Japan (blue). Each line connecting the haplotypes indicates a single mutational step, with hash marks representing additional mutational differences

Genetic diversity of rice yellow stem borer based on *Cox2* gene (Annamalai M, Parameswaran C, SD Mohapatra and PC Rath)

Genetic diversity of YSB from different locations of India was analysed using the mitochondrial *Cytochrome c oxidase subunit 2* (*COX2*) gene, and these were compared with YSB populations from other countries (Indonesia). Phylogenetic analysis revealed three major clades among the global YSB populations. Nucleotide sequence analysis identified 42 mutations and 40 variable sites (polymorphic sites), with Indian populations showing a higher number of variable sites. The overall haplotype diversity (Hd) and the nucleotide diversity were 0.893 and 0.00749.respectively, while for Indian populations they were 0.849 and 0.00441. Neutrality test statistics revealed significant negative values of Tajima's D (-1.86938), Fu and Li's D (-3.52370**), and Fu and Li's F (-3.49440**) and for Indian populations, the corresponding values were -2.24986**, -3.8709**, and -3.93345**, respectively indicating significant deviation from neutrality. In contrast, the Indonesian population exhibited positive and non-significant values. Significant and negative values of Indian population indicate viable expansion in the population size and geographic range of the YSB population with no evidence of genetic bottlenecks. Therefore, mitochondrial *COX2* gene-based genetic diversity analysis revealed substantial genetic variation among the yellow stem borer (YSB) populations across countries as well as within India. This study represents the first kind report comprehensively characterizing genetic variation in YSB using mitochondrial *COX2* gene.

Effect of potassium silicate amendment in wide range of rice varieties (Annamalai M, PC Rath and SD Mohapatra)

The effect of potassium silicate amendment on rice plants, in terms of growth parameters and defense responses against the yellow stem borer (YSB) and brown planthopper (BPH), was evaluated across a diverse set of rice varieties. A total of 100 CRRI rice varieties were supplemented with foliar application of potassium silicate and significant variation in the percentage increase of silica content was observed among the varieties. Based on the magnitude of silica accumulation on amendment, high responder (CR Dhan 907), low responder (CR Dhan 505), susceptible variety (TN1; susceptible to YSB and BPH), and resistant varieties (PTB-33 resistant to BPH and YSB; TKM-6 resistant to YSB) were subjected for further experiments and recorded plant growth parameters, including plant height, stem diameter, chlorophyll content, and number of leaves; insect defense such as dead heart incidence caused by YSB, honeydew excretion, total egg deposition, and egg hatchability of BPH. In addition, biochemical and molecular defense responses were analyzed. Potassium silicate amendment significantly improved plant growth parameters and reduced dead heart damage by YSB, as well as honeydew excretion, total eggs laid, and egg hatchability of BPH across susceptible, resistant, low- and high-responsive varieties. Furthermore, potassium silicate treatment enhanced phenol and lignin contents and increased the activity of defense-related enzymes across the tested rice varieties. An up-regulation of defense-related gene expression was also observed in the susceptible variety following potassium silicate amendment against both YSB and BPH, indicating enhanced induced resistance.

Influence of potassium silicate amendment on rice plant volatile organic compounds (PVOCs) and YSB behaviour (Annamalai M, Totan Adak and SD Mohapatra)

Foliar application of potassium silicate (1%) on the susceptible rice variety TN1 significantly altered the settling behavior of yellow stem borer (YSB) female moths under both cage experiments and olfactometer assays. GC-MS analysis of crude volatile extracts revealed distinct qualitative differences between potassium silicate–treated and untreated plants. Treated plants showed an increased presence of repellent compounds such as naphthalene and limonene, along with altered levels of short-range attractants and oviposition-stimulant compounds, including tetracosane, octacosane, eicosane, and hexatriacontane and these changes in volatile profiles most likely contributed to the disrupted host-selection behaviour of YSB females.

Identification of volatile compounds responsible for tritrophic interactions among rice plant, rice leaf-folder, and parasitoid (SD Mohapatra)

Chemical ecology studies revealed distinct roles of plant-derived volatile organic compounds (VOCs) in mediating interactions between rice plants, the rice leaf folder, and its parasitoid *Habrobracon hebetor*. Among the volatiles tested, the rice leaf folder showed strong attraction towards green leaf volatiles (GLVs), particularly trans-2-hexen-1-ol, (Z)-3-hexenyl acetate, and xylene. In contrast, herbivore-induced plant volatiles (HIPVs) such as methyl jasmonate, β-caryophyllene, and β-ocimene elicited strong repellent responses from the pest.

Interestingly, the parasitoid *H. hebetor* responded in an opposite manner. Electro-antennographic and olfactometry assays demonstrated that β-ocimene, β-caryophyllene, and 1,2,3,4-tetrahydronaphthalene acted as strong attractants for the parasitoid. These findings clearly indicate that *C. medinalis* is attracted to constitutive GLVs but repelled by HIPVs, whereas *H. hebetor* preferentially responds to HIPVs emitted by herbivore-damaged rice plants. This differential perception of volatiles highlights their potential utility in designing a selective push–pull strategy for rice leaf folder management.

Use of precision tools and techniques in rice insect pests and diseases management

Identifying sensitive spectral bands for detection of rice brown spot, *Helminthosporium oryzae* (SD Mohapatra)

The hyperspectral analysis of rice canopies using ASD data successfully identified sensitive spectral regions and optimal bands for early detection of rice brown spot (RBS) disease through a combination of derivative analysis, sensitivity analysis, continuum removal, and feature selection algorithms. Owing to the presence of hundreds of contiguous spectral bands, hyperspectral data enabled more detailed characterization of disease-induced spectral variations compared to conventional multispectral approaches. Derivative analysis (DA) proved particularly effective in enhancing subtle spectral differences by reducing background effects and illumination noise. Both first- and second-order derivatives of reflectance were computed to capture changes in reflectance rate and curvature with respect to wavelength, respectively. Pearson's correlation analysis between disease severity (DS) and derivative spectra revealed spectral regions that were highly sensitive to BS damage. Regions showing correlation coefficients greater than 0.60 in both first- and second-order derivatives were considered robust indicators for differentiating healthy and diseased samples. Based on this criterion, three key sensitive regions were identified at 500–550 nm, 680–780 nm, and 800–840 nm, with significance confirmed at the 0.01 level. Within these regions, distinct spectral features were

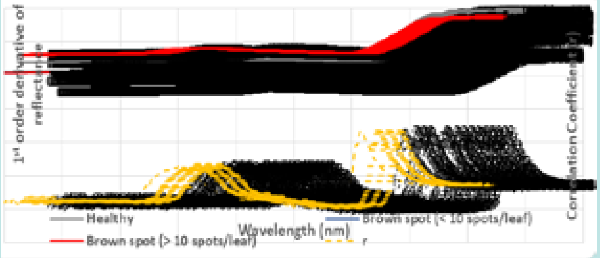


Fig. 3.6. Spectral reflectance from the combined leaves and the correlation coefficients (r) between the reflectance and disease severity of rice brown spot

observed, including prominent derivative peaks at 522, 720, and 732 nm, along with a pronounced dip at 812 nm, indicating maximum spectral separation between healthy and BS-infected leaves across different severity levels. Complementary sensitivity analysis further quantified the relative influence of BS on reflectance by normalizing reflectance differences against healthy samples. The analysis demonstrated positive sensitivity values in the visible region, particularly near the blue and red bands, indicating increased reflectance in BS-affected samples compared to healthy rice, while reduced sensitivity near the green region suggested limited discrimination. Beyond the red edge (~684 nm), sensitivity values indicated higher reflectance for healthy samples in the near-infrared (NIR) region, reflecting structural degradation of diseased canopies. Continuum removal (CR) analysis normalized reflectance spectra to a common baseline and enhanced absorption features, enabling clearer discrimination between healthy and RBS-infected samples across damage scales. CR results showed a rapid decrease in absorption feature amplitude in the visible and short-wave infrared regions with increasing disease severity, while healthy samples consistently exhibited higher reflectance in the NIR region. Using CR, multiple sensitive bands were identified across the VIS–NIR spectrum, including 498, 673, 708, 763, 816, and 936 nm, highlighting the combined role of pigment degradation and canopy structural changes induced by BS infection. To refine band selection and improve predictive performance, a backward sequential feature selection approach coupled with the RELIEFF algorithm was employed. This method systematically evaluated combinations of sensitive bands derived from DA and CR to identify the most informative subset. Among all tested combinations, the four-band set comprising 498, 522, 673, and 708 nm achieved the highest classification accuracy of 75.96%, outperforming larger band combinations and demonstrating the advantage of optimal feature reduction. Overall, the results confirm that hyperspectral derivative-based approaches, supported by sensitivity analysis, continuum removal, and machine learning-based feature selection, are highly effective for identifying BS-sensitive spectral bands (Fig. 3.6). The identified optimal bands enable early and accurate detection of rice brown spot disease, offering strong potential for precision disease monitoring and targeted pesticide application under field conditions.

Search for novel mediators in plant defense response to pathogenic infections in rice through molecular techniques

Genome analysis of *Streptomyces caeruleatus* S14

(Prabhukarthikeyan SR, Keerthana U, Manas Kumar Bag and Parameswaran C)

The complete genome of *Streptomyces caeruleatus* S14 was obtained using Illumina NovaSeq 6000 paired-end sequencing (PE 150), resulting in an assembled genome of 9.75 Mb. The genome comprises 9,191 predicted protein-coding genes, 68 tRNA genes, and 6 rRNA genes, with a high G+C content of 71.03%. Annotation performed using RASTtk (genetic code 11) and evaluated through PATRIC confirmed the high quality of the assembly, showing 99.9% completeness and strong consistency metrics. Functional categorization revealed genes associated with key biological processes such as primary and secondary metabolism, energy production, stress adaptation, membrane transport, regulation and signaling, cell envelope biogenesis, and defense-related functions. Importantly, multiple biosynthetic gene clusters involved in secondary metabolite synthesis were identified, highlighting the strain's capacity to produce antibiotics and other bioactive compounds. Overall, this genome analysis emphasizes the biotechnological and agricultural potential of *S. caeruleatus* S14, particularly for applications in biocontrol and plant growth promotion, and represents the first whole-genome sequencing report of this species from rice rhizosphere soil in India. (Fig. 3.7).

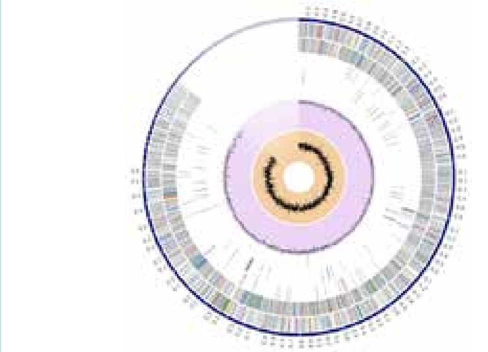


Fig. 3.7. A circular graphical display of the distribution of the genome annotations: The circular genome map displays, from outer to inner rings, contigs, CDS on forward and reverse strands, RNA genes, CDS associated with antimicrobial resistance and virulence factors, followed by GC content and GC skew. Colors denote the functional subsystems of the CDS

Characterization of cuticular wax of contrasting rice genotypes against Bacterial Blight Disease (Arup Kumar Mukherjee and Totan Adak)

Scanning Electron Microscopy (SEM) analysis reveals distinct cuticular wax morphology between resistant and susceptible rice genotypes (Fig. 3.8). Resistant genotypes (CR Dhan 800-R and MPI-37-R) show dense, well-organized crystalline wax structures, contributing to higher surface roughness and hydrophobicity. Susceptible genotypes (CO-39-S and TN1-S) exhibit sparse or irregular wax deposition with smoother surfaces, leading to lower hydrophobicity and potential vulnerability to pathogen entry.

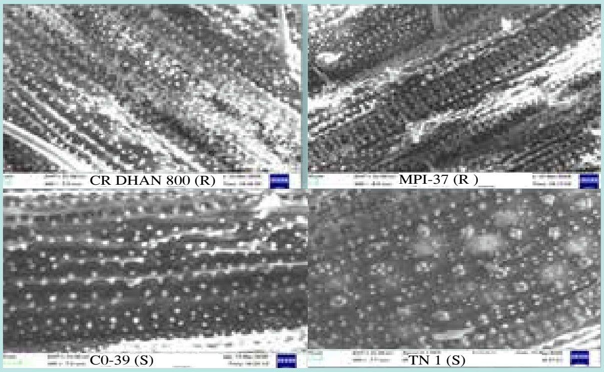
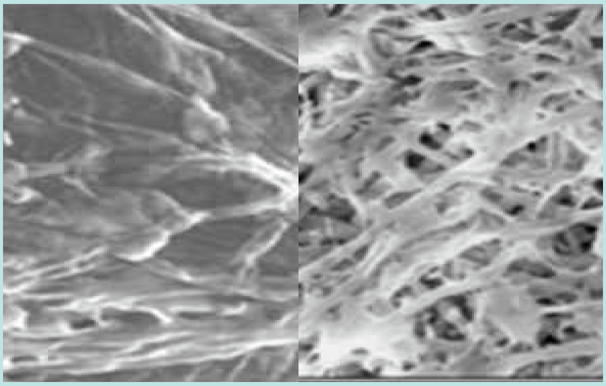


Fig. 3.8. Scanning Electron Microscopy (SEM) analysis reveals distinct cuticular wax morphology between resistant and susceptible rice genotypes

Trichoderma VOCs for growth promotion and biocontrol (Arup Kumar Mukherjee and Totan Adak)

Fumigation effect of volatiles released from *Trichoderma* sp. against pathogenic soil borne fungus *R. solani* was tested and it was observed that the VOCs emitted by the *Trichoderma* sp. showed clear-cut disintegration of fungal mycelium (Fig. 3.9). In addition, fumigation with VoCs of *Trichoderma* sp. showed growth promotion in rice seedlings as evidenced by higher root and shoot length and root and shoot weight (Fig. 3.10 and 3.11)



R. solani without volatiles *R. solani* with volatiles

Fig. 3.9. Trichoderma showed clear-cut disintegration of fungal mycelium

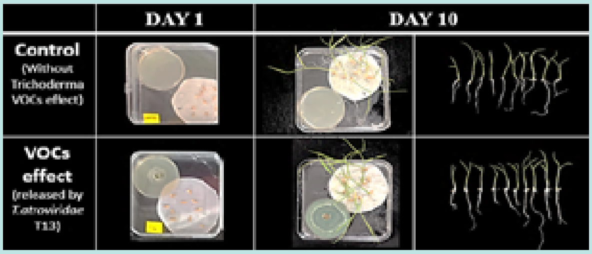


Fig. 3.10. Effect of VOCs on rice plant length and biomass in a closed square Petri plate

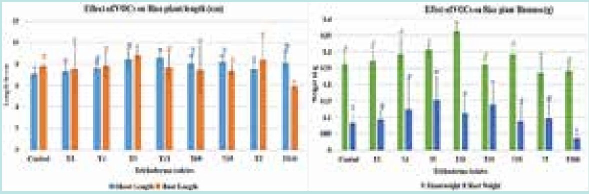


Fig. 3.11. Effect of VOCs on (A). Plant length and (B) Plant biomass of rice plant [error bars represents the standard deviation from the mean of three replicate plates. Statistical significance was assessed using univariate analysis followed by DMRT test (p<0.05)

Plant Volatiles and bacterial leaf blight resistance (Arup Kumar Mukherjee and Totan Adak)

The volatiles (VOC) were collected from eight different genotypes, susceptible (S) (Nidhi, Tetep, Hanseswari, Chaka akhi) and resistant (R) (CR DHAN-800, MPI-37, NSN-2-114 (IET NO- 28463), IR-29). VOCs like Ethylbenzene, p-Xylene, o-Xylene, Benzene, 1-ethyl-3-methyl-, 1-Octanol, 2-Carene, Nonanal, Eicosane, etc., were present in both resistant and susceptible plants. p-Cymene, n-Pentadecanol, Heptadecane, n-Tridecan-1-ol, Dodecanal, and Tetradecane were found in higher quantities in the resistant varieties.

Collection, isolation, and morphological characterization of *Rhizoctonia solani* isolates causing sheath blight disease in rice (Jeevan B and Raghu S)

Sheath blight–infected rice samples were collected from multiple rice-growing regions across different Indian states. A total of 40 *R. solani* isolates were recovered and subjected to pathogenicity testing and morphological characterization. All forty isolates induced typical sheath blight symptoms on the susceptible rice cultivar Swarna *Sub1*, thereby fulfilling Koch's postulates. Morphological characterization revealed substantial diversity among the *R. solani* isolates with respect to mycelial texture, colony pigmentation, and sclerotial characteristics. Colony coloration ranged from pale white and translucent to greyish white, pale brown, and dark brown. Most isolates exhibited appressed, web-like mycelial growth at the colony periphery, accompanied by dense, cottony, or fluffy aerial mycelium towards the center. Considerable variation was also observed in sclerotial development. Some isolates produced abundant, dark brown, coarse, and irregularly shaped sclerotia arranged in distinct rings, arcs, or dense central clusters, whereas others formed small, light cream to whitish immature aggregates or failed to produce mature sclerotia. The spatial distribution of sclerotia varied among isolates, appearing scattered across the colony surface, localized at the periphery, or densely aggregated near the point of inoculation.

A rapid and simplified detection of *Sclerotium rolfsii* causing seedling blight in rice nurseries by loop mediated isothermal amplification (LAMP) assay

(Raghu S, Jeevan B and Amrita Banerjee)

Seedling blight is emerging as a severe problem in rice nurseries of Odisha leading to complete loss of sown seeds. This puts farmers to go for second time seed bed preparation which not only delays crop transplanting, but also leads to the incidence of several foliar diseases at late season. Hence, we developed a loop mediated isothermal amplification (LAMP) assay for early detection of *Sclerotium rolfsii* from soil and infected plants. LAMP primers were designed targeting the ITS region of the rDNA of the *S. rolfsii* using LAMP primer designing tool (Primer Explorer V5; Eiken Chemicals, Tokyo, Japan) and performed LAMP assay in at 60°C for 1 hr in a water bath. Negative controls were kept using *Rhizoctonia solani* and *Fusarium fujikuroi*. A positive reaction that showed the green color of the visible dye ((SYBR® green I). The detection sensitivity of the LAMP assay was 1000 times higher than that of conventional PCR (Fig. 3.12 and 3.13).


Incidence of Early seedling blight in rice nurseries


Incidence of Early seedling blight in rice nurseries

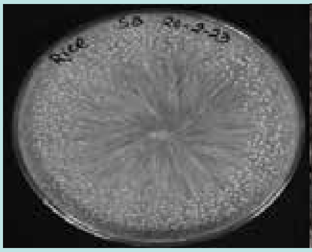


Fig. 3.12. Culture of *Sclerotium oryzae*


Fig. 3.13. Tube 1: color change (green) of the visual dye indicates positive reaction for *S. rolfsii*. Tube 2-3: Negative reaction for *Rhizoctonia solani* and *Fusarium fujikuroi*

Field evaluation of Streptomyces-based bioformulations for the management of rice blast

(Prabhukarthikeyan SR and Keerthana U)

Two consecutive field trials were conducted to evaluate liquid formulations of *Streptomyces* isolates (S-3, S-14 and S-20) along with recommended fungicides for the management of rice blast in the susceptible rice variety *Tapaswini*. Across both trials, all treatments significantly enhanced growth and yield parameters and reduced rice blast incidence compared to the untreated control. Bioagent-treated plots showed consistent improvement in agronomic traits. Among all treatments, the liquid formulation of *Streptomyces* isolate S-14 applied as seed treatment, seedling root dip and foliar spray recorded the highest plant growth, biomass accumulation, yield and seed index in both trials. Significant reduction in rice blast incidence was observed in all treated plots. Tebuconazole 50% + trifloxystrobin 25% WG recorded the maximum disease reduction (72.58% in Trial I and 76.79% in Trial II), followed by isoprothiolane 40% EC. Among bioagents, the liquid formulation of S-14 was the most effective, reducing disease severity by 64.52% (PDI 16.30%) in Trial I and 66.07% (PDI 14.07%) in Trial II. The untreated control recorded the highest disease incidence with PDI values of 45.93% and 41.48% in Trials I and II, respectively.

Plant protection molecules: efficacy, distribution, toxicity and remediation

Effect of exogenous melatonin application as seed priming against rice root knot nematodes *(Meloidogyne graminicola)*

(Rupak Jena, Totan Adak and Milan Kumar Lal)

Seed treatment with melatonin (150 ppm) and foliar application (100 µM) at 30, 60, and 90 days after sowing (DAS), alone or in combination, were evaluated for their effects on *Meloidogyne graminicola* infection in rice. Foliar application of melatonin at 30, 60, and 90 DAS did not significantly influence root galling index, number of egg masses per root system, or eggs per egg mass. In contrast, seed treatment with melatonin significantly reduced galling parameters up to 35 days after sowing. Foliar application at 30 and 60 DAS significantly enhanced physiological traits, including photosynthetic rate, transpiration rate, stomatal conductance, and intercellular CO_2 concentration, compared with the control. Moreover, repeated foliar sprays of melatonin (100 µM) at 30, 60, and 90 DAS consistently improved plant physiological performance. Biochemical analyses revealed that foliar application markedly increased the activities of superoxide dismutase (SOD), catalase, peroxidase, glutathione, phenols, hydrogen peroxide–scavenging enzymes, and total chlorophyll content.

In-vivo efficacy of combination fungicides against sheath blight disease under artificial inoculation (Srikanta Lenka)

Out of seven combination fungicides taken repeatedly for evaluating in vivo (field) efficacy of combination fungicides against sheath blight disease (*Rhizoctonia solani* Kuhn) under artificial inoculation during *kharif*, 2024, the combination fungicide azoxystrobin 5.1% + tebuconazole 9.1% + prochloraj 18.2% EC @ 3.5mL/L was the best to inhibit sheath blight severity by 73.4%, sheath blight disease incidence by 69.7% with production of maximum grain yield of 5.08 t ha^{-1}. The 2nd best treatment was azoxystrobin 14% + epoxyconazole 9% SC @1.5mL/L which reduced sheath blight severity by 70.2%, sheath blight disease incidence by 65.3% along with production of grain yield of 4.86 t ha^{-1}. In control, grain yield was obtained as 3.52 t ha^{-1}. Sheath blight susceptible variety Tapaswini was taken up for this field experiment (Table 3.3).

Table 3.3. Field evaluation of new molecules of fungicide against sheath blight disease.

	Treatments	Dose (g or ml/L)	Dis. Severity (%)	Reduction in dis. severity over control (%)	Disease incidence (%)	Reduction in disease incidence over control (%)	Grain yield (t/ha)
T-1	Mancozeb 50% + Thiophanate methyl 25% WG	3.0g	34.3	49.8	37.6	48.2	4.02
T-2	Kasugamycin 5% + copper oxychloride 45% WP	1.5g	37.0	45.9	45.4	37.5	4.0
T-3	Azoxysrobin 5.1% + tebuconazole 9.1% + prochloraz 18.2% EC	3.5g	18.2	73.4	22.0	69.7	5.08
T-4	Fenoxanil 5% + Iso-prothiolane 30% EC	2.0ml	25.6	62.6	33.4	53.9	4.24
T-5	Azoxystrobin 14 % + Epoxiconazole 9 % SC	1.5ml	20.4	70.2	25.2	65.3	4.86
T-6	Picoxystrobin 7.05% + Propiconazole 11.7% SC	2.0ml	23.8	65.2	28.8	60.3	4.55
T-7	Tebuconazole 50%+ Trifloxystrobin 25% w/w WG	0.4g	30.6	55.3	36.3	50.0	4.17
T-8	Untreated control	-	68.4	-	72.6	-	3.52
CD at 5%				3.74		4.82	

Multigenerational exposure of insecticides on resistance and gut microbiota in *Nilaparvata lugens* (Guru Pirasanna Pandi G, Basana Gowda G and Totan Adak)

This study explored how continuous exposure to five insecticides *viz*., imidacloprid, pymetrozine, buprofezin, triflumezopyrim, and dinotefuran affects resistance mechanisms and gut microbiota across five generations (F0–F5). Resistance assays showed higher LC_{50} values for imidacloprid and dinotefuran. Gene expression analysis revealed strong upregulation of detoxification genes, particularly P450 variants, in later generations. Microbial profiling identified 20 phyla and 273 genera, dominated by Proteobacteria, Actinobacteria, and Firmicutes, with diversity declining under chemical stress. Specific taxa such as Enterobacteriaceae and Pseudomonadaceae became enriched, reflecting adaptive shifts. These findings highlight how long-term insecticide pressure reshapes microbial ecosystems and resistance, offering insights for sustainable pest management strategies.

Simultaneous removal of imidacloprid, carbendazim, and bispyribac sodium using zinc and bentonite functionalized rice husk biochar composite (Totan Adak)

The increasing use of pesticides in intensive cultivation practices poses significant environmental risks due to their persistence, leaching, and adverse impacts on non-target organisms. Rice husk, an agricultural by-product, was functionalized with zinc chloride and bentonite for the removal of three commonly used pesticides; imidacloprid, carbendazim, and bispyribac sodium. Engineered rice husk biochar (ERHB) was produced via the co-pyrolysis of 10 g of rice husk, 5 g of bentonite and 5 g of $ZnCl_2$at 500 °C for 2 h, and it removed 96.43, 84.47 and 78.94% of spiked bispyribac sodium, carbendazim, and imidacloprid, respectively, from water. Physico-chemical characterization revealed significant structural and surface chemistry changes upon modification and their role in enhancing adsorption. Elemental analysis of ERHB confirmed the incorporation of clay minerals along with Zn. Adsorption experiments showed that pesticide removal was mainly influenced by initial concentration, contact time, and adsorbent dosage, while solution pH had little effect. Kinetic and isotherm models further explained the adsorption mechanisms. ERHB demonstrated a maximum adsorption capacity of 57.69 µg mg^{-1} in the mixed-pesticide system. ERHB could also remove over 95% of 50 pesticides and three synthetic dyes including bromocresol green (44.6%), allura red (75.3%), and methylene blue (89.7%) from water. Thus, the ERHB can be used as a multi-class pesticide and dye removal agent from aqueous media, offering potential for integrated water remediation strategies in agro ecosystems (Fig. 3.14).

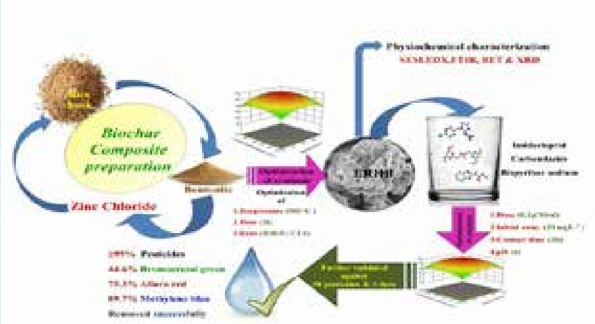


Fig. 3.14. Engineered rice husk biochar (ERHB) for multi-contaminant removals from water

Efficiency of lignin-degrading fungal strains isolated from biomixture for myco-remediation of pesticides (Totan Adak)

Pesticides play a crucial role in sustaining global food production; however, their improper handling leads to point-source pollution. A total of eight fungal colonies were isolated from contaminated biomixtures, and named as F1-F8 to degrade pesticides from point-source pollution. All isolates exhibited tolerance to bispyribac-sodium (BS), carbendazim (CAR), and imidacloprid (IMI), across concentrations ranging from 1 to 10 ppm. Pesticide degradation efficiency was evaluated by inoculating isolates into broth fortified with the three pesticides (10 ppm) and incubating for 10 days, followed by UHPLC residue analysis. Among the isolates, F6 and F7 were the most effective. Over 21 days, F6 degraded 93% CAR, 82% BS, and 60% IMI, while F7 degraded 92% CAR, 71% BS, and 61% IMI. Laccase activity assays revealed a strong correlation between ligninolytic potential and pesticide degradation, with F7 exhibiting the highest laccase activity (6507 U kg^{-1} on day 14). Further, bioaugmentation studies showed that pesticide half-lives were significantly reduced in biomixture compared to topsoil and were further accelerated by inoculation with F6 and F7.

Salicylic acid and methyl jasmonate seed priming induces systemic acquired resistance to bakanae disease caused by Fusarium fujikuroi in non-basmati rice (Raghu S and Jeevan B)

Efficacy of salicylic acid (SA) and methyl jasmonate (MJ) as seed priming agents for control of bakanae disease was evaluated in two non basmati varieties *i.e.*, Pooja and Chandan. Seed priming was done with different concentrations (1.0 g, 2.0 g, 5.0 g, 10.0 g and 50.0 mg/L) for 12, followed by challenge inoculation with pure culture of *Fusarium fujikuroi*. The results showed significant reduction in bakanae disease incidence in elicitor treated plants with maximum efficacy at 10.0 mg/L in both the varieties. The seed priming has recorded significantly higher amount of Peroxidase, Polyphenol oxidase, PAL and Chlorophyll content. The treated plants also recorded reduced hydrogen peroxide content, endogenous GA3 quantity. Hence, the elicitor seed priming can be a promising alternative to chemical fungicides for management of this important seed borne disease of rice.

Effect of sublethal acephate on demographic and behavioural characteristics of *Habrobracon hebetor* (Say) (Basana Gowda G)

The transgenerational effects of acephate on demographic and behavioural traits of the gregarious parasitoid *Habrobraconhebetor* (Say) were assessed over five generations (F1–F5). Probit analysis estimated LC$_5$, LC$_{30}$ and LC$_{50}$ values at 0.01, 0.15 and 0.52 mg L^{-1}, respectively. Sublethal concentrations shortened developmental duration and enhanced fecundity, while higher concentrations lowered fecundity, reduced longevity, and decreased adult walking speed (Fig. 3.15). Nevertheless, major population growth indices (r, λ, R$_0$, GRR) showed little variation across generations. Overall, acephate produced concentration-dependent sublethal effects with transgenerational consequences in *H. hebetor*, which could alter its efficiency as a biological control agent. Such insights are important for incorporating parasitoids into IPM and reducing unintended impacts of insecticide applications.

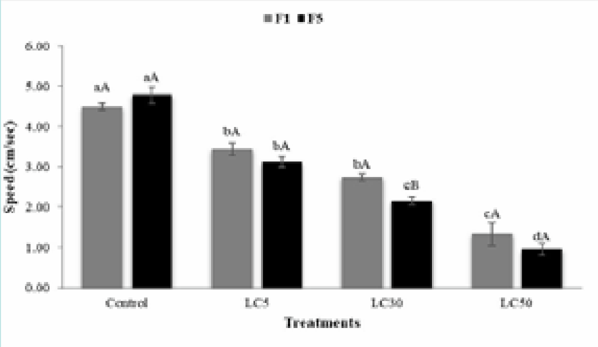


Fig. 3.15. Higher concentrations lowered fecundity, reduced longevity, and decreased adult walking speed

Dissemination of integrated pest management strategies for insect pests, diseases and nematodes in rice

Climate Variability and Distribution of Brown Plant hopper in India (Guru Pirasanna Pandi G)

This study evaluates brown planthopper potential distribution under CMIP6 climate scenarios for 2050 and 2070 using species niche modeling across four SSPs. Results showed temperature-related factors contribute 60% to habitat suitability, with annual mean temperature

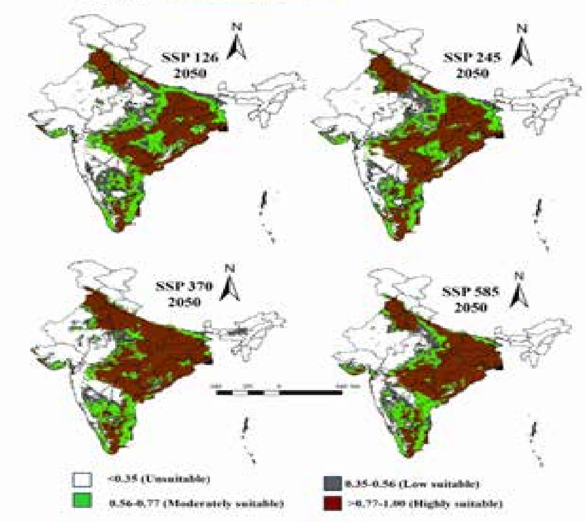


Fig. 3.17. Expected shifts in the habitat distribution of Nilaparvata lugens across India by 2050, as predicted by the Beijing Climate Center Climate System Model under the four different climate scenarios. SSPs, socioeconomic pathways

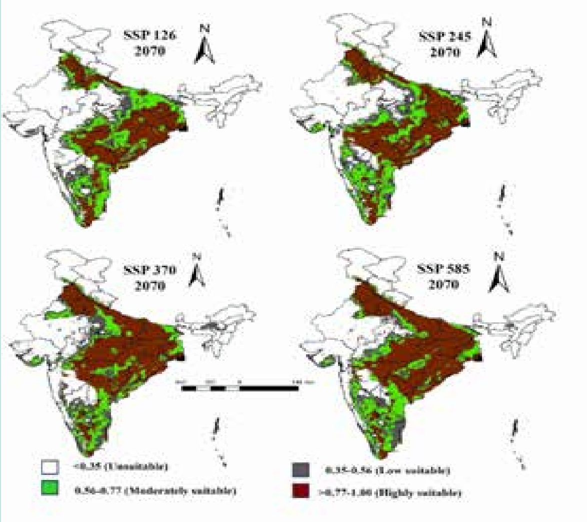


Fig. 3.18. Expected distributional changes of Nilaparvata lugens across India by 2070, as modelled using the Beijing Climate Center Climate System Model under four different climate scenarios. SSPs, socioeconomic pathways

being most critical, while precipitation accounts for 40%. Currently, half of India's land is suitable for *N. lugens*, with 7.80% at high risk. Projections indicate expansion of high-risk zones to 30.35% (2050) and 27.24% (2070), particularly in Odisha, West Bengal, Tamil Nadu, and Andhra Pradesh, with emerging risks in the northeast. Effective adaptation strategies are urgently needed (Fig. 3.17 and 3.18).

Temperature-Dependent Development of Brown Planthopper (*Nilaparvata lugens*) (Guru Pirasanna Pandi G)

This study examined thermal constants and their effects on life table parameters using five constant temperature regimes (18–34°C) for *Nilaparvata lugens*. Developmental rates, mortality, and fecundity were modeled through linear and non-linear functions with ILCYM software, which generated a phenology model to simulate life cycle parameters. Lower temperature thresholds (LTT) and thermal constants (k) were estimated for each stage from egg to adult. Results showed that developmental duration shortened with rising temperatures, with optimal growth between 22–30°C. Maximum fecundity occurred at 26°C, while intrinsic growth rate (rm) and net reproductive rate (R0) peaked at 26–30°C. Model validation confirmed close agreement between observed and simulated values. These findings provide critical insights for risk assessment under climate change and support the development of monitoring and decision-support systems for rice pest management.

Effect of various combinations of neem oil cake and neem oil for management of nematode (*M. graminicola*) (Rupak Jena)

A combination of neem oil cake @ 30 gm/pot and neem oil @ 3 ml/lit were tested against *M. graminicola* and it was observed that seed treatment of neem oil @ 3 ml/lit during sowing and soil treatment of neem oil cake @ 30 gm/kg after 5 days of sowing expressed significantly improved morphological parameters and alleviated nematode infection i.e. reduced galling, egg mass and reproductive factor at 35 and 60 days after sowing. The disease index and control efficacy were studied and reciprocated to have positive correlation with initial treatments of neem oil and cake applications while at 60 DAS the plants had non-significant difference in galling index, egg masses/root system and eggs/egg mass.

Molecular characterization and Effect of varied levels of moisture and temperature on EPN survival (Rupak Jena)

Four entomopathogenic nematodes *Oscheius chongmensis*, *Heterorhabditis bacteriophora*, *Steinernema carpocapsae* and *Steinernema khoisanae*were were identified and tested for formulation development at various moisture and temperature levels @ 3000/100 gm. *Heterorhabditids* sp. exhibited best survivality till 240 days while it recorded 50% mortality at 150 days at 30% moisture while *Oscheius* sp. survived best in 30% moisture till 195 days and 50% mortality was reached by the EPN at 135-140 days. At 4^{o}C, *Heterorhabditis* sp. survived till 210 days while *Oscheius* sp. survived till 110 days and exhibited 50% mortality at 80-90 days.

Biological Control of early seedling blight of rice Induced by Sclerotium rolfsii (Raghu S, Jeevan B and Totan Adak)

Bacterial and fungal biological control agents like *Trichoderma asperellum*, *Trichoderma harzianum*, *Pseudomonas fluorescens*, and *Bacillus megaterium*, applied either individually or in mixed combinations, against *Sclerotium rolfsii* causing seedling blight. The treatment with *T. harzianum* and *P. fluorescens* resulted in the highest mycelial growth inhibition (100%), followed by *T. asperellum* and *B. megaterium* (85.25 and 83.50%). Seed treatment and soil application of *T. harzianum* and *P. fluorescens* @ 10 (5 + 5) g kg^{-1} and soil application @ 10 (5 + 5) kg ha^{-1}, followed by seed treatment and soil application of *T. asperellum* and *B. megaterium* at 10 (5 + 5) g kg^{-1} soil application @ 10 (5 + 5) kg ha^{-1}, resulted in the lowest disease incidence (15.25 and 18.50%) (Fig. 3.19). Therefore, an integrated disease management module with these BCAs needs to be developed and validated with a farmers' participatory mode under field conditions.

Fig. 3.19. Seed treatment + Soil application of Biocontrol agents

Untreated control Bed

Activities of plant essential oil (PEO) on false smut pathogen (*U. virens*) (Manas Kumar Bag)

Cinnamon oil (CO) is found as highly effective in inhibiting mycelial growth of the pathogen *Ustilaginoidea virens* causing false smut diseases of rice. LC_{50} value for CO is calculated as 53.6ppm. All 21 isolates collected from different parts of eastern Indian states were tested at 5 different concentrations of CO based on the LC_{50} value. Only 3 isolates were found not sensitive at or below LC_{50} value (Table 3.4, Fig. 3.20)

Fig. 3.20. Isolates found not sensitive at or below LC_{50} value

Table 3.4. Sensitivity of *Ustilaginoidea virens* to cinnamon oil.

Isolates	Location	LC_{50} value
FS117	Jeypore, Odisha	45.8
FS57	Sankrail, Howrah, W.B.	46.3
FS83	Dhemaji, Assam	46.5
FS10	Ranital, Bhadrak, Odisha	46.5
FS14	Anlamara, Nayagarh, Odisha	49.7
FS47	Pundibari, Coochbehar, W.B.	49.9
FS34	Pundibari, Coochbehar, W.B.	49.9
FS45	Pundibari, Coochbehar, W.B.	50.1
FS114	CRRI, Cuttack, Odisha	50.2
FS8	Salipur, Cuttack, Odisha	50.5
FS63	Gosaba, 24 Parganas (South), W.B.	51.9
FS19	Satyapur, Dhubri, Assam	52.6
FS17	Basanti, South 24-Pargana, W.B.	53
FS119	Jagatsinghpur, Odisha	53.7
FS66	Chinsurah, Hooghly, W.B.	54
FS56	Kalyani, Nadia, W.B.	54.3
FS116	Jeypore, Odisha	54.6
FS65	Polba, Hooghly, W.B.	54.8
FS4	Darang, Assam	55.3
FS118	Sambalpur, Odisha	57.2
FS59	Uluberia 1, Howrah, W.B.	58

Impact of sheath blight (ShB) and bacterial blight (BB) pathogen infection at different rice growth stage on grain production (Manas Kumar Bag)

Impact of sheath blight disease at different rice growth stages was studied under artificial inoculation condition on Tapaswini variety at four different stages *viz.,* Early tillering (T1), Maximum tillering (T2), 50% flowering (T3), and100% flowering (T4) with control (no infection-T5). Sheath blight disease severity was significantly higher when inoculated at tillering stages over flowering stages. Grain production was significantly lower when inoculated at tillering stage than early flowering stages. ShB disease severity and grain production is non-significantly different when inoculated at 50% and 100% flowering stages.

Similarly, impact of bacterial blight disease at different rice growth stages was studied under artificial inoculation condition on Tapaswini variety at four different stages *viz.,* Early tillering (T1), Maximum tillering (T2), 50% flowering (T3), and100% flowering (T4) with control (no infection-T5). BB disease severity was significantly higher when inoculated at maximum tillering stage followed by early tillering and flowering stages. Grain production was significantly lower when inoculated at tillering stage than flowering stages. BB disease severity and grain production were non-significantly different when inoculated at 50% and 100% flowering stages (Fig. 3.21).

Validation of need based IPM modules in shallow low land ecologies (Srikanta Lenka and PC Rath)

IPM module under shallow low land ecosystem was tested in the farmer's fields of the village Talasanga of Block-Marshaghai, Dist-Kendrapara with Swarna and Pooja (20 acres) during *Kharif,* 2024 involving 25 farmers. In IPM practice, seed treatment with *Trichoderma* formulation @10 g/kg seed before sowing and need based application of pesticides were undertaken by the farmers in the affected areas only. Carbendazim 50 WP @1.0 g liter^{-1} water against brown spot, sheath blight, sheath rot diseases; cartap hydrochloride @ 1kg ai ha^{-1} water against YSB, leaf folder, BPH and need based foliar application of chloropyriphos 20% EC @ 0.5 kg ai ha^{-1} against gundhi bug were applied. Also, sex pheromone traps @ 8 nos. ha^{-1} with lure and bio-control agents (*T. viride* and *Pseudomonas fluorescens*) formulations were provided to the farmers.

In need based IPM practice in both the varieties Swarna and Pooja, less infestation of diseases such as brown spot (4.8-5.4%), sheath blight (7.4-8.2%), sheath rot (4.4-4.5%), false smut (5.0-7.6%) and insects namely, dead heart (3.1-3.4%) and white ear head (3.1-3.7% due to YSB and gundhi bug (3.4-4.2%) were observed as compared to farmer's practice. Higher grain yield of 5.8-5.9 t/ha, straw yield of 5.0-5.2 t/ha with B:C ratio 2.82-2.9 were obtained due to following IPM practices. Need based IPM outperformed the farmer's practice with grain yield advantage of 0.8-1.5 t/ha.

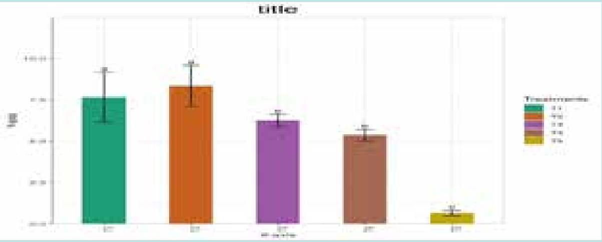


Fig. 3.21 a. Per cent disease progress of sheath blight

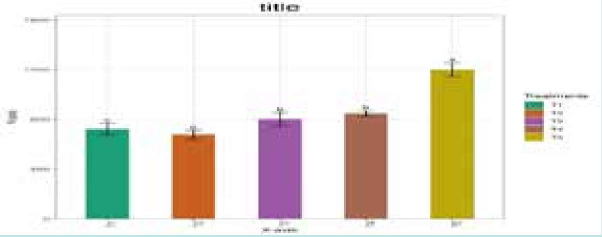


Fig. 3.21 b. Grain production (g/plot)

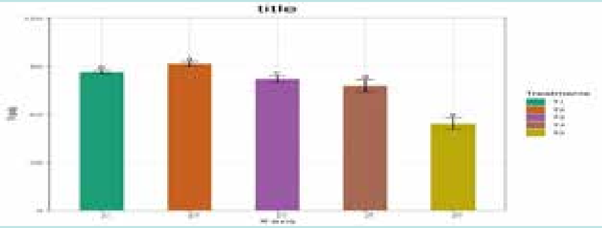


Fig. 3.21 c. Per cent disease progress of bacterial blight

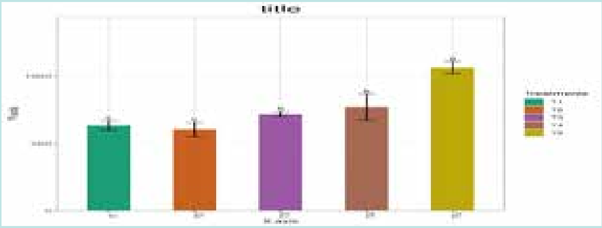


Fig. 3.21 d. Grain production (g/plot)

Table 3.5. Comparison of need based IPM with farmers practice against different insect pest and diseases.

	Treatments	Brown spot (%)	Brown spot (%)	Brown spot (%)	Brown spot (%)	DH (%)	WEH (%)	Gundy Bug (%)	NE	G-Yield (t/ha)	S-Yield (t/ha)	B:C ratio
Swarna	Need based	4.8 (12.08^{b})	7.4 (15.87^{b})	4.3 (13.08^{c})	5.0 (13.04^{c})	3.1 (10.19^{d})	3.7 (11.14^{d})	3.4 (10.62^{c})	3.4 (10.57^{c})	5.9^{a}	5.0^{b}	2.9
	Farmer's Practice	11.8 (17.96^{a})	13.6 (21.02^{a})	7.8 (15.98^{ab})	10.3 (17.74^{ab})	5.3 (13.35^{b})	5.6 (13.64^{b})	7.2 (15.56^{a})	6.0 (14.13^{a})	4.4^{c}	4.1^{c}	2.46
Pooja	Need based	4.6 (11.92^{b})	8.2 (15.04^{b})	4.5 (14.42^{bc})	7.6 (14.0^{b})	3.4 (10.62^{c})	3.1 (10.19^{c})	4.2 (11.77^{b})	4.4 (12.06^{b})	5.8^{b}	5.2^{a}	2.82
	Farmer's Practice	10.8 (18.76^{a})	11.7 (19.72^{a})	9.6 (18.87^{a})	12.9 (21.34^{a})	5.8 (13.93^{a})	5.9 (14.05^{a})	7.2 (15.56^{a})	6.0 (14.13^{a})	4.2^{d}	4.1^{c}	2.36
CD at 5%		2.12	2.28	2.24	2.43	0.22	0.52	0.31	0.24	0.28	0.20	

Conclusion

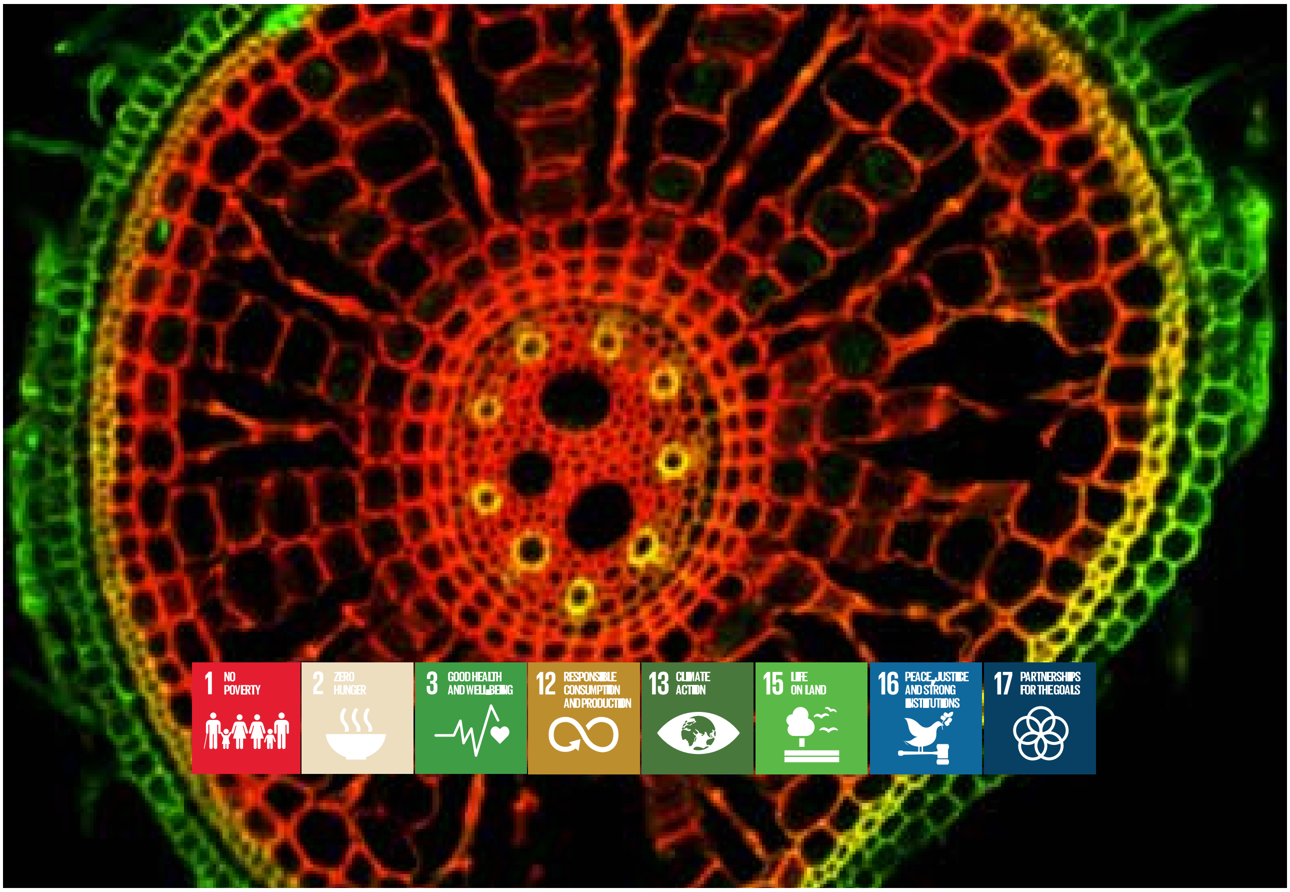
The program on biotic stress management in rice involved the evaluation of over 2000 rice entries against major insects, diseases, and nematodes to identify resistant donors, aiding in the development of biotic stress-resistant rice varieties. The division also identified key markers associated with resistance to BPH, WBPH, Leaf folder, gall midge, Bakanae, sheath blight offering valuable resources for marker assisted breeding. The complete genome of Streptomyces caeruleatus S14 revealed its potential role in plant growth promotion and disease suppression activities against blast. The hyperspectral analysis of rice canopies using ASD data successfully identified sensitive spectral regions and optimal bands for early detection of rice brown spot (RBS) disease through a combination of derivative analysis, sensitivity analysis, continuum removal, and feature selection algorithms. Exogenous melatonin application as seed priming significantly reduced root knot nematode infestation in rice. Significant reduction in bakanae disease incidence and plant growth promotion in elicitor treated plants with maximum efficacy at 10.0mg/l in was recorded. Foliar application of potassium silicate (1.0%) on the susceptible rice variety TN1 significantly altered the settling behavior of yellow stem borer (YSB) female moths under cage experiments and olfactometer assays. LAMP based early detection assay was developed for Sclerotium rolfsii causing seedling blight disease. Cinnamon oil (CO) was found as highly effective in inhibiting mycelial growth of the pathogen Ustilaginoidea virens causing false smut diseases of rice.

PROGRAMME

04

Photosynthetic Enhancement, Abiotic Stress Tolerance and Grain Nutritional Quality in Rice

Rain-fed rice cultivation faces multiple environmental challenges that have intensified in recent years due to changing climatic conditions. The extensive genetic diversity and rich germplasm resources available in rice provide a valuable platform for identifying and elucidating unique tolerance mechanisms that enable rice to withstand a range of abiotic stresses, occurring either individually or in combination. These stresses significantly reduce crop growth and productivity by impairing photosynthesis and other essential metabolic processes, and they also adversely affect grain yield and nutritional quality. Grain quality is a critical criterion for evaluation from the perspectives of farmers, millers, and consumers. Accordingly, a comprehensive assessment of physicochemical, nutritional, and sensory attributes, along with key biochemical components such as resistant starch, amylose, and phytic acid, is essential. In light of the rapidly increasing diabetic population, particularly among communities where milled rice constitutes a major dietary staple, there is an urgent need to investigate the factors contributing to the high glycaemic index of rice. These research challenges are being addressed through three institutional and five externally funded projects supported by the active involvement of eight scientific and nine technical personnel, with the overarching goal of developing sustainable solutions.



Photosynthetic efficiency and productivity of rice under changing climate

Prime editing for enhancing photosynthesis (KA Molla and MJ Baig)

Previous research suggests that acquiring more significant PEP substrate saturation constants and increased tolerance towards feedback inhibition are vital achievements in the evolution of C4 PEPC from the C3 ancestors. The conversion of alanine to serine at position 774 (Ala774 to Ser774) reduces the Km for phosphoenolpyruvate (PEP) in C4 PEPC enzymes. This study aimed to validate whether mutations at Ala774 and Arg884 in rice PEPC can switch its functionality from C3-like to C4-like with the help of precise genome editing. Prime editing offers precision but suffers from low efficiency in plants. Enhancements in vector design are crucial to improve editing success rates. Therefore, enhancing the efficiency of prime editing through vector modifications is another targeted goal in this study.

Previously, multiple vector modifications were made. Additionally, the pegRNA promoter was replaced with a composite promoter for higher PE efficiency, and extra mutations were introduced in the SpCas9 enzyme. Twelve vectors engineered with pegRNA targeting Ala774 and Arg884 were transfected into rice protoplasts. Genomic DNA from transfected protoplasts was amplified and analyzed using deep sequencing, and the vector with the highest efficiency was selected for *Agrobacterium*-mediated rice transformation. Edited plants with the desired nucleotide changes were identified. Seeds from T_0 plants were harvested and grown for the next generation in a climate-controlled greenhouse and analyzed for the presence of prime editor (PE) components and Cas-9. The PE components and Cas-9-free homozygous lines were used for further analysis. Crude protein extracts were prepared from both wild-type and edited plants and subjected to malate inhibition assays. The PEPC isoform derived from the edited lines exhibited less sensitivity compared to the wild-type enzyme. In the presence of 0.5 and 1 mM malate, the edited lines showed approximately 49.4% and 32% reduction in malate sensitivity, respectively, and retained a substantially higher catalytic activity.

The photosynthetic pigment content was significantly higher in the edited lines compared to the wild-type, which was also visually evident from the darker green coloration of the edited plants (Fig. 4.1A-B). Measurements of photosynthetic rate (A), stomatal conductance (gs), and transpiration rate (E) were obtained. Leaf gas exchange data clearly demonstrated that the edited lines outperformed the wild type. Specifically, the wild type exhibited a photosynthetic rate of approximately 22 µmol CO_2 m^{-2} s^{-1}, whereas the edited lines achieved rates around 29 µmol CO_2 m^{-2} s^{-1} (Fig. 4.1C). Stomatal conductance was also markedly higher in the edited lines, showing an improvement of about 38% relative to the wild type (Fig. 4.1D). Similarly, the transpiration rate increased by approximately 30% in the edited plants (Fig. 4.1E). Furthermore, analysis of light use efficiency revealed that the edited lines exhibited an enhancement of nearly 21% compared to the wild type (Fig. 4.1F).

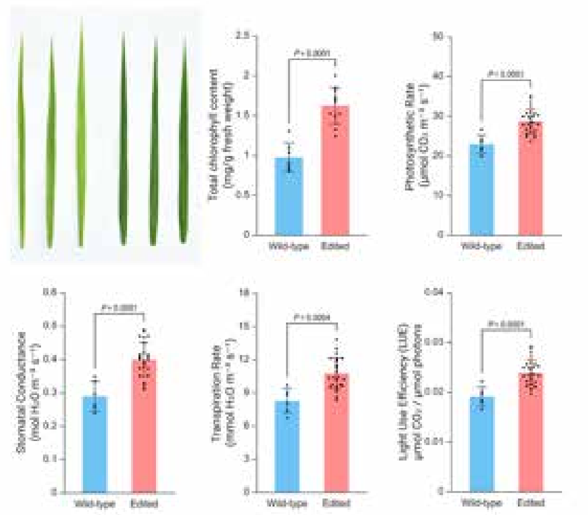


Fig 4.1 Comparative analysis of the photosynthetic efficiency between the edited lines and the wild-type. (A) Comparative analysis of the colour variation among edited and wild-type plants. (B) total chlorophyll content, (C) Photosynthetic rate, (D) Stomatal conductance, (E) Transpiration rate, (F) Light use efficiency

The edited lines exhibited an early flowering phenotype compared with the wild-type plants. In addition, a significant reduction in plant height was observed at maturity, with the edited plants averaging approximately 24% shorter than the wild type. While the total tiller number did not differ markedly between the two groups, the edited lines produced a slightly higher number of effective tillers, suggesting an improvement in tiller productivity. The panicles of the edited lines were shorter in length but more densely packed compared to those of the wild type, while the overall seed yield per plant remained unchanged (Fig. 4.2A-C, I). In the edited lines, the spikelets on the primary branches arise from the base of the branch, making them more compact compared to the wild-type plants (Fig. 4.2E-F). Furthermore, the seeds of the edited plants were slightly larger than those of the wild type (Fig. 4.2G-J, K). The seeds for edited lines also exhibited higher accumulation of nitrogen, depicting enhanced protein content (Fig. 4.2L).

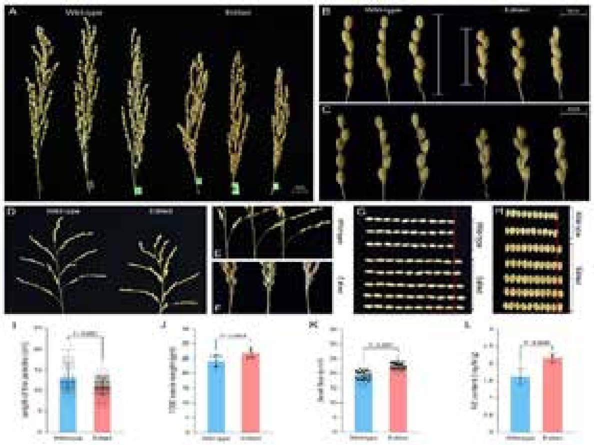


Fig 4.2 Phenotypic and agronomic characterization of wild-type and edited rice plants

Identification of high-vigour rice genotypes through comparative growth rate and assimilation studies (MK Lal and MJ Baig)

Evaluation of growth parameters across diverse rice genotypes revealed marked variability in crop growth rate (CGR), relative growth rate (RGR), and net assimilation rate (NAR), reflecting differences in vegetative vigor and physiological efficiency. CGR ranged from 0.33 g m^{-2} d^{-1} (SL-V13) to 5.53 g m^{-2} d^{-1} (NP-56), with genotypes such as B-67, B-77, NP-56, and DTL-45 exhibiting strong biomass accumulation. Moderate CGR in B-162, B-183, and BCM-177 indicated suitability for moderate-input systems, while consistently high CGR in DTL-31 and B-77 suggests potential for high-yield breeding. RGR varied from 0.01 to 0.05 g g^{-1} d^{-1}, with DTL-233, B-67, NP-56, and NI-DBT-44 showing superior growth efficiency, whereas IR-20, P-DTL-285, and B-112 exhibited poor performance. NAR ranged widely (6.84–115.37), with B-67, NP-56, NP-21, and NI-DBT-44 demonstrating high photosynthetic efficiency (Fig. 4.3). Overall, NP-56, B-67, and NI-DBT-44 consistently outperformed other genotypes and emerged as promising candidates for high-yield and stress-tolerant breeding programs.

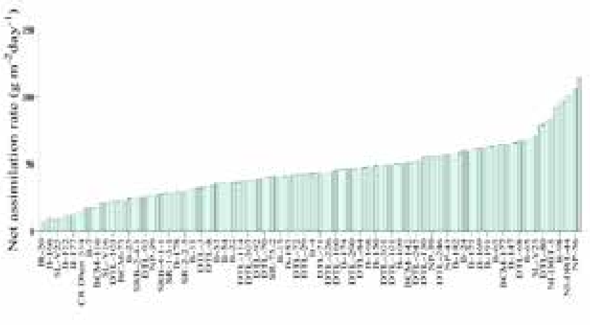


Fig. 4.3. Net assimilation rate of 135 genotypes

Physiological and morphological variation among rice genotypes based on leaf traits and yield components (MK Lal and MJ Baig)

Evaluation of physiological and yield-related traits among diverse rice genotypes revealed pronounced variability in leaf development, biomass partitioning, and canopy architecture. Leaf Area Ratio (LAR) varied widely at 30 and 60 days, indicating contrasting early growth strategies, with genotypes such as B-7, DTL-243, and SL-V6 exhibiting rapid leaf expansion, while B-55 and NP-45 showed more conservative growth. Leaf Weight Ratio (LWR) also differed among genotypes, reflecting variation in biomass allocation to leaves, with IR-20, NI-DBT-55, and B-112 maintaining higher LWR at later stages (Fig. 4.4). Differences in Specific Leaf Weight (SLW) and Specific Leaf Area (SLA) further highlighted structural variation in leaves, distinguishing dense, potentially stress-tolerant leaves from thinner leaves favoring rapid canopy development. Leaf Area Index (LAI) increased substantially from 30 to 60 days, with B-25, DTL-152, and SR-1-3-1 showing rapid canopy expansion, whereas NI-DBT-5 and SL-V25 maintained lower LAI. Significant genotypic variation was also observed in tiller and panicle production. Overall, these results demonstrate broad physiological diversity among genotypes, providing a strong basis for selection under diverse management and stress environments.

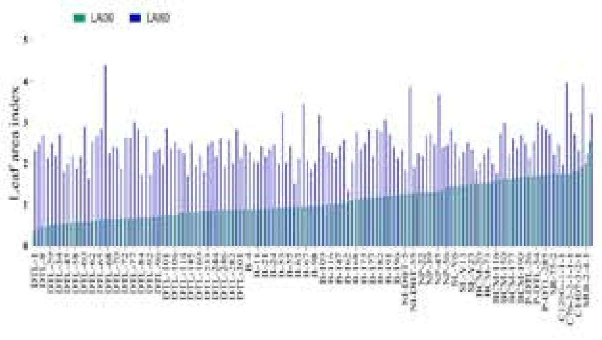


Fig. 4.4. Leaf area index of 135 genotypes at 30 days and 60 days after planting

Evaluation of rice genotypes for new sources of multiple abiotic stress tolerance and understanding the underlying mechanism

Evaluating lowland rice genotypes for prolonged submergence and stagnant flooding stresses (K Chakraborty, K Chattopadhyay and MK Lal)

Rice cultivation in lowland and deepwater ecologies is highly constrained by submergence and stagnant flooding stress. In this study, 60 rice genotypes of lowland ecology (varieties, land races, germplasm

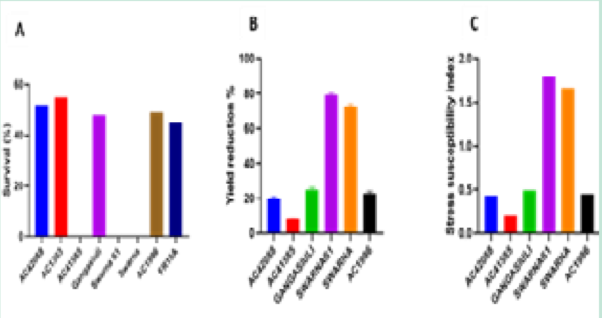


Fig. 4.5. Survival percentage of rice genotypes under prolonged submergence stress (A), yield reduction percentage (B), and stress susceptibility index (C) under stagnant flooding stress

accessions) were evaluated for prolonged submergence stress at the early seedling stage for 21 days (90 ± 5 cm) and tillering to maturity stage stagnant flooding stress (45 ± 5 cm). Upon genetic profiling of this panel, it was identified that seven genotypes carry the functional allele of only *SUB1* QTL, two genotypes carry the functional alleles of only *SNORKELs* (SK1 and SK2), whereas 16 genotypes carried the functional alleles of both *SUB1* and *SNORKEL* (either or both SK1 and SK2). It was noted that, under prolonged submergence stress, the genotypes AC 1303 and AC 42088 performed better with a high survival percentage of 52-55%, surpassing the survival ability of FR13A (45%). Interestingly, all the genotypes that showed prolonged submergence stress tolerance carry the functional allele of both *SUB1,* along with either of the *SNORKEL* (SK1 or SK2 or both) QTL. When these genotypes were subjected to stagnant flooding stress, AC 41585, which carried only the functional allele of SNORKEL (both SK1 and SK2), performed better with lower yield reduction and stress susceptibility index compared to the genotype AC42088 having the functional allele of both *SUB1* and *SNORKEL* QTL in the genetic background.

Response of rice genotypes towards combined stresses of saline water flooding (K Chakraborty, MK Lal and K Chattopadhyay)

In coastal areas, rice plant growth and yield are severely hampered by salinity and flooding stresses. With an aim to distinguish the combined effect of salinity and stagnant flooding from their individual effects, 12 rice genotypes were subjected to salinity, flooding, and saline water flooding stress. As evident from the grain yield, salt tolerance indices, chlorophyll, and malondialdehyde content under stress, it was found that saline water flooding was more harmful to the rice plant than either of the individual stresses. Gangasiuli, Rahaspanjar, AC 39416A, and FR13A were found to be tolerant under individual as well as combined stress conditions (Table 4.1). Whereas, salt-tolerant genotypes like FL478, SR26B, and AC 39293 were susceptible to flooding stress, and highly susceptible to saline water flooding conditions. Ravana was found to be tolerant to flooding but susceptible to salinity stress, and moderately tolerant to combined stress. It was identified that K^+-retention in leaf, leaf sheath, and stem has a dominant role in individual and combined stresses of saline water flooding tolerance than the upward Na^+ transport. Selective uptake of K^+ from the root to different parts over Na^+ is a major factor that contributes to saline and

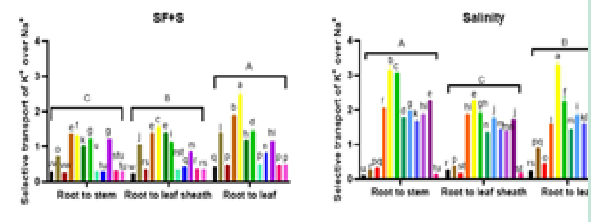


Fig. 4.6. Selective transport of potassium over sodium from root to different plant parts in different rice genotypes under combined stresses of salinity and stagnant flooding

Table 4.1 Characterization of different rice genotypes under combined stresses of salinity and stagnant flooding

Genotypes	Stagnant flooding	Salinity	Saline water flooding
Pantara	Moderately Tolerant	Highly Susceptible	Highly Susceptible
Ravana	Moderately Tolerant	Susceptible	Moderately Tolerant
Varshadhan	Moderately Tolerant	Susceptible	Highly Susceptible
FR13A	Moderately Tolerant	Moderately Tolerant	Moderately Tolerant
Gangasiuli	Tolerant	Tolerant	Tolerant
AC39460	Moderately Tolerant	Moderately Tolerant	Moderately Tolerant
Rahaspanjar	Moderately Tolerant	Moderately Tolerant	Moderately Tolerant
AC 39293	Susceptible	Moderately Tolerant	Susceptible
SR26B	Susceptible	Moderately Tolerant	Highly Susceptible
AC 39416A	Moderately Tolerant	Moderately Tolerant	Moderately Tolerant
FL478	Highly Susceptible	Moderately Tolerant	Highly Susceptible
IR29	Highly Susceptible	Highly Susceptible	Highly Susceptible

combined stress tolerance (Fig. 4.6). It was identified that tolerance to flooding stress, rather than salinity, was more important in tolerating the combined stresses of saline water flooding in rice.

Exploring the possible role of aerenchymatous gas spaces in salt tolerance in rice (K Chakraborty and K Chattopadhyay)

In plants, roots are extremely important for nutrient and water acquisition and act as the primary interface of stress sensing. As a sink, roots may utilize the majority of the photo assimilate produced by the plant. Therefore, in the era of climate change, understanding the root system architecture may provide an alternative to optimize the performance of the plant under salinity stress. To understand, an experiment was initially conducted with eight rice genotypes, and the root aerenchymatous gas space, Na^+ and K^+ concentrations of roots and leaves were measured (Fig. 4.7). Furthermore, an experiment was performed with four selected rice genotypes (FL478, AC 39416A, Rahaspanjar and Naveen) based on morphological, physiological, biochemical, and molecular traits. Based on the results, it was identified that, in salinity stress, the aerenchyma formation in roots provides some additional spaces for Na^+ storage in salt-tolerant rice genotypes such as FL478, Rahaspanjar, and AC 39416A, as compared to salt-susceptible Naveen. A strong and significant correlation of root porosity and root aerenchymatous gas spaces was observed with leaf Na^+ ion concentration and leaf and root K^+ ion retention. Molecular studies identified that NADPH oxidases such as *OsNOX5* and *OsNOX9* can function as key players for aerenchyma development in roots under salt stress.

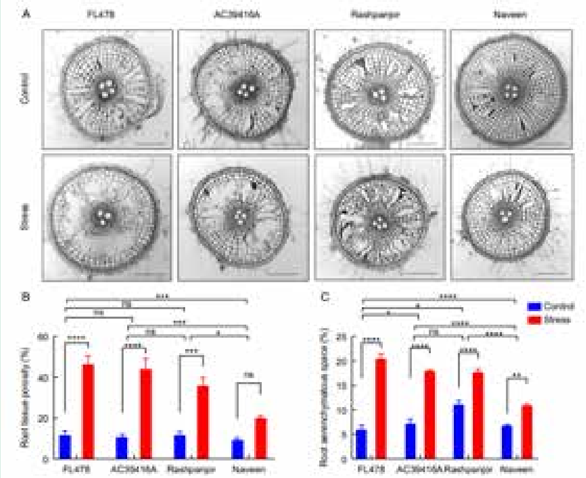


Fig. 4.7. Freehand section images of roots for four different rice genotypes in control and stress conditions (A). Changes in root porosity (B) and root aerenchymatous gas space (C) for four different rice genotypes in control and stress conditions

New rice genotypes identified for pre-harvest sprouting resistance (MK Lal and K Chakraborty)

Pre-harvest sprouting (PHS) is a physiological disorder observed in rice and other cereal crops, characterized by seed germination while still on the panicle before harvest. PHS significantly compromises grain quality, reduces yield, and results in substantial economic losses for producers. To address this critical issue, a study was conducted in both *Kharif and Rabi* seasons of 2024–25. The investigation was done on a set of 50 rice genotypes, encompassing both PHS-susceptible and -resistant lines, which were earlier identified as drought-tolerant.

The genotypes were assessed under controlled laboratory conditions at three distinct time points *viz.,* 21, 28, and 35 days after anthesis (DAA). Based on observed phenotypic variation in seed germination, the genotypes were categorized as tolerant. Highly Tolerant: Five genotypes namely, *DTL-49* (IC-410060), *DTL-50* (IC644772)*, DTL-150* (IC-516278)*, DTL-175* (EC-306378)*, DTL-265* (IC356059) exhibited 0% germination across all stages and were classified as highly PHS-tolerant (Fig. 4.8). Temporal patterns of germination revealed that highly susceptible genotypes initiated sprouting as early as 21 DAA, while moderately resistant and susceptible lines germinated progressively later. Notably, the highly tolerant genotypes remained completely dormant throughout the experimental period, indicating strong inherent resistance to PHS. These findings highlight the potential of the identified highly tolerant genotypes as valuable genetic resources for breeding programs aimed at developing climate-resilient rice varieties with enhanced resistance to pre-harvest sprouting.

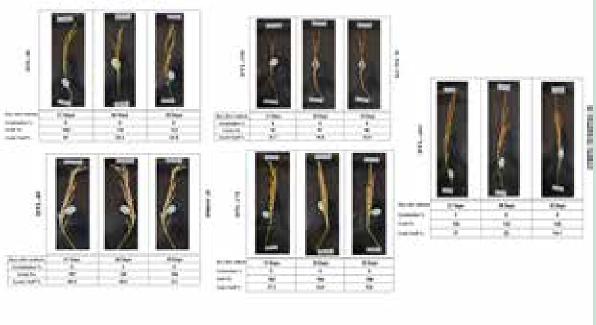


Fig. 4.8. Rice genotypes exhibiting preharvest sprouting resistance at 21, 28, and 35 days after flowering

Effect of Melatonin on root architecture under drought stress in the seedling stage (MK Lal and K Chakraborty)

Drought stress significantly reduced root length in Pooja, Swarna, and N22 by 34%, 32%, and 47%,

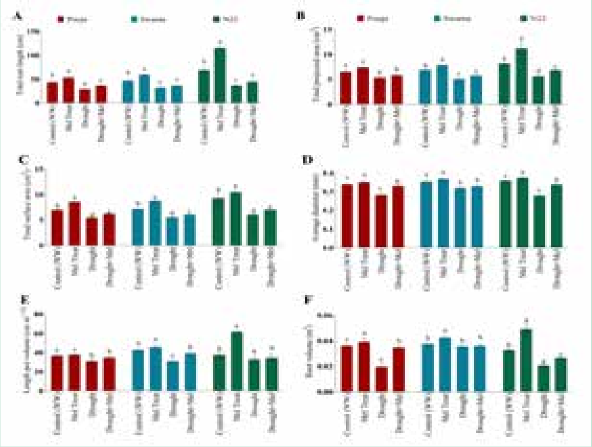


Fig. 4.9. Effect of application of drought and 100 µM melatonin treatment on three rice cultivars (Pooja, Swarna, and N22) on root architecture traits (A) total root length, (B) total projected area, (C) total surface area, (D) average diameter, (E) length per volume, (F) root volume

respectively. However, the application of 100 µM melatonin under drought improved root length by 26%, 12%, and 22%, indicating that melatonin alleviates drought-induced inhibition of root growth. The application of melatonin under well-watered conditions showed a significant increase in the total projected area (TPA) and total surface area (TSA) (Fig. 4.9). It was revealed that Pooja and Swarna showed around 21-26 % increase in the TPA and TSA. However, the drought-tolerant cultivar N22 showed 67 % increase in TPA and 12 % increase in TSA. On the contrary, the drought treatment in all three cultivars reduced TPA and TSA. In Swarna, the recovery of TPA and TSA was only 13 and 22 %, respectively.

Characterization of rice genotypes for improved physicochemical and nutritional properties

Molecular characterization of amylose biosynthesis and debranching enzyme genes in rice with variable amylose content (A Kumar)

Rice varieties with high resistant starch (RS) and low glycaemic index (GI) exhibit slower starch digestion and reduced postprandial glucose responses. In addition to amylose content (AC), the length and structure of amylopectin linear chains substantially influence starch digestibility. The starch debranching enzyme pullulanase (PUL) plays a key role in trimming long α-glucan chains, thereby shaping amylopectin fine structure. To elucidate the contributions of amylose and amylopectin linear chains to starch digestibility, GI, RS, and AC were estimated in 110 milled rice genotypes, revealing significant variation in GI (54.76–67.00), RS (0.40–2.19%), and AC (4.82–25.52%). Three contrasting genotypes (IG 72, IG 23, and IG 40) were selected for molecular analysis of *GBSSI* and *PUL*. A low-GI genotype, IG 23, harboured a single nucleotide substitution in the endosperm-specific promoter motif of *PUL*, which was associated with elevated *PUL* expression during grain filling (Fig. 4.10). This likely enhanced amylopectin branch trimming, promoting the accumulation of longer linear glucan chains, increased starch crystallinity, higher RS, and reduced GI. In contrast, reduced digestibility in the high-amylose genotype IG 40 was primarily associated with elevated *GBSSI* expression and amylose–lipid complex formation. Overall, these findings highlight IG 23 as a promising genetic resource for breeding rice with high RS and low GI through modulation of amylopectin structure rather than increased amylose content.

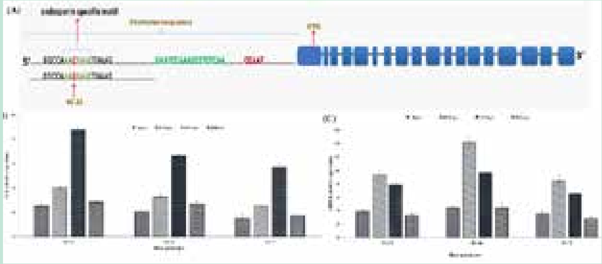


Fig. 4.10. (A) A SNP substitution indicated in the endosperm-specific motif (AAC/GA) in the promoter of the *PUL* gene of the IG23 rice genotype. (B) and (C) Expression pattern of *PUL* and *GBSSI* at different stages (7, 10, 14, and 28 DAF) of grain development in three rice genotypes

Effect of processing on protein fractions as well as the amino acid content in rice grains (TB Bagchi)

The impact of different methods of rice grain processing, like milling, cooking, and parboiling, on protein fractions like albumin, globulin, glutelin, and prolamin content and amino acid content in two contrasting rice cultivars (Naveen and CR Dhan 310) were investigated. Results showed that among different rice protein fractions, glutelin (61.2 to 83.1 % of total

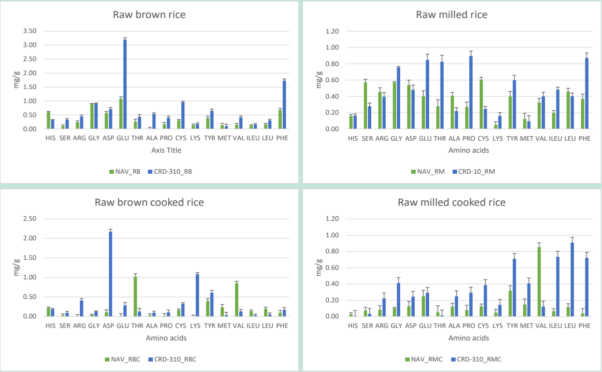


Fig. 4.11. Amino acid fraction (mg/g) of two rice varieties (CR Dhan 310 and Naveen) under different processing conditions

protein), followed by prolamin (1.9 to 18.9% of total protein), were the most abundant fractions. Albumin and globulin contents varied between 7.1 to 21.5% and 4.3 to 10.0%, respectively, in CR Dhan 310 (Fig. 4.11). The high protein rice variety CR Dhan 310 contained the highest protein (10.36%) and amino acids content (Glu, Arg, Asp) in brown rice, but after parboiling, the dominant amino acids were Asp, Lys and Val. Interestingly, it was observed that prolamin (less digestible protein fraction) content increased significantly under different hydrothermal processing. In general, prolamin content varied between 1 to 5% (on a total protein basis) in raw rice.

NIR calibration for prediction of protein and essential amino acids in rice grain (TB Bagchi)

Owing to the polygenic inheritance of grain protein and essential amino acids, high-throughput and cost-effective approaches are required to identify superior segregants and simultaneously improve protein quality and quantity in rice. Using chemical analysis data from 150 genetically diverse rice genotypes, near-infrared spectroscopy (NIRS)–based prediction models were developed for the rapid estimation of grain protein content (GPC) and essential amino acid (EAA) content. Modified partial least squares (mPLS) models with various mathematical pretreatments were evaluated, and optimal equations were selected based on minimal cross-validation error, maximal 1-VR, high coefficients of determination (R^2), and low calibration error. The optimal pretreatments for GPC and EAA were 1,6,6,1 and 2,8,8,1, respectively. Model validation using paired *t*-tests showed strong agreement between predicted and reference values (R^2 = 0.909–0.967) (Fig. 4.12). These models were subsequently applied to a mapping population to facilitate the identification of genomic regions associated with qualitative and quantitative improvement of grain protein.

Nutritional characterization of traditional rice landraces of the Jeypore tract, Odisha (N Basak, G Kumar, P Sanghamitra and S Sarkar)

The Jeypore tract of Odisha harbours diverse, underutilized traditional rice landraces with notable nutritional and nutraceutical potential. However, systematic documentation of their physical, phytochemical, and antioxidant properties remains limited. In this study, twenty pigmented and non-pigmented rice genotypes were evaluated for twenty-five attributes encompassing physical characteristics, phytochemical composition, and antioxidant activity, to assess inter-trait relationships and identify promising cultivars. Proximate components such as protein and total soluble sugars exhibited positive correlations with phytochemical content and antioxidant activity, whereas bulk density and amylose content showed negative associations with these parameters. Based on overall performance, two landraces- *Bodikaberi* and *Mahipaljeera* were identified as particularly promising candidates for nutritional enhancement and future utilization.

Efficient anthocyanin extraction from pigmented rice and its application in enhancing the nutritional quality of commonly consumed non-pigmented cooked rice (N Basak and G Kumar)

White rice is widely preferred due to its soft texture and mild taste; however, the milling process removes the aleurone layer, resulting in significant nutrient loss.

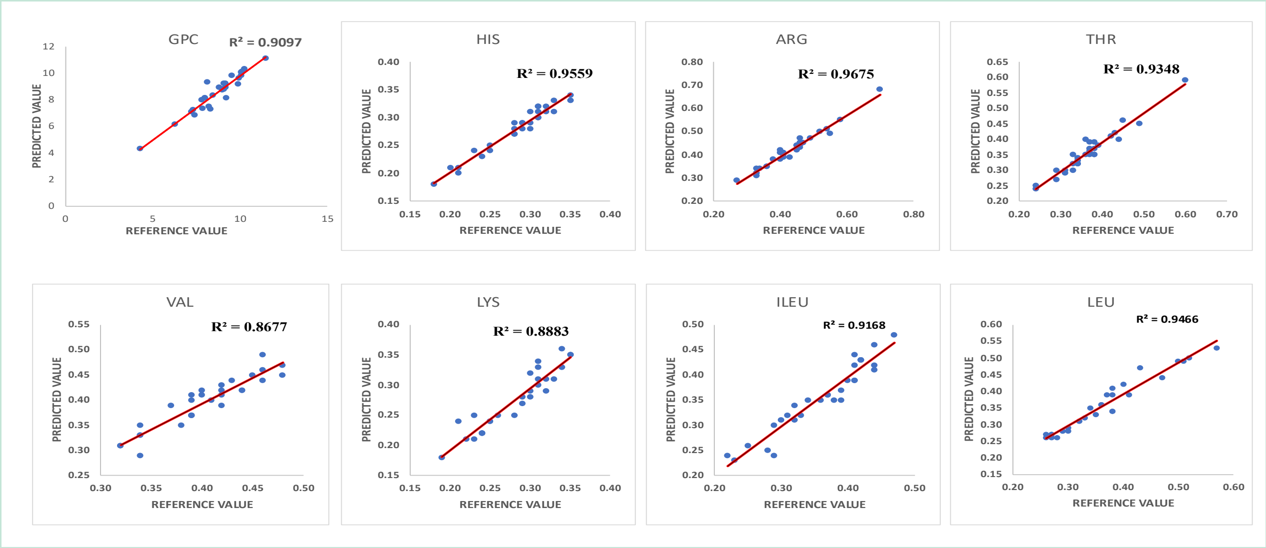


Fig. 4.12. Regression plot for grain protein content and all seven amino acids

In contrast, pigmented rice varieties possess high levels of health-promoting phytochemicals, yet their harder texture and stronger flavour often reduce consumer acceptance. In this study, *Mamihunger* was selected for anthocyanin extraction, while *Naveen*, a commonly consumed non-pigmented variety, served as the cooked base for anthocyanin enrichment trials. Extraction conditions were optimized, revealing that 90% ethanol combined with 1 mL of 0.5 N HCl achieved the highest anthocyanin recovery (108.16 mg/100 g). Incorporation of the extracted anthocyanin pigment during cooking substantially enhanced the total phenolic and flavonoid contents of white rice, along with improved DPPH radical-scavenging and FRAP activities, without compromising sensory acceptability. Moreover, the anthocyanin-fortified rice demonstrated a significantly lower glycemic index compared to untreated white rice (Fig. 4.13).

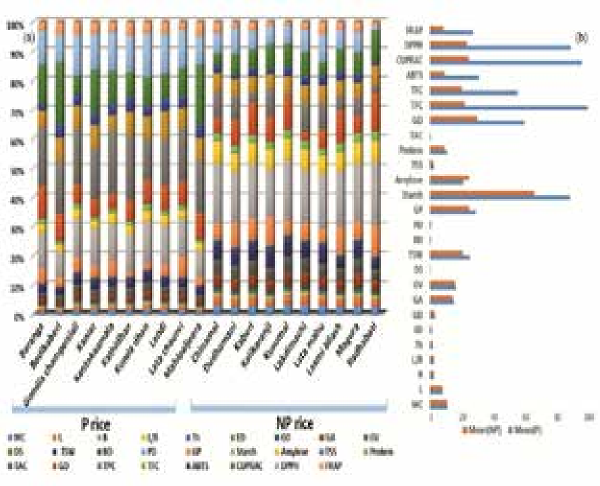


Fig. 4.13. (a) Physical properties, proximate composition, phytochemical, and antioxidant properties of pigmented and non-pigmented rice (b) comparison of means of pigmented and non-pigmented rice

Effect of moisture content on stabilization efficiency and oil quality of rice bran (G Kumar and N Basak)

Raw rice bran has a short shelf life, necessitating rapid stabilization to prevent rancidity. Microwave stabilization (600 W, 30 s) was applied to rice bran at two moisture levels—normal moisture (22%; M22 MW) and hot-air-dried bran (12%; M12 MW)—to evaluate the influence of moisture on stabilization efficiency. Oil content, γ-oryzanol concentration, and key physicochemical parameters affecting rice bran oil (RBO) shelf life, including acid and peroxide values, were assessed across 35 rice varieties (Fig. 4.14). Although hot-air-dried bran yielded higher oil recovery due to lower moisture content, microwave treatment did not adversely affect oil extraction. Notably, stabilization at 22% moisture resulted in superior oil stability, with higher average γ-oryzanol content (1.9%) compared with low-moisture bran (1.74%). Correspondingly, low-moisture bran exhibited higher acid (0.35 mg/g) and peroxide values (1.92 meq/kg) than normal-moisture bran (0.28 mg/g and 1.51 meq/kg). These results indicate that microwave stabilization is more effective when rice bran retains its normal moisture content.

Fig. 4.14 (A). Rice bran oil content (B) Gamma Oryzanol (C) Acid Value and (D) Peroxide value in raw and stabilized bran at 22% and 12% moisture

Conclusion

To overcome PEP substrate saturation and improve photosynthetic efficiency, a point mutation at Ala_{774} and Arg_{884} in rice PEPC was inflicted using a precise genome editing technique, which resulted in C4-like photosynthetic activity and yield enhancement in rice. Superior high-vigour rice genotypes were also identified based on leaf traits, comparative growth rate, assimilation pattern, and different yield components. In addition, several rice germplasm accessions were evaluated for multiple and combined stress tolerance abilities, *viz*., salinity and flooding, submergence and stagnant flooding, etc. It was identified that tolerance to flooding stress, rather than salinity, was more important in tolerating the combined stresses of saline water flooding in rice. The presence of both *SUB1* and *SNORKEL* QTLs in the genetic background seemed to have a positive effect on prolonged submergence tolerance in rice, whereas it might have a negative impact on tolerating stagnant flooding stress. It was identified that, under salinity stress, the aerenchyma formation in roots provides some additional spaces for Na^+ storage in salt-tolerant rice genotypes. New genotypes were identified for pre-harvest sprouting tolerance. It was shown that the external application of melatonin can influence root architecture and improve drought tolerance in rice. Several rice accessions were tested for low glycemic index (GI) and high RS content. Besides identifying superior genotypes, an elevated *PUL* expression in grain was found helpful in lowering the GI value of rice. The effect of different grain processing methods on grain amino acid composition was tested, along with calibration of the NIR-based technique for the prediction of protein and essential amino acids in rice grain. An efficient anthocyanin extraction method from pigmented rice was developed and standardized. The effect of moisture content on stabilization efficiency and oil quality of rice bran was tested, and it was found that microwave stabilization is more effective when rice bran retains its normal moisture content.

PROGRAMME
05

Socio-Economic Research to Aid Rice Stakeholders in Enhancing Farm Income

The Social Sciences Division undertakes technology dissemination and socioeconomic research by developing, testing, and refining innovative extension models, approaches, and strategies. Its primary objective is to strengthen outreach mechanisms that promote the adoption of new technologies by end users while generating feedback to improve research and development. The Division is supported by a multidisciplinary team of five scientists and 12 technical staff and implements its mandate through two in-house and 10 externally funded research projects.

During the period, a total of 7552 participants including farmers, extension officials, administrative personnel and others were imparted training through 182 programmes of different durations (2-8 days) conducted physically or through virtual mode on various aspects of rice production and protection technologies. A major achievement was the development of the "Aromatic Rice of Odisha for Export (arORIce)", a rice value-chain model to enhance the production of export-quality, non-Basmati, aromatic rice through improved seed systems. To support gender-inclusive agriculture, women-friendly farm machinery was demonstrated to tribal farm women, and drudgery reduction was assessed using a human physical drudgery index. The Division also developed a Kirkpatrick-based methodology to objectively evaluate farmer training programs. In addition, livelihood vulnerabilities were analysed across 472 districts, rice-growing districts were categorized, and a regional rice yield forecasting model was developed.

The Division also actively participated in national exhibitions, showcased CRRI technologies, disseminated agro-advisories through platforms such as CRRI Video *Barta*, managed rice-related databases, and contributed to inclusive development through SCSP, TSP, NEH, and Farmer FIRST initiatives.

Reaching stakeholders to Enhance their socio-economic CAPacities (RECAP) through rice technologies

Drudgery Assessment of Women-Friendly Farm Machineries in Rice Production (Supriya Priyadarshini and Sudipta Paul)

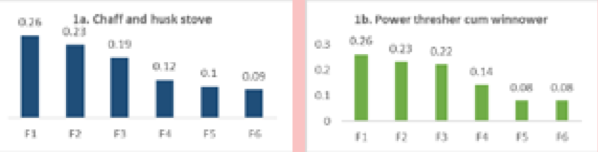
In an effort to promote gender-inclusive agricultural practices, women-friendly farm machineries (WFFMs) were demonstrated to tribal farmwomen. The extent of drudgery reduction was, thereafter, quantified using a human physical drudgery index (HPDI) (Table 5.1). Seven indicators namely, time spent (hrs/year), task performance score, difficulty score of activity, body posture adopted, frequency of postural change, postural discomfort, and load/force were used in the measurement, which highlights the significant improvements in work efficiency and comfort.

Table 5.1. Human Physical Drudgery Index (HPDI) of selected WFFTs.

WFFT	Mean HPDI	SD	CV	Max	Min
Chaff and husk stove (n = 31)	45.28	16.04	35.43	72.56	10.40
Power thresher cum winnower (n = 31)	42.75*	11.90	27.83	66.57	20.00
Mini rice mill (n = 30)	52.23	19.10	36.57	82.54	18.25
Pulveriser (n = 30)	44.65	16.62	37.22	75.14	10.00

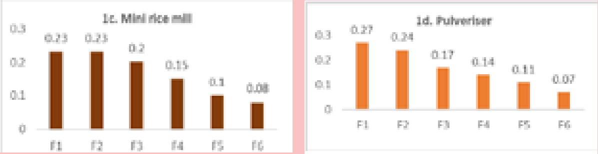
*HPDI score (42.75) of Power thresher cum winnower indicates a 25.25% reduction in HPDI score as compared to manual threshing.

Factors influencing the willingness to adopt WFFMs were identified and prioritized using the Fuzzy Analytical Hierarchy Process (Fuzzy-AHP), facilitating informed policy and design decisions (Fig. 5.1).



F1 = Waste utilization, F2= Efficient burning, F3=Improved health outcomes, F4 = Low cost, F5 = Portability and easy to use, F6 = Less use of fuelwood

F1 = Lower investment cost, F2= Energy saving, F3=User control, F4 = Space efficiency, F5 = Local market accessibility, F6 = Low maintenance



F1 = Dual functionality, F2= Compact and cost effective, F3= Ease to use, F4 = Minimal postharvest grain loss, F5 = Labour cost reduction, F6 = Affordable and low maintenance

F1 = High speed grinding mechanism, F2= Versatile, F3=Adjustable, F4 = Robust, F5 = Energy Efficient, F6 = Less dust and noise

Fig. 5.1. Mapping factors of willingness-to-adopt WFFM using the fuzzy-AHP methodology

Development of a Robust Methodology for Evaluating the Effectiveness of Farmers' Training Programmes (Sudipta Paul, Biswajit Mondal and NN Jambhulkar)

A novel methodology, based on the Kirkpatrick model, was developed to objectively evaluate training programmes for farmers across various organizations (Table 5.2). Kirkpatrick's training evaluation model provides us the foundation to design a four-dimensional composite framework based on range-based indicator normalization, principal component analysis-based indicator weight estimation, and rank correlation-based framework sensitivity testing (Table 5.3). This framework enables more structured assessment of learning outcomes and behavioural changes post-training. Further, the framework captures translation of the behavioural changes into practical livelihood measures taken by the participating farmers.

Table 5.2. Relative importance setting to the Kirkpatrick's levels and identified indicators.

Kirkpatrick's level	**Weight 1**	**Level indicator**	**Weight 2**	**W1 x W2**
Level 1: Reaction	0.19	Need fulfillment (X_1)	0.26	0.0494
		Course content (X_2)	0.24	0.0456
		Duration (X_3)	0.25	0.0475
		Timing (X_4)	0.25	0.0475
Level 2: Learning	0.23	Knowledge gain (X_5)	0.54	0.1242
		Skill development (X_6)	0.46	0.1058
Level 3: Behaviour	0.33	Change in attitude (X_7)	NA*	NA*
		Improved performance (X_8)	1.00	0.33
Level 4: Result	0.25	Product(s) and enterprise(s) diversification (X_9)	0.27	0.0675
		Business expansion (X_{10})	0.32	0.08
		New enterprise(s) (X_{11})	0.31	0.0775
		Increased income (X_{12})	0.10	0.025

Table 5.3. Reliability of the framework tested through Spearman's rank correlation.

Particular	Learning	Behaviour	Result	Effectiveness
Reaction	0.719***	-0.091	-0.006	0.392*
Learning	-	0.043	-0.113	0.467**
Behaviour	-	-	0.727***	0.844***
Result	-	-	-	0.745***

***sig. at 0.001, **sig. at 0.01, *sig. at 0.05

Analysis of ICAR-CRRI's e-Extension Platform, 'CRRI Barta' (GAK Kumar, Biswajit Mondal, NN Jambhulkar and Sudipta Paul)

The analysis covers 97 videos of which 31 videos are related to crop establishment (Estb), 58 videos are related to crop management (Mgmt), and the remaining 19 videos are related to harvest and post-harvest (HPH). The audience engagement index (AEI) of the videos was worked out using seven indicators, average number of views, average watch time per video (in hr.), average watch time per subscriber (in hr.), average number of likes, average number of comments, average number of subscribers added, and impression click-through rate. The AEI was same for the crop management (0.24) and harvest and post-harvest (0.24) stage videos (Fig. 5.2). It was comparatively lower for the crop management (0.22) stage videos. However, the difference in AEI of the videos crop stage wise was not statistically significant.

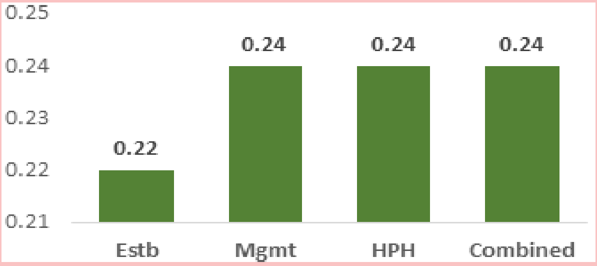


Fig. 5.2. Audience engagement index for different crop stages

The average watch time per subscriber is the highest for the harvest and postharvest stage videos (1:08 min.) whereas, the highest average watch time per video is the highest for the crop management stage videos (5.83 hr.). The highest average number of views is the highest for the crop management stage videos (307). The highest impression click-through rate is the highest for the harvest and postharvest stage videos (4.76) (Fig. 5.3).

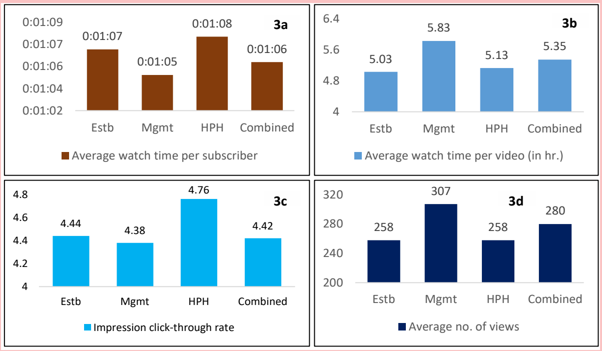


Fig. 5.3. Comparison of different crop stage videos on the basis of selected AEI parameters

Towards a Comprehensive Rice Policy: Vulnerability to Groundwater Depletion Assessment (Sudipta Paul and Biswajit Mondal)

A comprehensive assessment was undertaken to analyse livelihood vulnerabilities of farmers across 472 districts spanning 21 States and Union Territories, covering 18 of the 21 Agro-Ecological Regions (AERs) of India, with a specific focus on groundwater depletion. The study was conducted in collaboration with the ICAR–National Institute of Agricultural Economics and Policy Research (NIAP), New Delhi, and provides critical insights into regional disparities as well as the urgent need for adaptive water management strategies. The assessment adopted the IPCC vulnerability framework, where Vulnerability is defined as a function of Exposure, Sensitivity, and Adaptive Capacity. A total of 19 indicators were incorporated into the framework, comprising 8 exposure variables, 5 sensitivity variables, and 6 adaptive capacity variables. The analysis was based on cross-sectional and time-series secondary data. A weighted index-based approach using Principal Component Analysis (PCA) was employed, with data processing and spatial analysis carried out using RStudio and QGIS software. The results reveal that half of the total number of study districts have high to very high level of vulnerability to groundwater depletion (Fig. 5.4). The 10 most vulnerable districts, incidentally belong to one state i.e. Punjab. Similarly, the 10 districts with the highest exposure to groundwater depletion are also concentrated in Punjab. Among the 10 most sensitive districts, six are located in Haryana. States such as Chhattisgarh, Odisha and Bihar predominantly account for the bottom 25 districts with the lowest adaptive capacity. Furthermore, Andhra Pradesh, Haryana, Rajasthan, Punjab, Tamil Nadu and Uttar Pradesh have high proportion of districts affected by varying degrees of livelihood vulnerability to groundwater depletion (Fig. 5.5). The study has important implications for formulating a comprehensive rice policy for the entire country.

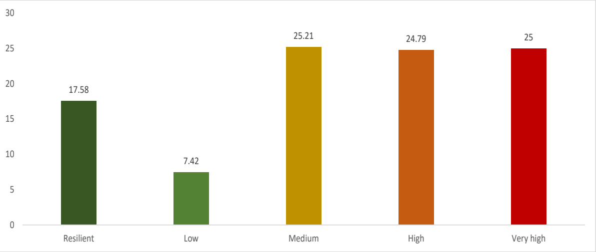


Fig. 5.4. Distribution of study districts across vulnerability categories (n=472)

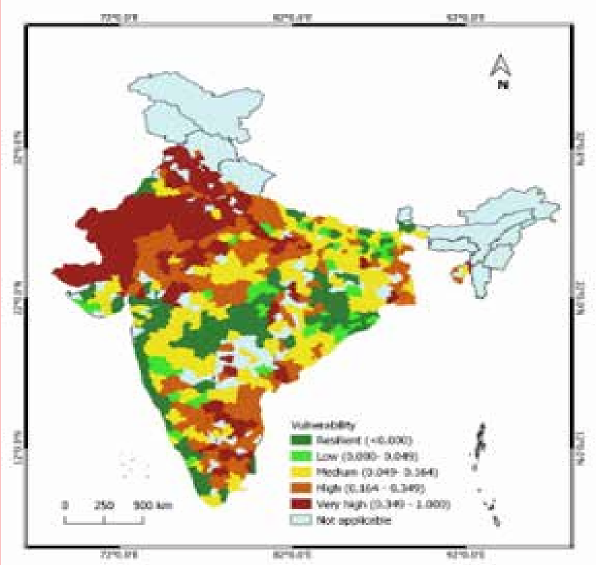


Fig. 5.5. Vulnerability to groundwater depletion map of India (n=472)

Working to Increase farm Net Gain through Socioeconomic research (WINGS)

Identification and categorization of districts in terms of rice area & productivity (Biswajit Mondal, Rahul Tripathi, NN Jambhulkar, Sudipta Paul and GAK Kumar)

An exercise was undertaken to classify rice-producing districts in the country based on their productivity levels and to compare these with the national average yield. For this purpose, the national average rice productivity was taken as 2.7 t ha^{-1}, and districts were grouped into four categories according to their yield performance relative to this benchmark.

The first group included districts with productivity levels up to 2.2 t ha^{-1}, which is 0.5 t ha^{-1} below the national average. This low-productivity category accounts for 26% of the total rice area, covering approximately 12 million hectares, and comprises 246 rice-producing districts. The second group consisted of districts with productivity ranging from 2.2 to 2.7 t ha^{-1}, representing yields from 0.5 t ha^{-1} below to equal to the national average. This group includes 132 districts and covers about 9.2 million hectares, which constitutes 19.6% of the total rice area in the country. The third group encompassed districts with productivity levels between 2.7 and 3.7 t ha^{-1}, that is, from the national average up to 1 t ha^{-1} above the national average. This category represents the largest share of rice cultivation, comprising 202 districts and accounting for nearly 39% of the total rice area, equivalent to about 18 million hectares. The fourth group included districts with high productivity levels exceeding 3.7 t ha^{-1}, or more than 1 t ha^{-1} above the national average. This group consists of 64 districts and covers approximately 7 million hectares, representing 15% of the total rice area (Fig. 5.6).

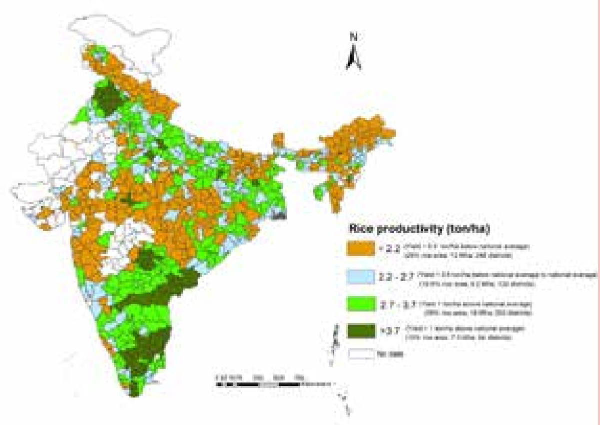


Fig.5.6. Distribution of districts in terms of rice area & yield

Overall, the classification highlights substantial variation in rice productivity across districts, with the majority of rice area concentrated in districts achieving yields at or above the national average, while a significant proportion still falls under lower productivity categories.

Development of Rice Yield Forecasting Models for Bargarh, Odisha (NN Jambhulkar, Biswajit Mondal, S Paul, AK Pradhan and GAK Kumar)

Forecasting model was developed for forecasting of rice production using weather variables of the period 1993 to 2019 in Bargarh district of Odisha. Four different models used for the forecasting were i) stepwise multiple linear regression (SMLR), ii) the least absolute shrinkage and selection operator (LASSO), iii) ridge regression and an iv) elastic net (ELNET) model. Maximum temperature, minimum temperature, rainfall and relative humidity were the four weather variables used for model development. Weighted and unweighted weather indices developed based on weather parameters were used for the model development. The equation for four different models is given in Table 5.4.

Table 5.4. Equation for different models based on weather variables for rice yield in Bargarh district.

Model	Equation
SMLR	Yield=-39640+20.55*Time+33.50*Z340+0.12*Z341
LASSO	Yield= −25474+12.95*Time−2.21*Z121−0.01*Z140 + 1.92*Z141 + 9.45*Z31 −0.07*Z40−1.13*Z240−0.05*Z340
Ridge regression	Yield= −6814*+3.51*Time +0.33*Z120−0.61*Z121 - 21.19*Z11+ 5.23*Z10 +0.02*Z130+0.04.*Z131 + 11.77*Z21+ 9.25*Z20+ 0.09*Z140+0.25*Z141 + 1.03*Z31 + 0.31*Z30+ 0.02*Z230+ 0.04*Z231 +4.06*Z41 + 0.26*Z40+ 0.01*Z240+ 0.11*Z241+ 0.0023*Z340 + 0.01*Z341
ELNET	Yield= −24558+12.65*Time -2.52*Z121+ 0.11*Z131 + 1.73*Z141+ 4.45*Z31-0.04*Z30 -8.81*Z40-0.59*Z240 -0.05*Z340+0.02*Z341

The four models were compared based on four criteria R^2, RMSE, nRMSE and MAE. The comparison of four models is shown in Table 5.5. In the calibration stage in the Bargarh district, LASSO and ELNET gave the highest R^2 value followed by ridge regression and SMLR. Similarly, in RMSE and nRMSE; LASSO and ELNET gave lower value followed by SMLR and ridge regression. The difference of value in LASSO and ELNET was very small. The similar results were found in validation stage also. Both in calibration and validation stage LASSO and ELNET performed better. Hence LASSO and ELNET are the best models for rice yield forecasting in Bargarh district.

Table 5.5. Comparison of different models for rice yield in Bargarh District.

Type	Models	R^2	RMSE	nRMSE (%)	MAE
Calibration	SMLR	0.564	265.31	0.26	211.48
	LASSO	0.746	203.15	0.11	164.81
	RIDGE	0.630	288.11	0.15	228.69
	ELNET	0.742	205.01	0.11	165.66
Validation	SMLR	0.084	540.91	0.80	494.21
	LASSO	0.628	338.20	0.37	311.20
	RIDGE	0.191	433.36	0.47	357.99
	ELNET	0.594	339.37	0.37	315.61

Farm Mechanization in Odisha: Distribution & Impact (Biswajit Mondal, GAK Kumar, NN Jambhulkar, Sudipta Paul, PC Jena and Asit Kumar Pradhan)

Eastern India has traditionally lagged in farm mechanization, but recent initiatives emphasize machinery adoption through demonstrations and subsidies. In Odisha, the Directorate of Agriculture's Agriculture Engineering Wing implements mechanization programs across all 30 districts under Sub Mission on Agricultural Mechanization (SMAM) and the Rashtriya Krishi Vikas Yojana (RKVY). To ensure seamless and automated subsidy transfers to farmers' bank accounts, Direct Benefit Transfer (DBT) initiatives have been implemented since 2016-17. A study was conducted utilizing secondary data on district-wise and machine-wise beneficiary lists provided by the Department of Agriculture, Government of Odisha and primary data gathered from 400 respondents across 101 villages, 14 blocks, and five districts in Odisha—Bargarh, Kandhamal, Koraput, Mayurbhanj and Nayagarh. Data were analyzed to examine the distribution of machines and subsidies across various districts and demographic groups and impact in terms of cost saving and yield increment.

Machinery distribution / subsidy disbursement: During the Pre-DBT period, Ganjam recorded the highest distribution of agricultural implements, followed by Bargarh and Balasore, together contributing nearly 25% of the total. In the Post-DBT period, Bargarh emerged as the leading district, with Ganjam and Balasore also receiving substantial shares. Bargarh received the highest subsidy in both the periods. Conversely, districts such as Phulbani, Gajpati, Kandhamal and Boudh consistently received lower subsidy allocations, with a significant portion directed towards power tillers.

Gender wise, during the Pre-DBT period, 87% of implements went to males and 13% to females, with 86% of the subsidy allocated to males and 14% to females. By the Post-DBT period, the distribution of implements to females increased to 21%, with 20% of the subsidy going to females, representing a nine percent rise in implement distribution and a 6% increase in subsidy for females. Caste-wise, during the Pre-DBT period, 62.4% of implements were distributed to the general category, 20.4% to ST, and 17.2% to SC farmers. In the Post-DBT period, these figures were 61%, 21%, and 18%, respectively.

Equipment purchases and subsidies saw a notable increase in the Post-DBT period, peaking in 2018-19. The most purchased machines included power tillers

(25.19%), rotavators (15.83%), and combine harvesters (15.08%). The highest subsidies were given to power tillers (28.66%), pump sets (18.57%), and rotavators (15.52%), with substantial allocations also for special power-driven equipment (7.61%), multi-crop threshers (6.36%), post-harvest machinery (5.92%), tractors (4.42%), and transplanters (4.12%).

Cost saving in machine purchase & cost reduction in cultivation: During **Pre-DBT period as well as Post-DBT period,** farmers saved significantly on purchase of machines; and farmers in Bargarh, Bhadrak, Rayagada, and Sambalpur were benefited the most. Total savings increased from Rs. 347 crores during pre-DBT period to Rs. 1,441 crores during post-DBT period, indicating the DBT mechanism's effectiveness in reducing leakages and expanding reach.

To assess the reduction in cultivation costs for various crops, we analyzed expenses for different inputs across three crop categories: paddy, vegetables, and oilseeds/pulses. This analysis was based on a survey of respondents who use their own machines for various farm operations. It was found that labour costs constitute a significant portion of the expenses, accounting for 48.5% of the costs for paddy, 39.5% for vegetables, and 37.5% for oilseed/pulse crops (Fig. 5.7). Machine labour costs were determined by calculating the time usage of different machines and their rental rates in the region. The results showed that machine use contributed to 25.5% of the costs for paddy cultivation, 9.5% for vegetables, and 13.5% for oilseed/pulse crops. This represents substantial cost savings for farmers, who would otherwise face these expenses if they did not own the machines. Other inputs made up 26% of the total costs for paddy, 51% for vegetables, and 49% for oilseed/pulse crops.

Fig. 5.7. Percentage share of human labour, machine labour & other inputs in cost of cultivation

Conclusion

The program aims to accelerate the dissemination of CRRI varieties and technologies through a combination of demonstrations, awareness campaigns, and capacity-building initiatives. Its primary objective is to influence policies that address the needs of various rice stakeholders. Beyond government involvement, the program has empowered private entities such as NGOs, CSR Units, and FPOs, fostering profitable and sustainable rice-based cropping systems.

An assessment of the economic impact of institute-developed varieties and technologies, along with the valuation of specialty and premium seed varieties, will guide future research priorities and key policy decisions in the rice sector. Drudgery assessment of women-friendly farm machineries in rice production examined gender-inclusive practices and evaluated women-friendly farm machineries (WFFMs) for improved work efficiency and comfort. The development of a robust methodology for evaluating farmers' training programmes was focused on translating behavioural changes into measurable livelihood outcomes. The categorization of districts based on suitability criteria revealed significant variation in rice productivity, with most rice area located in districts achieving yields at or above the national average, while a considerable share still remains in lower productivity categories. These findings will support strategic land allocation, promote crop diversification, and enhance the long-term sustainability of rice production.

PROGRAMME
06

Development of Climate Resilient Rice Technologies for Rainfed Upland, Rainfed Lowland and Coastal Saline Ecologies

Rice production in rainfed drought-prone areas is limited by erratic rainfall, poor soils, nutrient deficiency, weeds, and biotic stresses. To address these challenges, CRRI Regional Station, Hazaribag adopted integrated varietal, genetic, agronomic, and crop protection strategies. Climate-resilient varieties such as CR Dhan 111 and advanced DSR and aerobic lines were developed, supported by germplasm conservation and genetic studies on stress tolerance and disease resistance. Improved practices including brown manuring, integrated weed management, and nano-urea application enhanced soil fertility and input-use efficiency. Biological control using native Trichoderma and eco-friendly termite management strengthened crop protection, supporting sustainable rice production under rainfed conditions.

At RRLRRS, Gerua, significant progress was made in improving rice production in rainfed lowland ecosystems. During 2024–25 and *kharif* 2025, 821 rice germplasm lines, including Bao, scented, and Sali types, were conserved to strengthen genetic resources. Evaluation of submergence-tolerant varieties in *kharif* 2025 identified CR Dhan 801 as the best performer with the highest yield (5.71 t ha^{-1}), followed by CR Dhan 802. Seed production and distribution of biofortified, aromatic, and high-yielding varieties were strengthened during Boro 2024–25 and *kharif* 2025, supporting varietal dissemination and enhancing productivity.

The coastal rice ecosystem is highly vulnerable to biotic and abiotic stresses, requiring an integrated and data-driven management approach. At the Regional Coastal Rice Research Station, Srikakulam, research during 2025 focused on field experiments combined with weather and pest surveillance to assess varietal performance and identify key climatic drivers of pest incidence. The use of IoT-based insect monitoring, machine learning models, and on-farm IPM validation strengthened pest forecasting and evidence-based decision-making, enhancing productivity, resilience, and sustainability of coastal rice systems.

Development of resilient production technologies for rice under rainfed drought-prone agro-ecosystems

Varietal development and germplasm management (NP Mandal, S Roy and Priyamedha)

CR Dhan 111/ DRV07 (CRR708-1-B-2-B-B-1) developed at CRURRS was released for early direct sown conditions in Karnataka. It is an early maturing (98 days) variety with good grain quality (Hulling - 74.2%, Milling - 61.3% and HRR - 56.9%, SB grains, ASV-3.0, amylose content - 21.94% and medium GC of 48) and moderately resistant to Blast, BLB and BPH. CR Dhan 110 (IET 27523/CRR 514-6-1-1-1-6 for Early DSR) and CR Dhan 215 (IET 29396/CRR 820-20-1-2-2 for Aerobic) were considered for release through SVRC Jharkhand. And a set of 625 genotypes comprising of 208 boro rice accessions, 214 3K RGP accessions and germplasm collections from different states like Nagaland (73), Jharkhand (49), and Assam (81) were characterized and seed multiplied.

CR Dhan 111/ DRV07 for early direct sown conditions in Karnataka.

Genetic analysis of anaerobic germination potential (S Roy, NP Mandal, K Chakraborty and A Banerjee)

Significant genotypic variation and genotype × environment interactions were observed for germination percentage (GRP), mean germination time and rate (MGT, MGR), coleoptile length at multiple stages (LtD7, LtD14, and LtD21), anaerobic germination index (AGI), and vigour indices in 181 rice accessions. Multivariate analysis identified accessions 'Karangi', 'Natel boro', and 'Kharsu 80' with superior AG performance across environments. Genome-wide association mapping using ~458 K SNPs identified 84 QTLs across four traits (GRP, AGI, MGR, and LtD7), spanning all 12 chromosomes (Fig. 6.1). Several QTLs co-localized with known genes, including *OsTPP7*, *SnRK1A*, *OsETOL1*, *ERF53*, and *OsEE1*, and new candidate genes involved in energy metabolism, hormone signalling, and coleoptile elongation were identified. The identified QTLs, promising donors, and superior haplotypes offer new genetic resources for breeding climate-resilient, high-vigour rice cultivars suited for DSR.

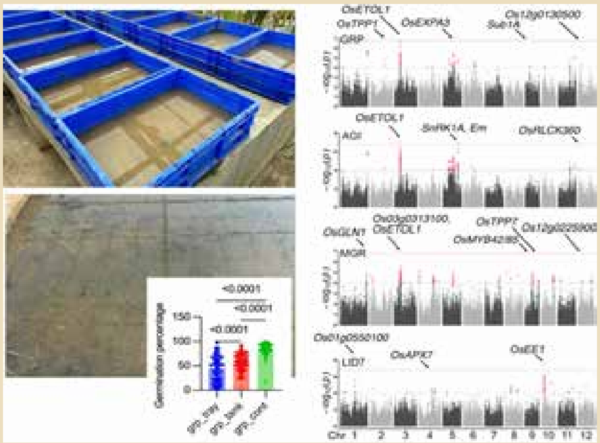


Fig. 6.1. AG experiment conducted in 181 *aus* accessions and germination percentage recorded under stress and control conditions. Manhattan plots for GWAS using the average (tray and tank) trait values under AG conditions (GRP, germination rate at day 7; AGI, AG index; MGR, mean germination rate; LtD7, seedling length at day 7)

Genetic variation for seed vigour in *aus* rice (S Roy, NP Mandal, A Banerjee and Priyamedha)

Previous GWAS on seedling vigour in *aus* genotypes highlighted the involvement of candidate genes like *OsPDR1, NCKAP1*, and *OsSAUR10*, which are involved in JA biosynthesis, ABA signalling, and BR pathways, for seedling vigour trait variation. Currently, GWAS analysis on seven seed vigour traits detected four significant QTLs on chromosome 3, 4, 11 and 12 for seed germination rate (Fig. 6.2). Notably SNPs on Chr 3 and Chr11 overlapped with genes *OsB12D*

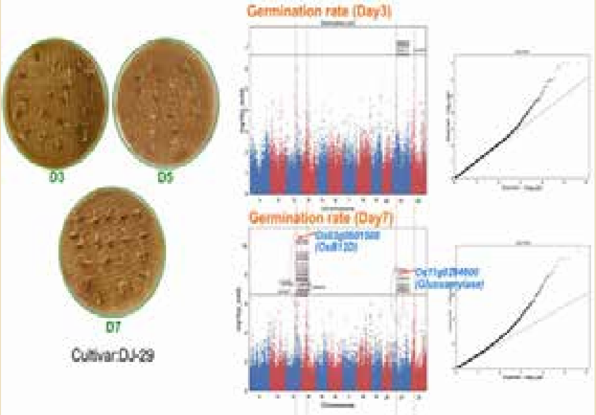


Fig. 6.2. High seed vigour recorded in *aus* cultivar DJ-29. GWAS analysis of germination rate revealed important genes like *glucoamylase* and *OsB12D*

and Glucoamylase, respectively. *B12D* is reported to influence seed germination and early seedling growth under flooded conditions, whereas, the Glucoamylase gene is responsible for breakdown of starch during germination. Germination rate was significantly associated with greater seedling vigour, grain yield and early flowering.

Screening germplasm for cold tolerance (Priyamedha, NP Mandal and S Roy)

A total of 120 cultivars from eastern and the NE Indian region were evaluated for grain yield, flowering, spikelet sterility under reproductive stage cold stress. Cold stress has resulted in significant reduction in grain yield, and grain filling was hampered in 23% of the genotypes. The correlation between yield under cold and normal conditions was low. EC 0268594, EC 0268605, AC 43256 and AC 43282 were found promising in terms of grain yield under RSCS, when compared with normal conditions.

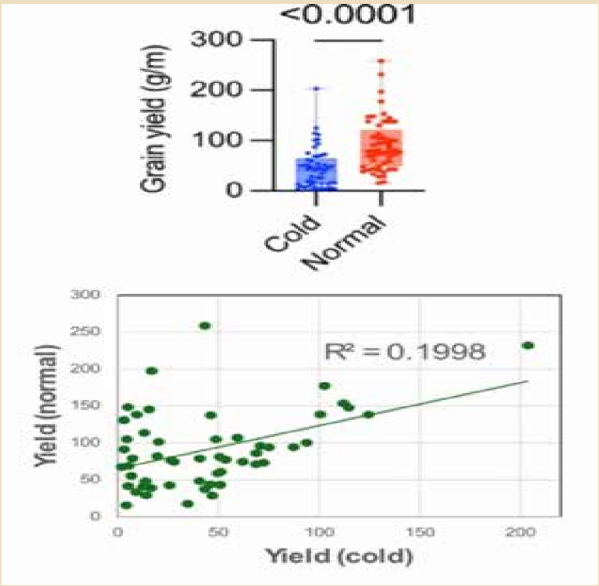


Fig. 6.3. Yield performance under cold stress

Screening hill rice germplasm for low-P tolerance (Priyamedha, NP Mandal and S Roy)

The rice germplasm accessions collected from Arunachal Pradesh were screened for low Phosphorus (P) tolerance and data were recorded for yield and attributing traits for both high P and low P conditions. The genotypes, *Nagaum1, Kolong* and *Serom* were found promising in terms of grain yield under low P conditions. Genotypic screening of the same set of accessions with *Pup1* gene linked markers, showed the presence of *PSTOL1* gene in 12 genotypes and total 29 genotypes amplified *Pup1* QTLs linked markers.

Development of NILs in Sahbhagidhan background (S Roy, A Banerjee, NP Mandal)

Two *Pi9* NILs of Sahbhagidhan (IET33259 and IET33260) tested in *kharif* 2024 under AICRIP showed superior blast resistance and overall superiority under moderate drought conditions over the recurrent parent. However, due to lower HRR values (37-45%) in these lines and also in the recurrent parent Sahbhagidhan (48% HRR), the entries were repeated in the trial for confirmation. The BC4 F2 generation of the other genes *Pi5, Pib Pi54, Pita2,* and *Pi2* were under evaluation for final selection.

IET33260/CRR840-4 – Sahbhagidhan NIL with blast resistance gene *Pi9*

Effectiveness of brown-manuring for improvement of soil fertility and moisture conservation in RBCS (BC Verma, SM Prasad and S Saha)

To assess the impact of brown manuring on soil organic carbon (SOC), available nitrogen (N), and productivity in a rice-based cropping system under drought-prone rainfed conditions, soil samples were collected from a three-year-old rice–mustard cropping system experiment at surface and sub-surface depths. Treatments included three fertilizer levels (no fertilizer, 50% RDF, and 100% RDF) with and without brown manuring. Brown manuring significantly increased SOC and available N, with manured plots recording higher SOC (0.55%) and available N (394 kg ha^{-1}) compared to non-manured plots (0.48% and 339 kg ha^{-1}). Significant interactions between brown manuring and fertilizer levels were observed across soil depths; notably, 50% RDF with manuring was comparable to 100% RDF without manuring. Brown manuring also improved sub-surface SOC and available N. Crop productivity, expressed as rice-equivalent yield, increased significantly from 2.42 to 2.70 t ha^{-1} with brown manuring. The highest yield (4.39 t ha^{-1}) was recorded under 100% RDF while 50% RDF with brown manuring remained at par with 100% RDF without brown manuring, demonstrating the potential of brown

Table 6.1. Effect of brown manuring and fertilizer management on SOC and available N content.

Fertilizers	No manuring			Manuring			Depth		
	Depth			Depth					
	Surface	**Sub surface**	**Mean**	**Surface**	**Sub surface**	**Mean**	**Surface**	**Sub surface**	**Mean**
	SOC (%) content								
T_1 (no fertilizer)	0.46	0.40	0.43	0.52	0.49	0.51	0.49	0.44	0.47
T_2 (50% RDF)	0.52	0.45	0.49	0.59	0.49	0.54	0.56	0.47	0.51
T_3 (100% RDF)	0.56	0.50	0.53	0.64	0.55	0.60	0.60	0.52	0.56
Mean	0.51	0.45	0.48	0.58	0.51	0.55	0.55	0.48	
CD (p=0.05)	F =0.03; M= 0.02, D= 0.02, D x M = 0.03, D x F = 0.04, M x F= 0.04, F x M x D =0.05								
	Available N (kg/ ha)								
T_1	299	260	279	356	314	335	327	287	307
T_2	369	314	342	425	388	406	397	351	374
T_3	438	354	396	470	410	440	454	382	418
Mean	369	309	339	417	371	394	393	340	
CD (p=0.05)	F = 14.9; M= 12.2, D= 12.2, D x M = 17.2, D x F = 21.1, M x F = 21.1, F x M x D = 29.8								

manuring to enhance soil fertility and productivity while reducing fertilizer inputs.

Development of soil fertility map of the CRURRS farm (BC Verma, SM Prasad and S Saha**)**

A total of 35 composite soil samples were collected from the Masipirhi farm and analysed for available nitrogen (N), phosphorus (P), and potassium (K). Based on the spatial distribution of these nutrients, a soil fertility map was developed (Fig. 6.4). The available N content was relatively higher in the lower reaches of the farm, covering E, F and G blocks, whereas, portions of the red soil zone near the office building (A and B blocks) exhibited low N levels. Available P was unevenly distributed across the farm, with most areas falling under the low fertility category. In contrast, available K showed a clear spatial pattern, with sufficient levels in the lower part (D, E, F and G blocks) of the farm and comparatively lower levels in the upper section with red acidic soil.

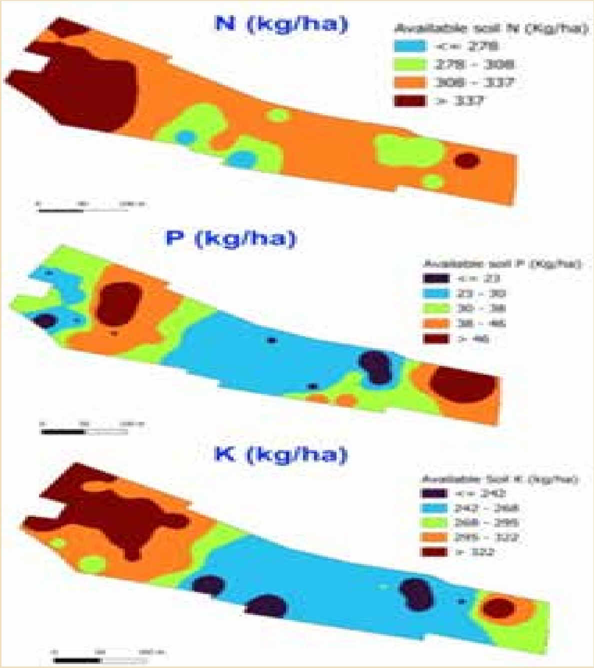


Fig. 6.4. Soil fertility map of CRURRS farm at Massipirhi

Evaluation of effectiveness and economics of IWM modules in rainfed DSR (SM Prasad, S Saha and BC Verma**)**

Seven weed management practices were evaluated in rainfed direct-seeded upland rice. The weed-free check (W6) recorded the highest grain (39.9 q ha^{-1}) and biomass yields (57.4 q ha^{-1}); however, these yields were statistically at par with W2, W3, and W5, which involved herbicide application in combination with cultural practices (Table 6.2). Weed indices were significantly highest under the weedy check (W7), resulting in the lowest grain (7.6 q ha^{-1}) and biomass yields (11.0 q ha^{-1}). Economic analysis revealed that the B:C ratio was significantly higher in W3 (1.54), indicating that integrated weed management (IWM) combining application of herbicides with cultural practices is the most effective and economically viable option for weed management in upland rice.

Nutrient Management options for sustainable rice production under direct seeded rainfed ecology (S Saha, SM Prasad and BC Verma**)**

A study on the effect of urea nano formulation (16% N w/w) in rainfed dry-direct seeded rice (cv. Sahbhagidhan) showed that T2 i.e., application of 100% RDN (NPK 60:30:30) recorded the highest grain yield, economic return, and nitrogen response (Table 6.3). However, grain yield under this treatment was statistically at par with '87.5% RDN' (T3), '87.5% RDN + one foliar spray of nano-urea' (T4), '75% RDN + one foliar spray of nano-urea' (T6), and '75% RDN + two foliar

Table 6.2. Performance and economics of IWM modules.

Treatments	Tillers/m^2	Grain yield (q ha^{-1})	Weed density (No./m^2)	Weed dry wt. at 60 DAS (g/m^2)	WCE (%)	Net return (Rs. ha^{-1})	B:C ratio
W1: Pendimethaline+Bispyribac- Na at 10-12 DAS	205.6	34.0	83.1	23.8	69.9	50042	1.47
W2: Bispyribac-Na at 10-12 DAS + one hand weeding	220.4	36.5	65.0	17.2	78.2	46010	1.03
W3: Bispyribac-Na+ Pyrazosulfuron ethyl at 10-12 DAS + One mechanical weeding (finger weeder)	226.0	38.1	60.2	17.1	78.3	57034	1.54
W4: Stale seedbed + One MW by finger weeder	179.6	23.8	107.3	37.2	52.9	27585	0.87
W5: Triafamone + Ethoxysulfuron (Council Active) + One MW	207.2	35.7	70.1	20.8	73.7	51613	1.40
W6: Weed Free check	229.1	39.9	41.4	14.1	82.2	56407	1.34
W7: Weedy Check	124.5	7.6	178.2	79.0	-	-3209	-
CD (P = 0.05)	NS	4.2	10.8	3.9	-	3676	0.10

sprays of nano-urea (T7)'. The most efficient use of N was found with 50% RDN + LCC based application of nano-urea (T8), which had the highest partial factor productivity and recovery efficiency, though yield and net returns were lower.

Evaluation of native *Trichoderma* isolates against *Magnaporthe oryzae* and *Bipolaris oryzae* (S Bhagat and A Banerjee)

Fifteen native *Trichoderma* isolates were evaluated in vitro against *M. oryzae* and *B. oryzae*, the causal agents of leaf blast and brown spot diseases of rice. All isolates significantly suppressed mycelial growth of both the pathogens, with Th-5 (*T. asperellum*) showing the highest inhibition, followed by Th-3 (*T. harzianum*), Th-77, Th-54, Th-90, Th-80, and Th-CTK, while Th-19 was the least effective. Non-volatile metabolites of *Trichoderma* caused significantly greater growth inhibition than volatile compounds. Promising isolates were further evaluated *in vivo* using susceptible varieties CO-39 (leaf blast) and Sahbhagidhan (brown spot). Th-5 recorded the highest disease reduction (68.5% for leaf blast and 67.0% for brown spot), followed by Th-3, Th-77, and Th-54, whereas Th-78 was the least effective.

Table 6.3. Effect of nano-urea (NU) application on growth, yield, NUE and profitability of rainfed DSR.

Treatment	Plant ht. (cm)	Panicle m^{-2}	Grains panicle^{-1}	Grain yield (t ha^{-1})	Total N uptake (kg ha^{-1})	Partial factor productivity (kg grain kg^{-1} N applied)	Recovery efficiency of applied N (%)	N response	Net return (Rs.)	B:C
T1: No Nitrogen (N)	86.3	163	68	1.51	23.0	-	-	-	3417	1.09
T2: RDN: 50% (30 kg N)-25% (15 kg N) – 25% (15 kg N)	106.9	237	87	3.03	52.6	50.5	49.5	2.02	37623	1.91
T3: 87.5% RDN: 30 kg N– 15 kg N – 7.5 kg N	102.4	233	81	2.86	45.8	54.5	43.5	1.90	33768	1.82
T4: 87.5% RDN: 30 kg N– 15 kg N– 7.5 kg N +NU	102.4	231	83	2.89	46.6	54.6	44.6	1.93	32351	1.76
T5: 75% RDN: 30 kg N– 15 kg N– 0 N	99.1	178	72	2.68	40.7	59.5	39.4	1.79	28785	1.70
T6: 75% RDN: 30 kg N– 15 kg N – NU	99.2	198	75	2.81	46.0	61.8	50.8	1.87	30695	1.72
T7: 75% RDN: 30 kg N– 7.5 kg N+NU – 7.5 kg+ NU	98.5	202	78	2.83	52.4	61.8	64.3	1.88	30370	1.69
T8: 50% RDN: 30 kg N– LCC based NU	95.8	163	66	2.30	46.3	**74.7**	75.8	1.53	18052	1.41
SEm±	2.5	14.4	2.5	0.09	2.0	2.0	4.1	0.06	2148	0.05
CD (p=0.05)	7.7	43.7	7.5	0.28	6.0	6.1	12.8	0.20	6517	0.16

Relative expression analysis of defence genes against *Bipolaris oryzae* infection (A Banerjee, S Roy, S Bhagat and NP Mandal)

A panel of 181 *aus* rice accessions from the 3K-RGP was screened for brown spot resistance, identifying one resistant (AUSRG127) and one moderately resistant (AUSRG91) genotype consistently over two years (Fig. 6.5). RT-qPCR analysis of six defence-related genes (*PAL, PR1b, PBZ1, JiOsPR10, LOX*, and *EIN2*) was conducted in resistant, moderately resistant, and susceptible genotypes (AUSRG127, AUSRG43 and HR12, respectively) following inoculation with *B. oryzae* (BoJH30) at 12, 24, and 48 h after inoculation (Fig. 6.5). In the resistant genotype, all genes except *EIN2* were strongly induced, with *PR1b* showing >5-fold upregulation at 12 h. The moderately resistant genotype showed significant induction of *PBZ1*, *JiOsPR10*, and *EIN2*, with *EIN2* peaking at 7.51-fold at 24 h. In contrast, susceptible genotypes exhibited negligible gene induction (<1-fold). Overall, the results indicated that early and strong activation of SA- and JA-associated defence pathways, rather than ethylene signalling alone, underpins effective resistance to *Bipolaris oryzae* in *aus* rice genotypes.

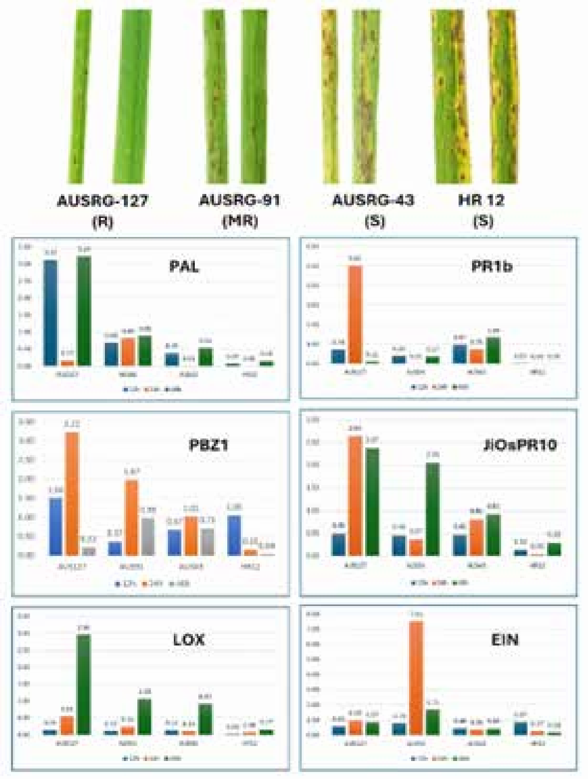


Fig. 6.5. Relative levels of expression of six defence related genes in *aus* rice accessions showing resistance (AUSRG127), moderate resistance (AUSRG91) and susceptible (AUSRG43) reaction following challenge inoculation by *B. oryzae*

Development of bait matrix for the management of termites in upland rice (Arunkumara CG, S Roy and NP Mandal)

Two termite species, *Odontotermes obesus* and *O. gurdaspurensis*, were identified from the upland rice ecosystem using dichotomous keys (Fig. 6.6). Laboratory studies demonstrated that a bait formulation comprising alpha cellulose (95–99%), dipotassium phosphate (4–9%), and carboxymethyl cellulose (1%) was highly palatable, attracting more termites and resulting in greater bait consumption. Optimized bait stations (26 cm length, 11 cm diameter, four slits, and nylon mesh at the base) installed at a distance of 1 ft from termite mounds effectively attracted termites. Following initial attraction using pine wood planks, a cellulose-based bait matrix containing the chitin synthesis inhibitor diflubenzuron (0.1%) was applied at 100 g per station, while control mounds received cellulose-only bait. Fortnightly monitoring indicated an average bait consumption of 700 g per mound, and within eight weeks, treated mounds showed no repair activity or live termites. Colony collapse was confirmed in 88.88% of treated mounds (n = 9).

Fig. 6.6. Management of termites through bait matrix

RPA-based rapid diagnosis technologies/process registered (A Banerjee and S Roy)

A recombinase polymerase amplification (RPA) assay protocol was developed to detect *U. virens* (based on the *UvG-β1* gene) directly from rice spikelet, and detection of the *BADH2* functional mutation causing aroma. The following ICAR certified techniques (Fig. 6.7) enable reliable, easy and resource efficient diagnosis of the false smut pathogen and the aroma gene in rice.

INDIAN COUNCIL OF AGRICULTURAL RESEARCH

Certified that
Dr Amrita Banerjee
(Lead Developer)
Associate Developers
Dr M.K. Bag
Dr Somnath Roy
Dr Raghu S.
Dr N.P. Mandal
of
ICAR-National Rice Research Institute
Cuttack (Odisha)
has developed the technology
RPA-based rapid diagnosis of false smut pathogen directly from rice spikelet

(Poonam Jasrotia)
Assistant Director General
(Plant Protection & Biosafety)

(D.K. Yadav)
Deputy Director General
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Certified that
Dr Amrita Banerjee
Dr Somnath Roy
(Lead Developers)
Associate Developers
Dr N.P. Mandal
Dr Priyamedha
Dr S. Sarkar
Ms. S. Bharti
of
ICAR-National Rice Research Institute
Cuttack (Odisha)
have developed the technology
Simple template based rapid detection of aroma gene in rice

New Delhi

(Poonam Jasrotia)
Assistant Director General
(Plant Protection & Biosafety)

(D.K. Yadav)
Deputy Director General
(Crop Science)

Fig. 6.7. ICAR-CS-NRRI Technology/Process Certificates

Rice production and productivity improvement in rainfed lowland ecosystem

Maintenance of germplasms (K Saikia)

A total of 64 rice germplasm lines were conserved at RRLRRS, Gerua during the *Boro* season of 2024–25. In addition, 757 rice germplasms comprising 114 Bao, 37 scented and 606 Sali were maintained during *kharif* 2025.

The performance evaluation of submergence-tolerant varieties at RRLRRS (K Saikia)

During *kharif* 2025, five submergence-tolerant rice varieties were evaluated at RRLRRS, Gerua to assess their growth performance, yield attributes and productivity. Considerable variation was observed among the entries. CR Dhan 801 recorded the highest grain yield (5.71 t ha^{-1}) with superior tiller number (12.6), higher panicle density (355 panicles/m^2) and 308 grains per panicle, maturing in 135–140 days. CR Dhan 802 was the next best performer with a yield of 5.13 t ha^{-1} and the highest panicle density (364 panicles/m^2). Ranjit Sub-1, though taller (145.4 cm) with longer panicles (31.2 cm) and higher grains per panicle (318), yielded 4.43 t ha^{-1} and had a longer duration (180–185 days). Bahadur Sub-1 yielded 4.62 t ha^{-1}, while Swarna Sub-1 recorded the lowest yield (3.57 t ha^{-1}) under the experimental conditions.

Seed production (K. Saikia)

During the Boro season 2024–25, a total of 3,258 kg of quality seed was produced and distributed, comprising 1,118 kg of biofortified varieties, 440 kg of aromatic rice and 1,700 kg of high-yielding varieties (HYVs). Produced 1600 kg of biofortified variety seed (CR Dhan 310 and 311), 1231 kg aromatic rice and 3215 kg HYV in the *kharif* 2025.

Breeder seed production (NP Mandal)

The Central Rainfed Upland Rice Research Station, Hazaribag produced breeder seeds (315q), neucleus seeds (10q) and TL seeds (50.1q) of 14 rice varieties

Development of resilient technologies for costal rice ecology.

Evaluation of the rice varieties suitable for the Coastal ecosystems (Kiran Gandhi B., MK Kar, Krishnendu Chattopadhyay, BC Marndi and BB Panda)

Field evaluation of CRRI salt-tolerant rice varieties (CR Dhan 402, CR Dhan 403, CR Dhan 406, CR Dhan 412, and CR Dhan 414) indicated that there was no significant yield advantage over the local salt-tolerant variety MTU 1061 under the coastal ecology. Among the CRRI varieties, CR Dhan 412 recorded the highest yield (4.92 t ha^{-1}), which was at par with MTU 1061 (5.15 t ha^{-1}) (Fig. 6.8). Similarly, evaluation of CRRI shallow-irrigated rice varieties (CR Dhan 304, CR Dhan 307, CR Dhan 312, CR Dhan 317, CR Dhan 409, CR Dhan 800, and CR Dhan 802) showed no significant yield

Fig.6.8: Experimental field showing the evaluation of CRRI rice varieties at RCRRS, Naira

Table 6.4. Performance of flood tolerant varieties of Assam during *kharif* 2025.

Variety	Plant height (cm)	Tiller No.	Panicle length (cm)	Panicle /m^2	Grains/ panicle	Yield (t ha^{-1})	Duration (days)
CR Dhan 801	114.0	12.6	25.3	355	308	5707	135-140
CR Dhan 802	104.4	9.4	23.7	364	294	5133	135-140
Ranjit Sub-1	145.4	9.6	31.2	233	318	4434	180-185
Bahadur Sub-1	112.4	5.4	25.5	158	241	4615	180-185
Swarna Sub-1	105.8	8.0	24.0	231	233	3572	150-155

difference compared to the local variety MTU 7029, except for CR Dhan 800. Among the CRRI varieties, CR Dhan 312 recorded the highest yield (5.21 t ha^{-1}), which was at par with MTU 7029 (5.27 t ha^{-1}).

Nitrogen Management for Enhancing the Productivity of Direct-Seeded Rice in Coastal Ecologies (KK Rao, Shyam CS and BB Panda**)**

The nitrogen management trial under modern DSR revealed that the medium-duration variety CR Dhan 328 recorded the highest grain yield (4.9 t ha^{-1}), followed by the long-duration variety CR Dhan 409 (4.59 t ha^{-1}) and the medium-duration variety CR Dhan 305 (4.35 t ha^{-1}). Among the N management treatments, the application of 120 kg N in four split doses (17:33:33:17) at seedling, tillering, panicle initiation and heading stages resulted in significantly higher grain yield (53% increase over control) and was at par with the application of 120 kg N in three splits (25:50:25).

Seasonal patterns and forecasting rice pest in Coastal ecosystem (Kiran Gandhi B., KK Rao, Shyam CS and BB Panda**)**

To assess the influence of abiotic factors on rice leaf folder (RLF) incidence in rice, Pearson correlation analysis was conducted. The results indicated that surface air temperature ($r = 0.419$; $p = 0.002$) had a significant positive association with RLF damage. In contrast, relative humidity ($r = 0.149$; $p = 0.286$) and rainfall ($r = -0.015$; $p = 0.915$) showed no significant relationship with RLF damage. Further, both the statistical model (SARIMAX) and machine learning models (MLP and LSTM) identified the previous week's RLF damage and the current week's average surface air temperature as the most influential predictors in the north coastal region of Andhra Pradesh. Among all models evaluated, the LSTM model performed the best, achieving the highest prediction accuracy (80.01%), though it required comparatively higher computational resources (Fig. 6.9).

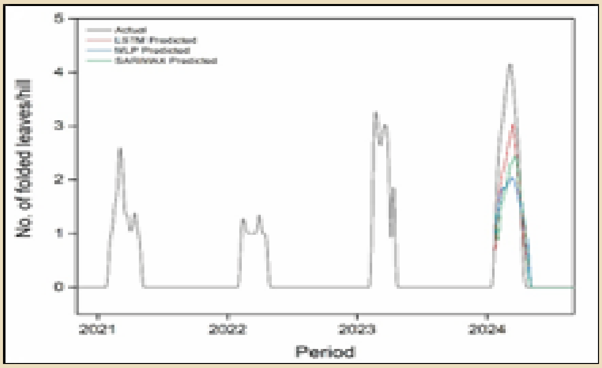


Fig. 6.9. Leaf Folder prediction capabilities of statistical and DL models

Fig. 6.10. A device for capturing nocturnal insect images

A design entitled "Device for Capturing Nocturnal Insect Images" was granted patent on 04 July 2025 (Design Registration No. 443493-001). The device, NoctiLens, captures images of nocturnal insect pests and automatically uploads them to Google Cloud Storage (Fig.3). A total of 2,895 images from the NoctiLens database were used to train a series of YOLO models—YOLOv8m, YOLOv9m, YOLOv10m, YOLOv11m, and YOLOv12m—for identifying major rice insect pests such as yellow stem borer, brown planthopper, green leafhopper, and rice gall midge (Fig. 6.10). Among all models, YOLOv10m performed the best, achieving an accuracy of 54.24%, precision of 63.11%, recall of 53.71%, and an F1-score of 0.58 on the validation dataset. Computational complexity analysis across models showed that YOLOv10m also had the lowest number of trainable parameters (16,455,016) and the shortest training duration (7.847 hours).

Validation and promotion of the IPM module in Coastal rice ecosystem (Kiran Gandhi B., KK Rao, Shyam CS and BB Panda**)**

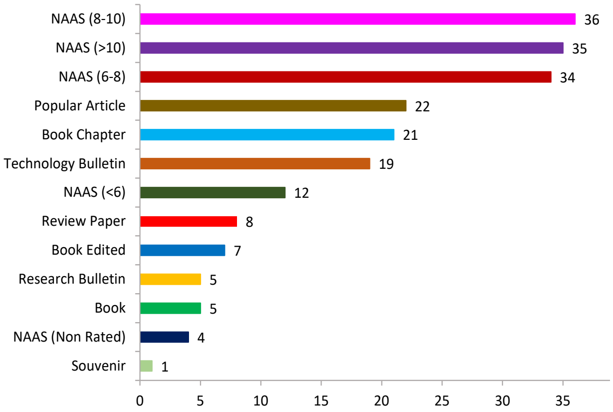
The implementation of Integrated Pest Management (IPM) practices in 10 different farmers' fields in Srikakulam district of Andhra Pradesh led to a considerable improvement in rice yield and a reduction in pest incidence compared to non-IPM practices. The average yield under IPM was 5.67 t ha^{-1}, which was higher than the 4.96 t ha^{-1} recorded in non-IPM fields. IPM plots also exhibited significantly lower pest infestations: brown spot (4.70% vs. 12.56%), sheath blight (7.46% vs. 15.03%), yellow stem borer (YSB) damage (4.30% vs. 12.78% %WEH), and rice leaf folder (RLF) incidence (0.56 vs. 2.36 number of folded leaves).

Conclusion

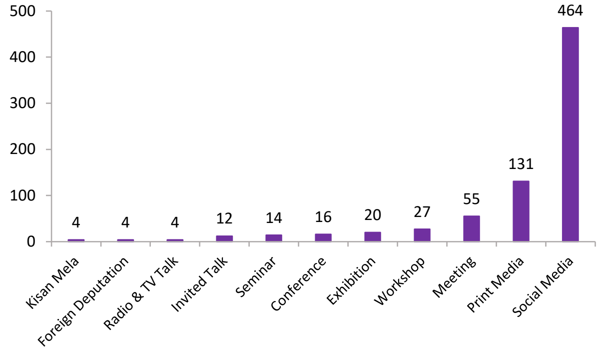
The CRRI research stations at Hazaribag, Gerua, and Naira have made significant contributions to developing climate-resilient rice production systems for rainfed, drought-prone, and coastal ecosystems. Through integrated research, the stations developed and validated stress-tolerant varieties supported by genetic studies on key adaptive traits, thereby strengthening the breeding pipeline. Agronomic innovations such as brown manuring, integrated weed management, and nano-urea-based nutrition improved soil health and input-use efficiency, while effective management of major diseases and pests enhanced system resilience. The integration of weather-based analysis, AI, IoT, and IPM-based strategies further optimized varietal selection, nutrient management, and pest surveillance, leading to improved productivity. Additionally, extensive research and extension activities, including demonstrations, training programmes, and workshops, benefited farming communities and students, collectively establishing a holistic and scalable framework for sustainable and climate-resilient rice production.

PUBLICATIONS & PARTICIPATION IN SCIENTIFIC EVENTS

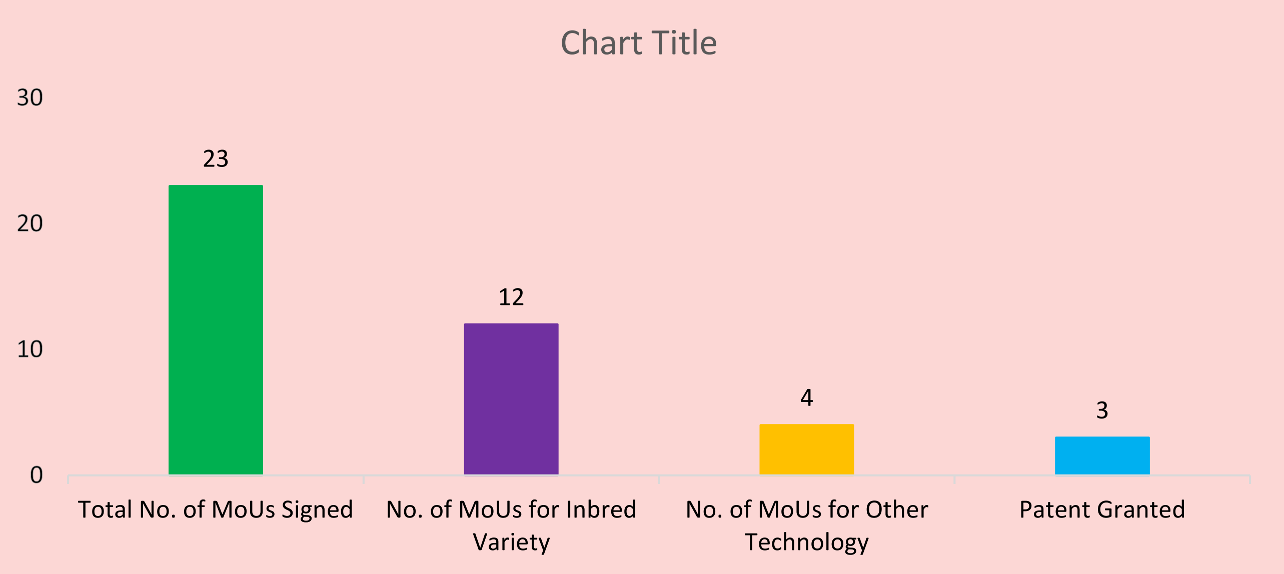
During the year 2025, the institute has published research, technology and extension materials which is shown by the below given figure.



Participation in Conference/ Workshop/ Exhibition/Kisan Mela/Radio & TV talks/ Media Coverages.



COMMERCIALIZATION OF ICAR-CRRI TECHNOLOGIES



ACTIVITIES AND EVENTS UNDERTAKEN

Activities and Events Undertaken

During the year 2025, ICAR-CRRI organized several events and conducted diverse set of routine and extracurricular activities to comply with the Council's vision and the Government of India programmes. The brief account of the events and activities are as follows-

A) **Activities:**

Activities	Distinguished participants
The 30th Research Advisory Committee (RAC) Meeting of ICAR-CRRI was held during 18-19 February 2025	Dr. T. Mohapatra, Chairperson, PPV&FRA, Govt. of India (Chairman), Dr. Shashidhar H.E., Ex-Professor, University of Agricultural Sciences, GKVK Campus, Bangalore; Dr. D.K. Sharma, Ex-Director, ICAR-CSSRI, Karnal; Dr. M.K. Naik, Vice Chancellor (Former), Keladi Shivappa Nayaka University of Agricultural & Horticultural Sciences Shivamogga and Professor (Higher Academic Grade) University of Agricultural Sciences, Raichur, Karnataka; Dr. V. Chinnusamy, Joint-Director (Research), IARI, New Delhi; Dr. N.P. Singh, Member Commission for Agricultural Costs and Prices (CACP), Govt. of India; Dr. S.K. Pradhan, ADG (FFC), ICAR, New Delhi; Dr. A.K. Nayak, Director, ICAR-CRRI, Cuttack; Shri Pawan Kumar Sahu, Farmer Representative from Jharkhand; Shri Amareswar Mishra, Farmer Representative from Odisha and Dr. R.M. Sundaram, Director, IIRR, Hyderabad as special invitee; Dr. (Mrs.) Sanghamitra Samantaray, Head, Crop Improvement Division, CRRI, Cuttack (Member Secretary)

37th Institute Management Committee (IMC) Meeting was held on 20 February 2025 in a hybrid mode	Dr. A.K. Nayak, Director, ICAR-CRRI, Cuttack (C), Dr. P.K. Roul, Vice Chancellor, OUAT, Bhubaneswar (online), Shri Balaram Subudhi, Joint Director, Special Programme, Director of Agriculture & Food Production, Govt. of Odisha, Shri A. Mishra, Bhubaneswar, Shri P.K. Sahu, Ranchi, Shri S. Ray, PS, National Bureau of Soil Survey & Land Use Planning Regional Centre, Kolkata, Dr. N. Ravishankar, PS, ICAR-IIFSR, Modipuram, Shri P.K. Nayak, FAO, ICAR-Central Institute for Women in Agriculture, Bhubaneswar and Dr. S. Samantaray, Head, Crop Improvement Division, Dr. M.J. Baig, Head, Crop Physiology & Biochemistry Division, Dr. P. Bhattacharya, Head, Crop Production Division, Dr. P.C. Rath, I/c Head, Crop Protection Division, Dr. G.A.K. Kumar, Head, Social Science Division, Dr. M.K. Kar, I/c PME Cell, Shri V Ganesh Kumar, Sr. AO, Shri R.K. Singh, Sr. F&AO, Shri D. Krishna R, and Shri D. Roy, CAO (SG), ICAR-CRRI, Cuttack (Member Secretary)
The Quinquennial Review Meeting (QRT) of ICAR-CRRI, Cuttack, was held from 8-10 April 2025 to review the institute's progress and achievements during the period from 1 April 2019 to 31 March 2024	The Chairman of QRT, Dr. A.K. Singh, Emeritus Professor, Division of Genetics, ICAR-IARI, New Delhi, along with a distinguished panel of experts, including Dr. P.V. Satyanarayana, Director of Research at Acharya NG Ranga Agricultural University, Guntur; Dr. A.R. Sharma, Director of Research at Rani Lakshmi Bai Central Agricultural University, Jhansi; Dr. V.V. Ramamurthy, Retd. Professor, Division of Entomology, IARI, New Delhi; Dr. S.G. Sharma, Former Head of Crop Physiology and Biochemistry Division at CRRI, Cuttack, and Emeritus Professor at GBPUAT, Pantnagar; Dr. R.K. Samanta, Former Vice-Chancellor of BCKV, West Bengal; and Mr. K.V. Iyer, Expert at the Agribusiness Foundation at IIT, Kharagpur (attended online); Dr. (Mrs.) Sanghamitra Samantaray, Head, Crop Improvement Division, CRRI, Cuttack (Member Secretary).
The 45th Meeting of the Institute Research Council (IRC) was held during 20–22 May 2025	Dr. M.J. Baig, (Director & Chairman), Dr. B Mondal (S, IRC & I/c PME Cell), Head of Divisions and Scientists of the Institute and KVKs; External experts Dr. K.K. Jena (Programme-1), Dr. K.K. Rout (Programme-2 & 6), Dr. Biranchi Kumar Sarma (Programme-3), Dr. R.K. Sarkar (Programme-4), and Dr. S.K. Rout (Programme-5)
The Institute Joint Staff Council (IJSC) Meeting was held on 18 September 2025	Dr. G.A.K. Kumar, Director, ICAR-CRRI, Cuttack as Chairman and other members of IJSC.
The 24th Scientific Advisory Committee meeting of KVK, Cuttack, 26 August 2025	Dr. G.A.K. Kumar, Director, ICAR-CRRI, Cuttack as Chairman and other KVK staff.

B) **Programmes and Events**

S. N.	Events	Participants
1.	ICAR-CRRI celebrated New Year Meet – 2025 on 2 January 2025	200
2.	A motivational and spiritual talk on "The Power of Mind: Its Secrets and Science" was organized at ICAR-CRRI, Cuttack, in collaboration with Prajapita Brahma Kumaris Ishwariya Viswa Vidyalaya on 21 January 2025	60
3.	Dr. Himanshu Pathak, Secretary, Department of Agricultural Research and Education (DARE) & Director General, Indian Council of Agricultural Research (ICAR), Government of India, inaugurated a newly constructed farmers' hostel, a state-of-the-art seed processing unit, and a Kisan Mela at Krishi Vigyan Kendra (KVK), Cuttack, on 8 February 2025	200
4.	The Kisan Samman Samaroh 2025 was held on February 24, 2025, at ICAR-CRRI, Cuttack, and KVK, Koderma to mark the release of the 19th installment of PM-KISAN by the Hon'ble Prime Minister	888
5.	The Drafting and Evidence Sub-Committee of the Hon'ble Parliamentary Committee on Official Language conducted an official language inspection of the office of the Chairman of the Town Official Language Implementation Committee (TOLIC) on February 27, 2025	50
6.	The ICAR-CRRI, Cuttack, organized the Eastern Zone Regional Agriculture Fair 2024-25 during February 27 to March 1, 2025 with the theme 5G Enabled Climate Smart Agriculture: Transforming Agri-Ecosystems for Sustainability and Resilience	2000
7.	ICAR-Krishi Vigyan Kendra (KVK), Koderma, in collaboration with the State Department of Agriculture and Agriculture Technology Management Agency (ATMA), organized a District Level Kisan Mela-cum-Horticultural Exhibition on 6 March 2025	800
8.	IARI-CRRI Cuttack Hub NSS Unit, KVK, Cuttack and KVK, Koderma celebrated International Women's Day Celebration on 8 March 2025 at ICAR-CRRI	150
9.	The Regional Rainfed Lowland Rice Research Station (RRLRRS), Gerua, Hajo, Assam, a regional station of ICAR-Central Rice Research Institute (CRRI), Cuttack, successfully organized a Farmers' Fair and Exhibition on 20 March 2025, at Medziphema, Nagaland under NEH Component	270
10.	KVK, Cuttack organized World Water Day events at Jamena and Haripur villages, Tangi Choudwar, on the theme *Water for All*	100
11.	A Hindi workshop on the topic "Progressive use of Hindi in e-office" was organized at CRRI, Cuttack on 28 March 2025	22
12.	The ICAR-CRRI, Cuttack, in collaboration with ICAR-ATARI, Umiam, Meghalaya, organized a workshop on "Collaboration Meeting for Strengthening Rural Agri-Business Incubation Initiatives in the Northeast Region" on 17 April 2025	25
13.	ICAR-CRRI, Cuttack observed the 7th Poshan Pakhwada 2025 from 8 to 22 April 2025	

14.	The ICAR-CRRI, Cuttack, celebrated its 80th Foundation Day and *Dhan Diwas* on April 23, 2025	300
15.	Celebrated Akshaya Tritiya at ICAR-CRRI on 30 April 2025	60
16.	ICAR-CRRI, Cuttack organized a tree plantation drive on the occasion of World Environment Day, on 5 June 2025 to promote environmental sustainability and eco-friendly practices	49
17.	"All Odisha Joint Hindi Workshop" was successfully organized at the Institute of Physics in Bhubaneswar, on June 11, 2025 as a new initiative and coordinated effort in the field of Hindi as the official language in Odisha. This event was initiated by the CRRI, Cuttack, and NARAKAS Cuttack, in collaboration with four other NARAKAS offices in Odisha	200
18.	ICAR-CRRI, Cuttack organized a brainstorming session on 18 June 2025 to finalize key indicators for establishing a Biofertilizer Model Village under the Jaiva-Poshak Project	40
19.	ICAR–CRRI, Cuttack organized a launching workshop of the project “Participatory Climate Risk Management using Abiotic Stress Resilient Varieties and Quality Seed Interventions” on 19 June 2025, funded by RKVY, Govt. of Odisha	32
20.	Dr. Devendra Kumar Yadava, Deputy Director General (Crop Sciences), ICAR, visited the Central Rainfed Upland Rice Research Station (CRURRS), Hazaribag on 21 June 2025	30
21.	ICAR-Central Rice Research Institute, Cuttack celebrated the 11th International Yoga Day (IYD) on 21 June 2025	50
22.	ICAR-CRRI Strengthens Rice Farming in Odisha with BPH resistant varieties- a successful outreach program across 17 villages in 10 districts of Odisha	343
23.	ICAR-CRRI, Cuttack successfully organized the livestreaming of the Hon’ble Prime Minister’s address and the release of the 20th instalment of the PM Kisan Samman Nidhi on 2 August 2025	95
24.	ICAR-CRRI, Cuttack celebrated 79th Independence Day on 15 August 2025	41
25.	ICAR-CRRI, Cuttack observed the 20th Parthenium Awareness Week during 16-22 August, 2025	100
26.	The Centre for Agriculture and Bioscience International (CABI), in collaboration with the ICAR– CRRI, organized a one-day Stakeholder Workshop on Gendered Analysis of Rice Crop Loss Burden Stakeholder Dialogue & Learning Exchange for Collaborative Reflection on 26 September 2025 at ICAR-CRRI, Cuttack	75
27.	ICAR-CRRI, Cuttack organized Swachhata Hi Seva-2025 with the theme “Swachhotsav” from 17 September to 2 October 2025	500
28.	ICAR–CRRI, Cuttack organized the live streaming of Hon’ble Prime Minister Shri Narendra Modi’s launch of two landmark agricultural initiatives - the *Pradhan Mantri Dhan-Dhaanya Krishi Yojana* and the *Self-Reliance in Pulses Mission* on 11 October 2025	665
29.	KVK, Cuttack celebrated Rashtriya Mahila Kisan Diwas 2025 on 15 October 2025	50
30.	KVK, Cuttack celebrated World Food Day–2025 on 16 October 2025	50
31.	Hon’ble MP, Kandhamal Mr. Sukanta Panigrahi visited ICAR-CRRI on 16 October 2025	50
32.	Hon’ble QRT members Dr. R.K. Samanta, Former Vice-Chancellor of BCKV, West Bengal; and Mr. K.V. Iyer, Expert at the Agribusiness Foundation, IIT, Kharagpur visited ICAR–CRRI, Cuttack on 22 October 2025	80
33.	Hon’ble QRT members, Dr. A.R. Sharma, Former Director of Research, RLBCAU, Jhansi; and Dr. P. V. Satyanarayan, Director of Research, ANGRAU, Andhra Pradesh along with Dr. P. Bhattacharya, Head, CPD and Dr. B. Mondal, Principal Scientist & I/c PME Cell from ICAR-CRRI visited CRURRS, Hazaribag on 22 October 2025	50
34.	Vigilance Awareness Week – 2025 was observed from 27th October to 2nd November 2025 on the theme “Vigilance: Our Shared Responsibility” (सतर्कता: हमारी साझा जिम्मेदारी).	300
35.	The National Unity Day (Rashtriya Ekta Diwas) was observed on 31st October 2025 at ICAR–CRRI, Cuttack and KVK, Cuttack	120
36.	KVK, Cuttack organized Swachhata and World One Health Day on 3 November 2025 at Ratnakar Vidyamandir, Biribati, Cuttack	50
37.	ICAR-CRRI and CABI jointly organized a Stakeholder Consultation Workshop during 4-6 November 2025 at Bhubaneswar and Cuttack	100
38.	The Hon'ble Union Minister for Agriculture and Farmers' Welfare Shri Shivraj Singh Chouhan inaugurated a high-level meeting on “Convergence Strategies for Implementation of PM Dhan-Dhanya Krishi Yojana, Mission for Atmanirbharta in Pulses and National Mission for Natural Farming” at to ICAR-CRRI, Cuttack on 10 November 2025	376
39.	ICAR–CRRI, Cuttack, celebrated National Education Day with a one-day workshop “Bridging Research and Innovation: From Knowledge to Technology and Start-up Ecosystem” on 11 November 2025	78
40.	KVK, Cuttack celebrated Janjatiya Gaurav Varsh Pakhwada–2025 from 1 to 15 November 2025 in tribal villages	200
41.	CRRI hosted the Live Streaming of 21st Installment Release of PM-KISAN Samman Nidhi Programme in the presence of Hon’ble Union Minister for Tribal Affairs Shri Jual Oram on 19 November 2025	286

42.	The ICAR-CRRI, Cuttack observed *Constitution Day (Samvidhan Divas)* on 26 November 2025	60
43.	ICAR–CRRI Cuttack, organised a national-level workshop on the eco-friendly utilisation of basic slag and fly ash for acid soil management on 2 December 2025 as a prelude to the World Soil Day 2025	85
44.	KVK, Cuttack celebrated World Soil Day–2025 on 5 December 2025	50
45.	A Mentorship Programme on Support Schemes for Agripreneurs was organized at ICAR–CRRI, Cuttack on 16 December 2025, with sponsorship from the Agribusiness Incubation Centre (ABI)	15
46.	On the eve of the birth anniversary of Shri Chaudhary Charan Singh, former Prime Minister of India, the ICAR-CRRI, Cuttack organized Kisan Samman Diwas on 23 December 2025 at CRRI, KVK, Cuttack and KVK, Koderma	300
47.	The 34th Dr. Gopinath Sahu Memorial Lecture was organized on 29 December 2025 at the ICAR–CRRI, Cuttack, by the Association of Rice Research Workers (ARRW) in association with the Dr. Gopinath Sahu Memorial Trust, Cuttack, at ICAR–CRRI, Cuttack	61
48.	ICAR-CRRI, Cuttack observed Swachhata Pakhwada-2025 from 16-31 December 2025	200

AWARDS AND RECOGNITIONS

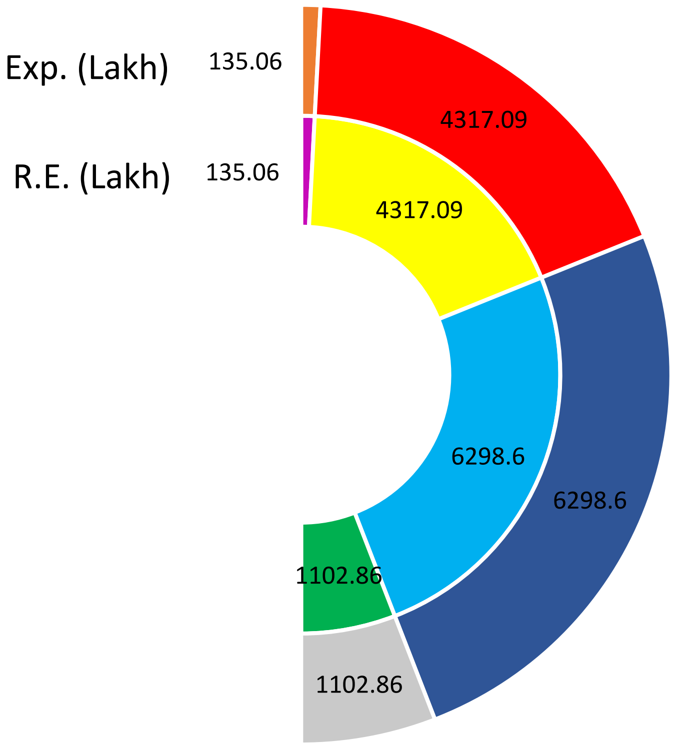
During the year 2025, ICAR-CRRI and its staff members bagged several prestigious awards and recognitions. The details of the awards are given below.

1	Dr. Sanghamitra Samantaray was honoured with the prestigious Samanta Chandra Sekhar Award for 2023 in the category of Life Sciences by the Odisha Bigyan Academy, Science & Technology Department, Government of Odisha
2	Dr. Krishnendu Chattopadhyay was elected Fellow of the National Academy of Agricultural Sciences (NAAS), New Delhi, in recognition of his impactful research in crop improvement
3	Dr. P. Panneerselvam was recognized as World top 2.0 % Scientists in the field of Agriculture by Stanford University (Year 2025)
4	Dr. Kutubuddin Ali Molla was awarded INSA Associate Fellow-2025 from Indian National Science Academy, New Delhi
5	Dr. Milan Kumar Lal was awarded the NAAS Young Scientist Award 2025 for his pioneering work in plant physiology, particularly in enhancing the nutritional quality of starchy crops and developing stress mitigation strategies
6	Dr. Koushik Chakraborty received CAR-LBS Foreign Visit and Best Editor Award for Plant Physiology Reports, Springer
7	Dr. D Chatterjee received Mosaic Company Foundation Young Scientist Award in the area of Plant Nutrition, Mosaic India Private Limited, Gurgaon, (Haryana), India and SM Sehgal Foundation
8	Dr. D Chatterjee received INSA Distinguished Lecture Fellowship 2025
9	Dr. Debarati Bhaduri was elected as Councillor, Indian Society of Soil Science (ISSS) for the biennium 2026-2027
10	Dr. Debarati Bhaduri was recognised as Editorial board member, Journal of Indian Society of Soil Science (JISSS) for the biennium 2025-2026
11	Dr. Awadhesh Kumar and Dr. Milan Kumar Lal have been recognized as World's Top 2% Scientists- 2025" by Stanford University, California, USA
12	Dr. Anilkumar C received NAPB travel grant cash award to participate in the NAPB annual meeting held during 19-23 May, 2025 at Kona Island of Hawaii, USA
13	Dr. N.P. Mandal was invited as Member, Expert Committee on Agriculture & Horticulture – DST, West Bengal
14	Dr. N.P. Mandal was invited to the Special Committee of Jharkhand State Agriculture Development Corporation Limited, Govt. of Jharkhand
15	Dr. S. Bhagat was awarded Fellow of National Academy of Biological Sciences, Chennai
16	Dr. A. Banerjee was awarded Young Women Scientist Award -2025 (Crop Protection) by Academy for Advancement of Agricultural Sciences, Kalyani, Nadia, West Bengal during National Conference on "Transformative Approaches and Smart Technology in Plant and Animal Health for Sustainable & Climate-Ready Agriculture" at PSB, Visva-Bharati, Shantiniketan, West Bengal
17	Dr. A. Banerjee was conferred with Fellow, Indian Virological Society in the field of Plant Virology at VIROCON 2025 held at ICMR-National Institute of Virology, Pune, Maharashtra
18	Dr. Priyamedha received Eminent Scientist Award by Indian Society of Agricultural Science & Technology Research (ISASTR) during International Conference on Agriculture & Veterinary: Transformative approach, Research & Innovations Forum
19	Dr. S. Roy was awarded Best Scientist Award -2025 (Crop Science) by Academy for Advancement of Agricultural Sciences, Kalyani, Nadia, West Bengal during National Conference on Transformative Approaches and Smart Technology in Plant and Animal Health for Sustainable & Climate-Ready Agriculture at PSB, Visva-Bharati, Shantiniketan, West Bengal

20	Dr. S. Roy was elected as Member of EC (Zonal Councillor-EAST), Indian Society of Plant Genetic Resources, New Delhi
21	Young Scientist Award-7
22	Best Poster/Oral Presentation Award-8

FINANCIAL STATEMENT (JANUARY-DECEMBER 2025)

Grand-in-Aid Capital

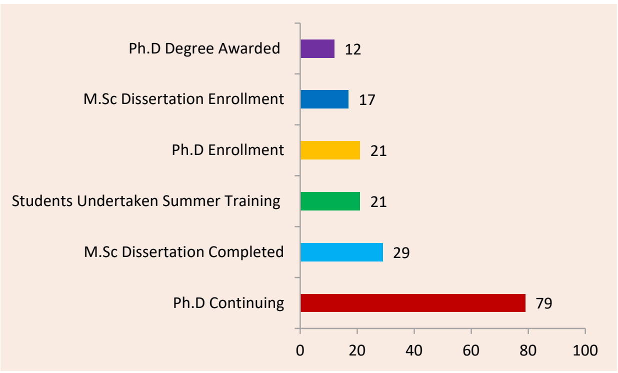


HUMAN RESOURCE DEVELOPMENT AND CAPACITY BUILDING

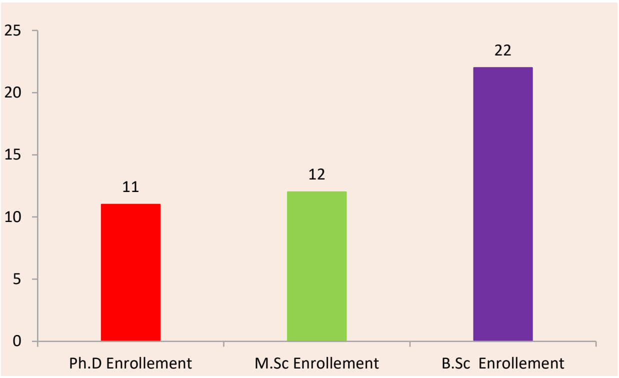
Human Resource Development (HRD) Cell of CRRI has been established to strengthen and facilitate the training and capacity building of the students/scientists/other staffs to work in the emerging areas of rice research and management.

Achievements of the HRD Programmes for the students during the year 2025.

Non - ICAR Students



ICAR Students



EXTENSION/OUTREACH ACTIVITIES

Extension/ Outreach Activities

To impart knowledge and develop skill to various groups of stakeholders, ICAR-CRRI, Cuttack had undertaken several extension activities during 2025 as detailed below:

Field demonstrations

During 2025, large-scale demonstrations in farmers' fields were conducted to promote improved rice varieties and climate-resilient cultivation practices, benefiting about 2,712 farmers across three states of the country, namely, Jharkhand, West Bengal and Odisha. These demonstrations were implemented in several districts of the respective states and covered a wide range of high-yielding and stress-tolerant varieties. Altogether, the programme brought nearly 1,386 acres under demonstration, providing farmers with hands-on exposure to improved production technologies, better crop management practices, and suitable varietal choices. The initiative not only enhanced farmers' technical knowledge and confidence in adopting new varieties but also contributed significantly to increasing productivity, resilience and sustainability of rice cultivation in the region.

Exhibitions

The institute participated in 20 exhibitions at different locations of the country and promising technologies and significant milestones were showcased to the visitors in the exhibitions.

Visitor's advisory services

A total of 4220 visitors comprising of farmers & farm-women, students and agriculture officers from the states of Jharkhand, Karnataka, Odisha, Andhra Pradesh, Tamil Nadu, Telangana, Bihar, Assam, Uttar Pradesh, Madhya Pradesh, Maharashtra and West Bengal visited experimental sites and demonstration plots, net houses, agricultural implement workshop and *Oryza* museum of the institute and regional stations during the year.

Fortnightly agro-advisory services

Overall, 24 agro-advisories on rice were issued on fortnightly basis in English as well as in Odia language during the year 2025. The advisories were sent by e-mail to the officials of Agriculture and related departments of the state as well as uploaded in Institute website for public awareness and reference. In addition, block wise weather forecast based Agro-met advisory bulletins of Cuttack district were issued 4-5 times per month. Advisories were also issued through 'NRRI Video *Barta*' every fortnight and circulated through social media for wider reach.

Training programmes for farmers and extension professionals

A total of 7552 participants including farmers, extension officials, administrative personnel and others were trained through 182 programmes of different durations (1-8 days) conducted physically or through virtual mode on various aspects of rice production and protection technologies.

Empowering Farmers, Transforming Agriculture: Viksit Krishi Sankalp Abhiyan–2025

Under the Viksit Krishi Sankalp Abhiyan–2025, the Institute carried out extensive outreach activities across nine districts of Odisha. The campaign witnessed the active involvement of 58 scientists and technical personnel of CRRI, who worked collectively to disseminate advanced agricultural technologies, interact with farmers, and promote sustainable and climate-resilient farming practices, making the programme a significant milestone in strengthening regional agricultural development.

Mera Gaon Mera Gaurav (MGMG) Programme

A group of 4-5 scientists has been constituted for a cluster of five villages who provide technical backstopping, training, advisories, etc. There are 21 such multi-disciplinary teams working at 21 clusters of villages (comprising 5 villages each) covering eight districts of Odisha.

Tribal Sub-Plan (TSP) Programme

ICAR-CRRI is carrying out the Tribal Sub Plan (TSP) activities in Aspirational Districts of Odisha (Through ICAR-CRRI Main Institute) & Jharkhand (Through ICAR-CRRI-RS Hazaribag). The institute has adopted 3 villages in Phulbani, Khajuripada block and 7 villages in Raikia Block in Kandhamal district. Similarly, 5 villages of Raigad Block and 3 villages of R Udayagiri block in Gajapati district and Maroda and Kusumi blocks of Mayurbhanj. In Jharkhand, TSP activities are being carried out in Ranchi and Khunti districts. More than 2000 tribal farmers were benefited in the program. During 2025, more than 100 tons of climate resilient, high yielding and short to medium duration paddy seeds were provided to the tribal beneficiaries. Activities like training and demonstration of cultivation of high yielding varieties (Seed distribution), Kitchen gardening, Organic farming, Vermicomposting, Honeybee production, Mushroom cultivation, Value addition of various agriculture products for higher market price, nature-based plant protection technologies, and improved poultry rearing were provided. Women self-help groups were formed to provide training and demonstration on drudgery reduction techniques like value addition, women friendly post-harvest processing of paddy and other products like, sal leaf plate making, sanitation, etc., Awareness programs on various govt. schemes, farmers field schools, frontline demonstrations have been organized. Life-saving irrigation facility to the kitchen garden and flower crops were provided through renovation of community pond, providing pump sets. Solar street lights were also provided. Keeping in mind the harmony of progress and environment, the TSP-programme especially focused on nature-based solutions in agriculture.

Scheduled Caste Sub-Plan (SCSP) Programme

During the year 2025, under SCSP programme several villages in Odisha and West Bengal were covered to strengthen the local seed chain. A total 27.18 tons of CRRI paddy seed were distributed in different villages of Cuttack, Jagatsinghpur, Khurdha and Cooch Behar districts covering a total of 1800 beneficiaries in *kharif* 2025. The varieties like Pooja, Sarala, CR Dhan 409, Dharitri, Varsadhan, Shatabdi, Gayatri, Savitri, Pradhan, CR Dhan 800, Swarna sub1, CR1009 sub1, CR Dhan 312, CR Dhan 313, CR Dhan 314, CR Dhan 316, CR Dhan 329, CR Dhan 317, CR Dhan 321, CR Dhan 507 and CR Dhan 508 were promoted in these districts. NRRI Biofertilizer of 500 L was distributed to promote organic farming in these areas. Total 11 User Groups (UGs) were created (a group of farmers) and twenty self-help groups (SHGs) were provided with solar thresher, power weeder, sewing machines, rubber roll sheller, petrol pump, pulverizer, electric paddy thresher cum winnower, etc. A total of 816 small, medium and large equipment/machinery like power weeder, solar thresher, battery sprayer, solar light trap, mini rice mill, power thresher, sickles, spades, etc. were distributed to promote farm mechanization in these areas. To support safe storage and crop protection from extreme weather situations tarpaulins were provided to 400 beneficiaries. Solar light traps and NRRI trichocard were promoted among 750 beneficiaries for chemical free crop protection from disease and pest. A total 2664 beneficiaries participated in different training, capacity building and exposure visit programs.

NEH Programme

Under the NEH component in 2025, extensive outreach and capacity-building activities were undertaken, including the distribution of 5,797 kg of paddy seeds to 700 farmers and 1,171 kg of HYV seeds to 11 KVKs across Assam and Meghalaya, as well as to Indian Agricultural Research Institute, Regional Station, Assam. Interaction, awareness, and training programmes on rice-based integrated farming systems, coconut cultivation, and rice–cum–fish farming were organized at RRLRRS, Gerua, benefiting farmers from Kamrup district, Barpeta district, and Baksa district. In addition, 530 coconut saplings, 300 spray machines, 150 raincoats, and 100 garden tool kits were distributed. A Farmer's Fair and Exhibition on livelihood improvement of tribal farmers was also organized at ICAR Research Complex for NEH Region, Nagaland Centre, Medziphema, Nagaland, with participation of 250 farmers and 20 officials, during which 350 kg of paddy and maize seeds, 11.8 kg of vegetable seeds, and 895 agricultural implements were provided, significantly strengthening technology adoption and livelihood security in the region.

Personnel (January- December 2025)

Dr. A.K. Nayak, Director (Up to April 2025)
Dr. G.A.K. Kumar, Director (Continuing)
Dr. B.C. Patra, Emeritus Scientist

CROP IMPROVEMNENT DIVISION

Scientist								
S Samantaray (retired on 31.10.2025)	MK Kar	L Behera	LK Bose	K Chattopadhyay	SK Dash	J Meher	M Chakaraborti	JL Katara
RL Verma	RP Sah	BC Marndi	P Sanghamitra	K Ali Molla	S Sarkar	Parameswaran C	Devanna	Reshmi Raj K.R.
Anil Kumar C	Shobharani M							
Technical Staff								
R Swain	PL Dehury	LK Singh	BC Behera	N Barik	KC Mallik	B Mondal	B Mishra	D Nayak
D Samal	B Behera	A Parida	D Majhi	B Hembram	M Patra	S Sarkar	R Rana	B Sethi
KC Munda	D Meena	KA Masud	M Kumar	R Kumar	MK Raj	A Alam		
Administrative Staff								
Nil								
Skilled Support Staff								
Nil								

CROP PRODUCTION DIVISION

Scientist								
P Bhattacharyya	AK Nayak	A Poonam	P Panneerselvam	R Tripathi	S Mohanty	M Shahid	D Bhaduri	U Kumar
A Kumar	S Munda	D Chatterjee	PC Jena	NT Borkar	S Chatterjee	M Debnath	R Khanam	M Sivashankari
BR Goud	S Priyadarsani	K Kumari	AK Das					
Technical Staff								
PK Sahoo	B Ghritalahre	M Sen	B Nayak	J Sai Anand	JP Behura	B Das	AK Moharana	P Moharana
SK Ojha	P Behera	KC Palaur	PK Jena	R Jamunda	S Panda	PK Parida	SC Sahoo	SP Lenka
P Samantaray	EV Ramaiah	S Baskey	G Mandi	PK Ojha	D Parida	D Baral	D Behera	G Bihari
S Mohanty	CK Ojha	S Pradhan	R Beshra	SK Sethi	S Barik	SK Tripathy	B Ray	JK Sahu
S Kumar	KK Meena	SP Sahoo	TK Behera	AK Suman	A Choudhary	A Maity	S Dawar	
Administrative Staff								
KC Behera								
Skilled Support Staff								
S Biswal	G Singh							

CROP PROTECTION DIVISION

Scientist								
SD Mohapatra	PC Rath	S Mondal	AK Mukherjee	MK Bag	S Lenka	T Adak	NKB Patil	Raghu S
Keerthana U	GP Pandi G	Basan Gowda G	Prabhu Karthikeyan SR	M Annamalai	G Prasanthi	Jeevan B	Rupak Jena	
Technical Staff								
EK Pradhan	H Pradhan	A Mohanty	AK Naik	MN Das	D Dash	JP Das	KC Barik	S Das

Md Shadab Akhtar	S Patwari	PK Mantry	RK Meena	PK Yadav	RK Meena	PM Meena	A Biswas	PK Biswakarma
Administrative Staff								
Nil								
Skilled Support Staff								
D Naik								

CROP PHYSIOLOGY & BIOCHEMISTRY DIVISION

Scientist							
MJ Baig (retired on 31.05.2025)	K Chakraborty	TB Bagchi	A Kumar	N Basak	G Kumar	MK Lal	B Singh
Technical Staff							
C Tudu	J Bhoi	J Senapaty	S Banerjee	DB Sahoo	S Haldhar	S Kumar	H Kumar
Administrative Staff							
Nil							
Skilled Support Staff							
G Sahoo							

SOCIAL SCIENCE DIVISION

Scientist								
GAK Kumar	B Mondal	NN Jambhulkar	Sudipta Paul	AK Pradhan	B Sen			
Technical Staff								
MK Nayak	SK Sethi	G Sinha	A Panda	AK Parida	SR Dalal	SK Rout	C Majhi	SK Mohapatra
A Anand	AK Panda	SK Roul	N Singh					
Administrative Staff								
Nil								
Skilled Support Staff								
Nil								

CRRI Research Station, Hazaribag:

Scientist								
NP Mandal	SM Prasad	S Bhagat	BC Verma	S Roy	A Banerjee	Priya Medha	Soumya Saha	Arun Kumar CG
Technical Staff								
S Oran	U Saw	J Kumar	J Prasad	S Akhtar	B Meena			
Administrative Staff								
DK Parida	R Paswan	S Kumar	CR Dangi	SK Pandey				
Skilled Support Staff								
Nil								

RRLRRS, Gerua, Assam:

Scientist								
K Saikia								
Technical Staff								
S Baruah	D Khan	TK Borah	B Kalita					
Administrative Staff								
J Das								
Skilled Support Staff								

M Das								

CRRI Research Station, Naira:

Scientist								
BB Panda	Kiran Gandhi B	B Gayatri	Shyam CS	KK Rao				
Technical Staff								
RP Rao	S Roy	B Bhukya						
Administrative Staff								
NP Behura								

KVK, Santhapur:

Scientist								
RK Mohanta								
Technical Staff								
S Sethy	DR Sarangi	TR Sahoo	R Kamboj	B Mounika	P Pradhan	A Bisoi	K Pradhan	S Rout
Administrative Staff								
BB Polai								

KVK, Koderma:

Scientist								
AK Rai								
Technical Staff								
C Kumari	B Singh	B Kumar	N Choudhary	D Ghosh	R Ranjan	M Kumar	S Kumar	BK Khuntia
Administrative Staff								
P Kumar								
Skilled Support Staff								
M Ram								

Administrative Section:

Administrative Staff								
V Ganesh Kumar (SAO)	D Roy	RK Singh (SFAO)	D Krishna R (AO)	SK Satapathy	Jayprakash TP	SK Behera	S Nayak	SK Sahu
RK Behera	RC Das	R Kido	SK Sahoo	M Mohanty	N Mahavoi	D Khuntia	N Jena	MB Swain
SP Sahoo	S Sahoo	SK Nayak	SK Lenka	SK Sahoo	M Das	RC Nayak	S Pradhan	A Sethi
R Sahoo	MK Sethi	PC Das	AK Pradhan	V Kumar	A Anand	S Jareda	R Gupta	R Yadav
A Pratap	R Singh	D Muduli	SK Bhoi	H Marandi	AK Sinha	RPS Sabarwal	SK Patra	SK Das
J Bhoi	B Daspattanayak							
Technical Staff								
BK Mohanty	DS Acharya	SK Sinha	AK Nayak	PK Sahoo	KC Das	B Pradhan	S Mahapatra	S Kumar
S Mishra								
Skilled Support Staff								
B Das	D Das	SR Das	G Singh	S Bhoi	R Soren	R Singh	B Naik	P Naik
B Naik	B Das							

Institute Research Programmes for 2025

Code No.	Title of the Projects	Principal Investigator(PI)	Co PIs
Programme 1: Genetic improvement of rice for enhancing yield, quality, and climate resilience			
1.1	Managing Rice genetic resources for sustainable utilization	P Sanghamitra	BC Marndi, S Samantaray, M Chakraborti, JL Katara, NN Jambhulkar, S Roy, Parameswaran C, Devanna, Anilkumar C
1.2	Maintenance Breeding and Genetic dissection of seed Quality Traits	BC Marndi	RP Sah, Anil Kumar C, Awadhesh Kumar, NKB Patil, Raghu S, Annamalai M, G Kumar, GAK Kumar
1.3	Pre-breeding for broadening the genetic base of rice by utilizing wild species of *Oryza*	MK Kar	LK Bose, M Chakraborti, S Samantaray, SK Dash, KA Molla, P Sanghamitra, JL Katara, Parameswaran C, Devanna, PC Rath, S Lenka, AK Mukherjee, GP Pandi G, S Sarkar, Priyamedha *Associates:* K Chakraborty, NP Mandal, Awadhesh Kumar, N Basak, G Kumar, BC Marndi
1.4	Developing genetic solutions for enhancing input use efficiency in rice for rainfed and irrigated ecologies	J Meher	RP Sah, Reshmi Raj KR, C Parameswaran, LK Bose, SK Dash, P Panneerselvam, Prabhu Kartikeyan SR, AK Mukherjee, S Samantaray, D Chatterjee, Devanna
1.5	Breeding for Aroma and Grain Quality in Rice	S Sarkar	K Chattopadhyay, P Sanghamitra, SK Dash, M Chakraborti, MK Kar, S Roy, J Meher, N Basak, TB Bagchi, A Banerjee, Basana Gowda G, M Sivashankari and Reshmi Raj KR *Associates:* S Samantaray, DR Pani, AK Mukherjee, L Behera, T Adak and G Kumar
1.6	Gene mapping and precision breeding for enhancing climate resilience in lowland varieties	SK Dash	RP Sah, P Sanghamitra, Resmi Raj KR, GP Pandi G, L Behera *Associates:* AK Mukherjee, MK Bag, K Chakraborty, J Meher, LK Bose, S Lenka, Annamalai M, Milan Lal
1.7	Genetic Enhancement for Multiple Stress Tolerance in Rice for Coastal Ecosystem	K Chattopadhyay	BC Marndi, K Chakraborty, LK Bose, A Poonam, KA Molla, Kiran Gandhi G *Associates:* AK Mukherjee, SD Mohapatra, Devanna
1.8	Hybrid rice for enhancing yield, quality and sustainability	RL Verma	JL Katara, Reshmi Raj KR, S Sarkar, S Samantaray, Parameswaran C, SK Dash, Devanna, Priyamedha, M Chakraborti *Associates:* AK Mukherjee, SD Mohapatra, BC Marndi, MK Kar
1.9	Development of New Generation Rice for enhancing yield potential in favourable ecology	LK Bose	SK Dash, MK Kar, J Meher, S Sarkar, L Behera, JL Katara, Parameswaran C, Devanna, Anilkumar C, RL Verma, S Roy, SD Mohapatra, A Banerjee, NN Jambhulkar, K Chakraborty *Associates:* NP Mandal, AK Mukherjee, N Basak, S Lenka, M Chakraborti, RP Sah
1.10	Utilization of genome editing, transgenics and doubled haploid technologies for rice improvement	S Samantaray	Devanna, Parameswaran C, JL Katara, KA Molla, RL Verma, Anilkumar C, Reshmi Raj KR, Awadhesh Kumar; *Associates:* S Lenka, Raghu S, Basana Gowda G
1.11	Development of Novel Genomic Resources for Rice Improvement	L Behera	Devanna, Parameswaran C, RP Sah, M Chakraborti, J Meher, Anilkumar C *Associates:* GP Pandi G, Raghu S, A Kumar, SK Dash, MK Kar
Programme 2: Enhancing the productivity, sustainability and resilience of the rice-based system			
2.1	Enhancing nutrient use efficiency in rice through advance agronomy using smart sensors, models and nano fertilizers	S Mohanty	AK Nayak, R Tripathi, D Bhaduri, D Chatterjee, U Kumar, Anjani Kumar, BC Verma, R Khanam, B Raghavendra Goud, Shyam Shiddaiah
2.2	National level zonation of rice ecologies, site specific planning and development of cropping and farming system models	A Poonam	R Tripathy, D Chatterjee, N Jambhulkar, B Raghavendra Goud, Kavita Kumari *Associates:* M. Nedunchezian (RC of CTCRI), G Acharya (CHES), SC Giri (RC of DPR), AK Nayak, Soumya Saha, SM Prasad, Basana Gowda G, U Kumar, S Paul
2.3	Vulnerability analysis and assessment of climate smart agricultural technologies for enhancing resilience in stress prone rice ecologies	D Bhaduri	AK Nayak, R Khanam, D Chatterjee, S Mohanty, S Munda, R Tripathi, P Bhattacharyya, BB Panda, B Mondal, M Debnath, B Raghvendra Gouda, S Chatterjee
2.4	Developing agronomy for new generation rice and rice-based cropping systems	B Raghavendra Goud	BB Panda, S Munda, Anjani Kumar, SK Dash, Soumya Saha and Shyam CS
2.5	Ecosystem services quantification and analysing the nexus of climate change-land use change-food security in rice production systems	R Tripathi	AK Nayak, M Debnath, Supriya Priyadarsani, S Mohanty, P Bhattacharyya, D Bhaduri, D Chatterjee, BB Panda, B Mondal
2.6	Environment friendly management of rice straw and value addition for income generation to rice-farmers	P Bhattacharyya	P Panneerselvam, S Munda, D Bhaduri, Supriya Priyadarsani, Kavita Kumari, BC Verma, AK Nayak *Associates:* T Adak, S Lenka

2.7	Harnessing microbiome for enhancing rice productivity and improving soil health	P Panneerselvam	U Kumar, GP Pandi G, Parameswaran C, Anjani Kumar, AK Nayak
2.8	Development of weed management strategies and assessing the risk of herbicide resistance in rice weeds	S Munda	B Mondal, Kavita Kumari
2.9	Development and Refinement of Farm implements, Post-harvest and Value addition Technologies for small farm mechanization	Sivashankari M	PC Jena, M Debnath, Supriya Priyadarsani, Awadhesh Kumar, TB Bagchi, R Khanam *Associates:* P Panneerselvam, S Sarkar
2.10	Enhancing water use efficiency in rice-based cropping system	Anjani Kumar	AK Nayak, R Tripathi, BB Panda, Kavita Kumari, D Chatterjee, BC Verma, R Khanam, M Debnath, B Raghavendra Goud, S Chatterjee *Associates:* D Bhaduri, S Munda, S Mohanty, P Panneerselvam
Programm 3: Biotic Stress Management in Rice			
3.1	Identification and characterization of donors against biotic stresses	MK Bag	PC Rath, AK Mukherjee, SD Mohapatra, S Lenka, S Mandal, A Banerjee, Raghu S, GP Pandi G, Basana Gowda G, NBK Patil, Prabhukarthikeyan SR, Keerthana U, P Golive, R Jena, Arun Kumar GC *Associate:* MK Kar
3.2	Ecology, diversity and interaction of plant, pests & natural enemies in rice	P Golive/ Annamalai M	SD Mohapatra, MK Bag, G Kumar, Prabhukarithikeyan SR, Kiran Gandhi B *Associates:* T Adak, Basana Gowda G, GP Pandi G
3.3	Use of Precision Tools and Techniques in Rice Insect Pest and Disease Management	SD Mohapatra	R Tripathi, Raghu S *Associate:* NN Jambhulkar
3.4	Search for novel mediators in plant defense response to pathogenic infections in rice through molecular techniques	AK Mukherjee	S Mandal, Raghu S, GP Pandi G, Prabhukarthikeyan SR, KA Molla, P Golive, TB Bagchi, Devanna *Associates:* MK Kar, MK Bag, A Banerjee, Parameswaran C, K Chakraborty, T Adak
3.5	Plant protection molecules: efficacy, distribution, toxicity and remediation	T Adak	PC Rath, MK Bag, S Lenka, Prabhukarthikeyan SR, Annamalai M, Raghu S, Basana Gowda G, NKB Patil, GP Pandi G, U Kumar, R Jena, Jeevan B, Keerthana U *Associates:* AK Mukherjee, P Bhattacharyya
3.6	Dissemination of integrated pest management strategies for insect pest, diseases and nematodes in rice	Guru Pirasanna Pandi G	PC Rath, AK Mukherjee, S Mandal, S Lenka, SD Mohapatra, MK Bag, T Adak, Annamalai M, Prabhukarthikeyan SR, Raghu S, Basana Gowda G, NKB Patil, R Jena, Jeevan B, GAK Kumar *Associate:* A Banerjee
Programm 4: Photosynthetic Enhancement, Abiotic Stress Tolerance and Grain Nutritional Quality in Rice			
4.1	Photosynthesis and productivity of rice under changing climate	MJ Baig	K. Chakraborty, N Basak, Gaurav Kumar, Millan Kumar Lal
4.2	Evaluation of rice genotypes for new sources of multiple abiotic stress tolerance and understanding the underlying mechanism	K Chakraborty	MJ Baig, M Chakraborti, KA Molla, Anilkumar C, Millan Kumar Lal *Associates:* K Chattopadhyay, Awadhesh Kumar, BC Marndi, NP Mandal, S Roy
4.3	Characterization of rice genotypes for improved Physico-chemical and Nutritional properties	Awadhesh Kumar	TB Bagchi, N Basak, G Kumar, RP Sah, Sivashankari M, Milan Kumar Lal *Associates:* L Behera, S Sarkar, K Chattopadhyay
Programm 5: Research to enhance socio-economic wellbeing of rice stakeholders			
5.1	**R**eaching stakeholders to **E**nhance their socio-economic **CAP**acities (**RECAP**) through rice technologies	S Paul	GAK Kumar, B Mondal, NN Jambhulkar, AK Pradhan, AK Mukherjee, S Lenka, Anjani Kumar, Supriya Priyadarsani, Sivashankari M, SM Prasad, K Saikia
5.2	Working to Increase farm Net Gain through Socioeconomic research (WINGS)	B Mondal	GAK Kumar, NN Jambhulkar, S Paul, AK Pradhan, SM Prasad, K Saikia *Associates:* MK Kar, S Saha, K Chattopadhyaya, SK Dash, S Sarkar, MK Bag, S Roy, RP Sah, Basana Gowda G
Programme 6: Development of climate resilient technologies for rainfed upland, rainfed low land and coastal rice ecology			
6.1	Development of resilient production technologies for rice under rainfed drought-prone agro-ecosystems	S Roy	NP Mandal, SM Prasad, S Bhagat, BC Verma, A Banerjee, Priyamedha, Soumya Saha, K Chakraborty, N Basak, L Behera, D Bhaduri
6.2	Rice production and productivity improvement in Rainfed lowland ecosystem	K Saikia	K Saikia
6.3	Development of Resilient technologies for Coastal Rice Ecology	Kiran Gandhi B	B Gayatri, Shyam CS, BB Panda, KK Rao *Associates:* MK Kar, K Chattopadhyay, BC Marndi, R Tripathi

Ongoing Externally Aided Projects (EAPs) 2025-26

SL. No.	Project No.	Title of the Project	Source of Funding
1.	EAP-27	Revolving fund scheme for seed production of upland rice varieties at CRURRS, Hazaribagh- NP Mandal, Priyamedha	AP Cess
2.	EAP-49	Revolving fund scheme for breeder seed production. - B C Marndi, RP Sah, Anil Kumar	NSP/Mega seed ICAR
3.	EAP-130	All India Network Project on Soil Biodiversity – Bio fertilizers - B C Verma	ICAR
4.	EAP-139	AICRP on energy in agriculture and agro-based industries - PC Jena, Manish Debnath	AICRP (DRET-SET/ DRET-BCT) ICAR
5.	EAP-140	Intellectual Property Management and Transfer/ commercialization of agricultural technology under National Agricultural Innovation Fund (NAIF) - GAK Kumar	IP&TM (ICAR)
6.	EAP-141	DUS Testing of Rice under Centrally sponsored scheme of PPV&FRA under "Sub-Mission on Seeds and Planting Material" - Anilkumar C, Reshmi Raj KR, P Sanghamitra	PPV&FRA
7.	EAP-197	Consortia Research Platform (CRP) on bifortification - K Chattopadhyay, S Samantaray, TB Bagchi, M. Chakraborty, A Kumar, N Basak, LK Bose, A Poonam, S Sarkar, BC Marndi, D Bhaduri	ICAR Plan-CRP
8.	EAP-198A	Incentivizing Coordinating Unit - KA Molla	ICAR
9.	EAP-198B	Incentivizing Research in Agriculture: Study of rice yield under low light intensity using genomic approaches - L Behera, MJ Baig, A Kumar, S Samantaray, RP Sah, Devanna	ICAR Plan
10.	EAP-199	Incentivizing Research in Agriculture: Towards understanding the C3-C4 intermediate pathway in *Poaceae* and functionality of C4 genes in rice - K Ali Molla , L Behera, Gaurav Kumar, A Kumar, K Ali Molla	ICAR Plan
11.	EAP-200	Incentivizing Research in Agriculture: Genetic modifications to improve biological nitrogen fixation for augmenting nitrogen needs of cereals - U Kumar, P Panneerselvam	ICAR Plan
12.	EAP-201	Incentivizing Research in Agriculture: Molecular genetic analysis of resistance/tolerance to different stresses in rice, wheat, chickpea and mustard including sheath blight complex genomics - M K Kar, L Behera, A Mukherjee, NP Mandal, S Samantaray, Devanna, K Ali Molla, M Chakraborti, LK Bose, Jeevan B, SK Lenka	ICAR Plan
13.	EAP-204	CRP on Agro-biodiversity: PGR Management and Use of Rice (Component I) - P Sanghamitra, BC Marndi, Raghu S	ICAR-NBPGR
14.	EAP-207	Conservation agriculture for enhancing the productivity of rice based cropping system in Eastern India - S Munda, AK Nayak, R Tripathi, BB Panda, M Shahid, S Saha, SD Mohapatra, P Guru, R Khanam, B R Goud	CAP - ICAR
15.	EAP-209	CRP on hybrid technology - RL Verma, JL Katara	CRP - ICAR
16.	EAP-211	CRP on molecular breeding - M K Kar, L Behera, A Mukherjee, M Chakraborti , P C Rath, LK Bose, SD Mohapatra, S Sarkar	CRP - ICAR
17.	EAP-215	Agri-Business Incubation Centre - GAK Kumar, BB Panda, B Mondal, AK Mukherjee, PK Guru, J P Bisen, G P Pandi, N N Jambhulkar	NAIF, IP&TM – ICAR
18.	EAP-227	Creation of seed hub for increasing indigenous production of pulses in India - S Sethi, DR Sarangi, T R Sahoo, M Chourasia, RK Mohanta	DAC &FW
19.	EAP-228	Increasing productivity and sustaining the rice-based production system through Farmer FIRST approach - B Mondal, SK Pradhan, S Saha, S Lenka, SD Mohapatra, BS Satapathy, R Tripathi, JP Bisen, NT Borkar, Supriya Priyadarsani, Lipi Das, GC Acharya, SC Giri, S Paul	ICAR-Farmer FIRST
20.	EAP-245	Strategic research component of National Innovation in climate resilient agriculture (NICRA) - P Bhattacharyya, A K Nayak, K Chattopadhyay, S Mohanty, D Chatterjee, K Chakraborty	ICAR Net work
21.	EAP-284	RKVY-RAFTAAR-Agribusinees incubation - G A K Kumar, A K Mukherjee, B B Panda, Narayan Borkar, M Sivashankari, B Mondal, Rameswar Sah, Sutapa Sarkar, G Prasanthi	RKVY
22.	EAP-291	Attracting and Retaining Youth in Agriculture (ARYA) - RK Mohanta , DR Sarangi, Rajan Kamboj, B Mounika	ICAR
23.	EAP-312	Mainstreaming rice landraces diversity in varietal development through genome wide association studies: A model for large scale utilization of gene bank collections of rice - L Behera, JL Katara, B C Marndi, Devanna, Amrita Banerjee, Somnath Roy, Kaushik Chakraborti, Manas Bag, Gourav Kumar, Aravindan S, Annamalai M, AK Mukherjee	DBT
24.	EAP-326	Accelerated genetic gain in rice (AGGRI- Alliance)- Irrigated rainfed (Drought, salinity & submergence) and DSR ecologies - SK Dash, NP Mandal, K Chattopadhyay, S Roy, RP Sah, LK Bose	IRRI
25.	EAP-328	Creation of seed infrastructure facility (only for construction) - RL Verma	Government of India Ministry of Agriculture & Farmers Welfare
26.	EAP-330	Formation and promotion of FPOs in Balasore - GAK Kumar, SK Dash, B Mondal, RP Sah, Basana Gowda, A K Mukherjee, Asit Pradhan, S R Dalal, S Paul	NCDC

27.	EAP-334	Generating C4 like PEPC enzyme in rice via precise genome editing - Sonali Panda (M J Baig)	DST Inspire
28.	EAP-337	Formation and promotion of FPOs in Odisha - GAK Kumar, S K Das, R P Sah, B Gowda, A K Mukherjee, A Pradhan, SR Dalal, Ankit Anand, S Sethi, S K Rout, B K Jha, S M Prasad, S Paul	Govt. of India (SFAC)
29.	EAP-339	Ph.D Dissertation work - Priya Das (M J Baig)	DBT JRF
30.	EAP-340	Targeting serotonin and senescence pathways for enhancing brown plant hopper resistance and yield in rice - Bijayalaxmi Sahoo (Parameswaran C)	DST Inspire fellowship
31.	EAP-343 (Merger of EAP-36 and EAP-100)	AICRIP on Seed (Crops) - B C Marndi, Anil Kumar C, AK Mukherjee, NKB Patil, RP Sah, Raghu S, Annamalai M	ICAR
32.	EAP-353	Network programme on precision agriculture (NePPA) -R Tripathy, A K Nayak, S Mohanty, S D Mohapatra, S R Raghu, B R Goud	ICAR
33.	EAP-357	Identification of genomic region(s) for 21 days submergence tolerance in rice using sequence based trait mapping approach - JL Katara, S Samantaray, Parameswaran C	SERB
34.	EAP-359	Enhancing resilience of smallholders to climate change through sustainable intensification and digital driven knowledge dissemination (E- CHASI) - S Mohanty, R Tripathi, S D Mohapatra, B Mondal, U Kumar, Anjani Kumar, Raghu S, PC Jena, P Panneerselvam	OIIPCRA, Deptt. of Water Resources Govt. of Odisha
35.	EAP-360	Biodegradable nanofibre encapsulated bio-fertilizer to enhance phosphorus and other micronutrient uptake in rice - P Panneerselvam	DBT, Govt. of India
36.	EAP-361	National mission mode program on nutritional improvement of digestible protein content and quality in rice - K Chattopadhyay, S Sarkar, TB Bagchi	DBT, Govt. of India
37.	EAP-364	Improving vegetative stage drought tolerance by integrating Genomic selection, GWAS and QTL mapping in rice - J L Katara	SERB, DST
38.	EAP-365	Nanoherbicide: A controlled release formulation to improve rice production - Totan Adak, S Munda	DST
39.	EAP-368	Comparative Assessment of Aldor as an Alternative to Urea on Rice growth, Yield, Nitrogen use efficiency and Soil Health - D Chatterjee, Mohammad Shahid as PI (up to 10.01.2025), A. K. Nayak	Sirius Minerals India Pvt Ltd (SMIPL)
40.	EAP-369	Popularization of BPH resistant rice variety for uplifting the Odisha rice farmers' income - SD Mohapatra, PC Rath, B Gowda, T Adak, GAK Kumar, Annamalai M Raghu S, MK Kar, N Patil, Parameshwaran, SK Mishra, R Sah, LK Bose	RKVY, Govt. of Odisha
41.	EAP-371	AICRIP (Rainfed) - S Samantaray, K. Chattopadhyay, SK Dash, M. Chakraborti, A. Kumar, AK Mukherjee, GP Padhi, Md. Shahid, K. Chakraborty, NN Jambulkar, AK Pradhan, N Basak	ICAR
42.	EAP-372	Development of haploid inducer rice lines using CRISPR/ Cas9 gene editing system for high induction frequency - S Samantaray, Devanna BN, Parameswaran C, JL Katara	DBT
43.	EAP-374	Allele mining for the epigenetic regulator NGR5 and other yield associated gene (GRF4) and their modulation using multiple genomic and molecular approaches to enhance rice yield under low nitrogen conditions – K Ali Molla, M J Baig	NASF ICAR
44.	EAP-377	Quantitative assessment of soil quality, yield sustainability and grain quality of rice in Eastern India: A unified triangular approach - Debarati Bhaduri	DST-SERB
45.	EAP-379	Deciphering and deploying low phosphorus tolerance and nitrogen use efficiency in rice - J Meher, Parameswaran C, D Chatterjee	NASF ICAR
46.	EAP-380	Blue carbon sequestration and climate change mitigation by managing mangrove-soil-algae system in coastal wetland - Sujit Kumar Nayak (P Bhattacharya)	DST-Inspire
47.	EAP-381	CRISPR Crop Network: Targeted improvement of stress tolerance, nutritional quality and yield of crops by using genome editing - Parameswaran C, S Samantray, Awadesh Kumar, K Ali Molla, Prabhukarthikeyan SR, Sushma M Awaji, P Hanjagi	NASF ICAR
48.	EAP-382	Identification and characterization of fungal effectors and host factors in rice- false smut pathosystem – Devanna, S Samantray (PI in absence of Devanna), M Bag	NASF ICAR
49.	EAP-384	Studying the Effect of Adopting Regenerative Agriculture Practices on Smallholder Farmer Livelihoods - Rahul Tripathi	J-PAL
50.	EAP-387	Computer vision for plant phonemics and smart agriculture" - Rahul Tripathi, SK Dash, Prashant K Hanjagi, P Swain, Sushma M Awaji	IIT, Jodhpur
51.	EAP-389	Establishment of hybrid rice seed system and state of art for genetic purity testing in Odisha - RL Verma, JL Katara, S Samantaray, BC Patra, GAK Kumar, AK Mukherjee, U Kumar	RKVY
52.	EAP-390	Outscaling of Natural Farming through KVKs **-** Dillip Ranjan Sarangi**,** Sujata Sethy, Tusar Ranjan Sahoo, RK Mohanta	ICAR
53.	EAP-391	4S4R Model for production, marketing and export of Odisha aromatic rice – GAK Kumar, BC Patra, B Mondal, T Adak, S Sarkar, M Chakraborti, S Priyadarshini, S K, Dash, S Sethy, JP Bisen, AK Pradhan	RKVY
54.	EAP-392	Improving rice genetics and its ecosystem through genome engineering and bioagents to reduce dependency on chemical N_2 fertilizer – K Ali Molla, MJ Baig, AK Mukherjee, T Adak, J Meher	Ignite Life Science Foundation

55.	EAP-393	Scaling of Natural Farming through KVKs (Kodarma) - Chanchilla Kumari, S Shekhar, B Singh, M Kumar, R Kumar	ICAR
56.	EAP-396	Engineered mesoporous silica nanoparticle-biochar complex for decontamination of phosphate and glyphosate in water - S Munda	DST
57.	EAP-399	Common Laboratory Services at ICAR-NRRI - P Bhattachatyya, T Adak	Service Providing Project
58.	EAP-400	Genome editing of rice targeting submergence and reproductive stage salinity tolerance for yield enhancement in coastal ecology - Swetapadma Sahu (S Samantray)	INSPIRE DST
59.	EAP-401	Transfer of bacterial leaf blight and sheath blight resistant gene(s) / QTL(s) into popular rice variety 'Maudamani' through marker assisted breeding. - Sushree Sangeeta, SK Pradhan, L Behera	INSPIRE DST
60.	EAP-402	Assessing the water productivity, GHG emission, yield and economics of rice based cropping systems under transplanted and direct seeded rice - Anjani Kumar, AK Nayak, S Mohanty, B Raghavendra Goud	IRRI
61.	EAP-403	Tackling emerging diseases and insect-pest problems in rice through innovative genomic approaches - Amrita Banerjee, NP Mandal, S Roy, Priya Medha, M K Bag	DBT
62.	EAP-404	Developing precision nitrogen management protocols for rice using remote sensing and geospatial tools (LBS Award- 2021) - Rahul Tripathi	ICAR
63.	EAP-405	Deciphering the role of OsSnRK (Sucrose nonfermenting-1 [SNF1] related kinase) gene family as a potential master regulator governing multiple abiotic stress tolerance in rice - Koushik Chakraborty	ICAR
64.	EAP-406	Identification and quantification of different volatiles emitted by Trichoderma and utilization of identified isolates/volatiles for plant growth promotion and soil borne pathogen management - Totan Adak, Arup Kumar Mukherjee	BRNS, BARC
65.	EAP-407	Ecosystem, Agribusiness and Institutions Component I: Impact assessment of Agricultural technology, Biswajit Mondal (PI), Sudipta Paul, Mridul Chakraborty	ICAR-NIAP
66.	EAP-408	Demonstration ,capacity building and Up-scaling of Integrated Farming Systems for Livelihood Security of Small and Marginal Farmers in Rainfed Ecosystem of Jharkhand' - SM Prasad, Soumya Saha, Bibhash Chandra Verma, Someshwar Bhagat, Chanchila Kumari, Sudhanshu Shekhar, Bhoopendra Singh , R K Singh, V P Rai	RKVY, Jharkhand
67.	EAP-409	Strengthening the entrepreneurship in the production, promotion and marketing of biocontrol agents in the rainfed ecosystem of Jharkhand - Someshwar Bhagat, Amrita Banerjee, BC Verma, SM Prasad, NP Mandal, Sushma Saroj Surin, Arti Beena Ekka, Raghav Kumar, Rajesh Kumar	RKVY, Jharkhand
68.	EAP-410	Sulphur enriched bio-nanoformulation of methanotrophs for greenhouse gas emission, mitigation and sustains production in rice - Monalisha Rath, Pratap Bhattacharyya	BPRF (Govt. of Odisha)
69.	EAP-411	Economic and Environment-Friendly Utilization of Basic-slag and Fly Ash as Soil Amendments to Reclaim Acid Soils of Odisha - Pratap Bhattacharyya Rubina Khanam, Debarati Bhaduri, Mohammad Shahid, G A K Kumar, Amaresh Kumar Nayak	Department of Agriculture and Farmers'Empowerment (DAFE), Government of Odisha
70.	EAP-412	Development of liquid formulation of Halotolerant Plant Growth Promoting Rhizobacteria (H-PGPR) Consortia to alleviate salt stress for sustainable rice production in saline coastal soil - U Kumar, G Rastog, P Panneerselvam, A K Nayak, K Chakroborty, A Poonam, Mahesh Dharne	DST, Odisha
71.	EAP-413	Bio-efficacy of PIX-20002 20% SC and PII 070 70% WG against insect pest of rice and their natural enemies through drone and conventional spraying - SD Mohapatra, Totan Adak	PI Industries Pvt. Ltd.
72.	EAP-415	Atlas of climate adaptation in South Asian Agriculture (ACASA) - Rahul Tripathi, Manish Debnath, NN Jambhulkar	BISA
73.	EAP-416	Production, popularization and supply of quality bioinoculants for rice based cropping and farming system of Odisha - Upendra Kumar, P Panneerselvam, GAK Kumar, B Mondal, A K Mukherjee, Annie Poonam, Md. Shahid, D Chatterjee, S Paul, RL Verma, A K Nayak	DAFE, Govt. of Odisha
74.	EAP-418	Map-based cloning and functional characterization of Pi-42; a novel blast resistance gene from rice genotype 'DHR-9' – Devanna, Parameswaran C, Rajeev Rathour	DST-SERB
75.	EAP-419	AICRIP on Bio Control - M Annamalai, Prabhukarthikeyan SR	ICAR
76.	EAP-420	Enhancing climate resilience and ensuring food security with genome editing tools -Parameswaran C	ICAR
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80.	EAP-424	Deciphering master regulators governing tolerance to multiple abiotic stresses in rice - K Chakraborty, K Chattopadhyay, K Ali Molla	SERB-CRG
81.	EAP-425	Deciphering the resistance mechanism through leaf volatiles and wax components in rice against bacterial leaf blight disease - AK Mukherjee, T Adak, Arabinda Mohanty	DST-SERB

82.	EAP-426	Integrated direct seeded rice systems for India - BB Panda, J Meher, PC Jena, AK Nayak	IRRI
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86.	EAP-430	Popularization of High Yielding Climate-Resilient Rice Cultivars in Aspirational Districts of Jharkhand and Feedback based Genetic Improvement - Priyamedha, N.P. Mandal, Somnath Roy, SM Prasad, BC Verma, Soumya Saha, S Bhagat , A Banerjee, Arun Kumara C G , Chanchila Kumari, Sudhansu Sekhar, RK Singh	RKVY-Jharkhand
87.	EAP-431	Establishment of state-of-art biocontrol laboratory for the management of insect-pests in Jharkhand - Arun Kumara C G, N.P. Mandal, S.M. Prasad, S. Bhagat, Somnath Roy, A. Banerjee, B.C. Verma, Priyamedha,, Soumya Saha	RKVY-Jharkhand
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105.	EAP-450	Trials for hybrids and HYVs in Eastern India, INVO74107 - RL Verma, S Samantaray, JL Katara	BMGF
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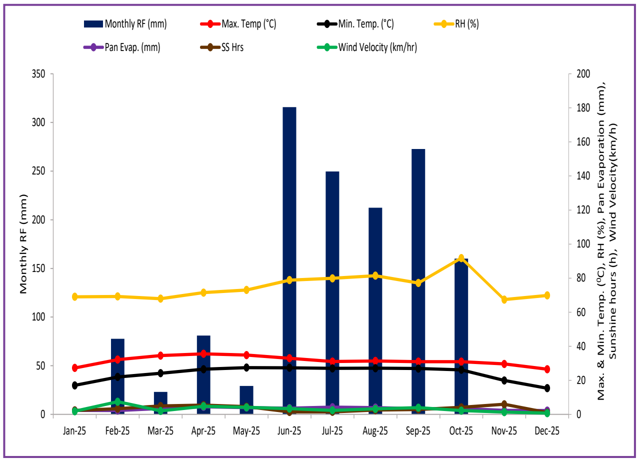

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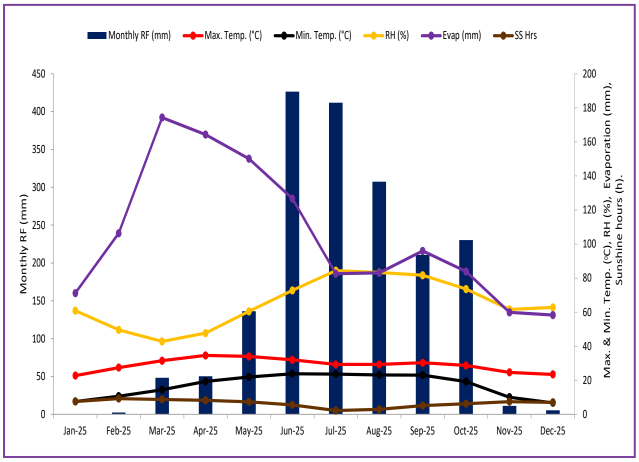

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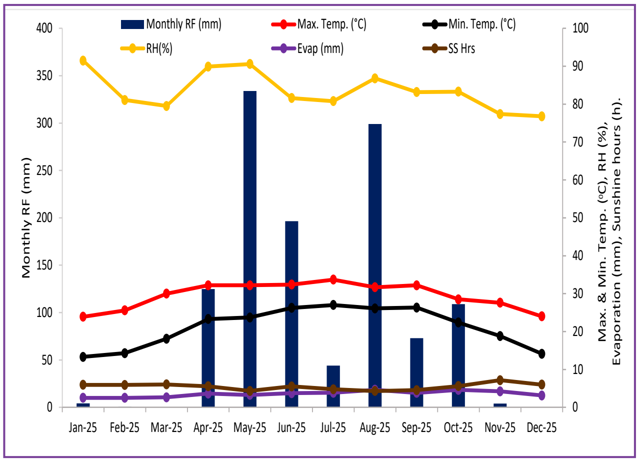

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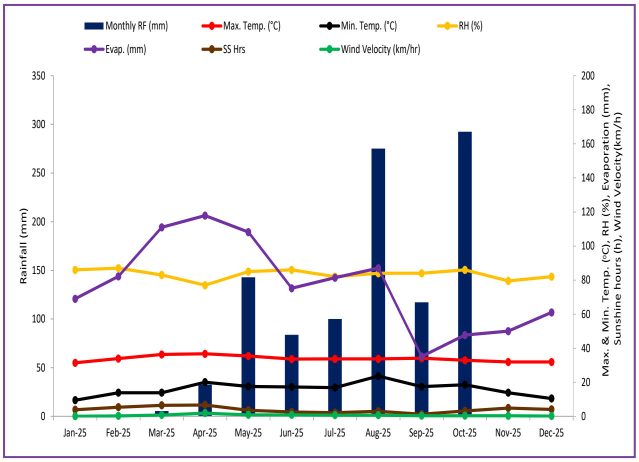

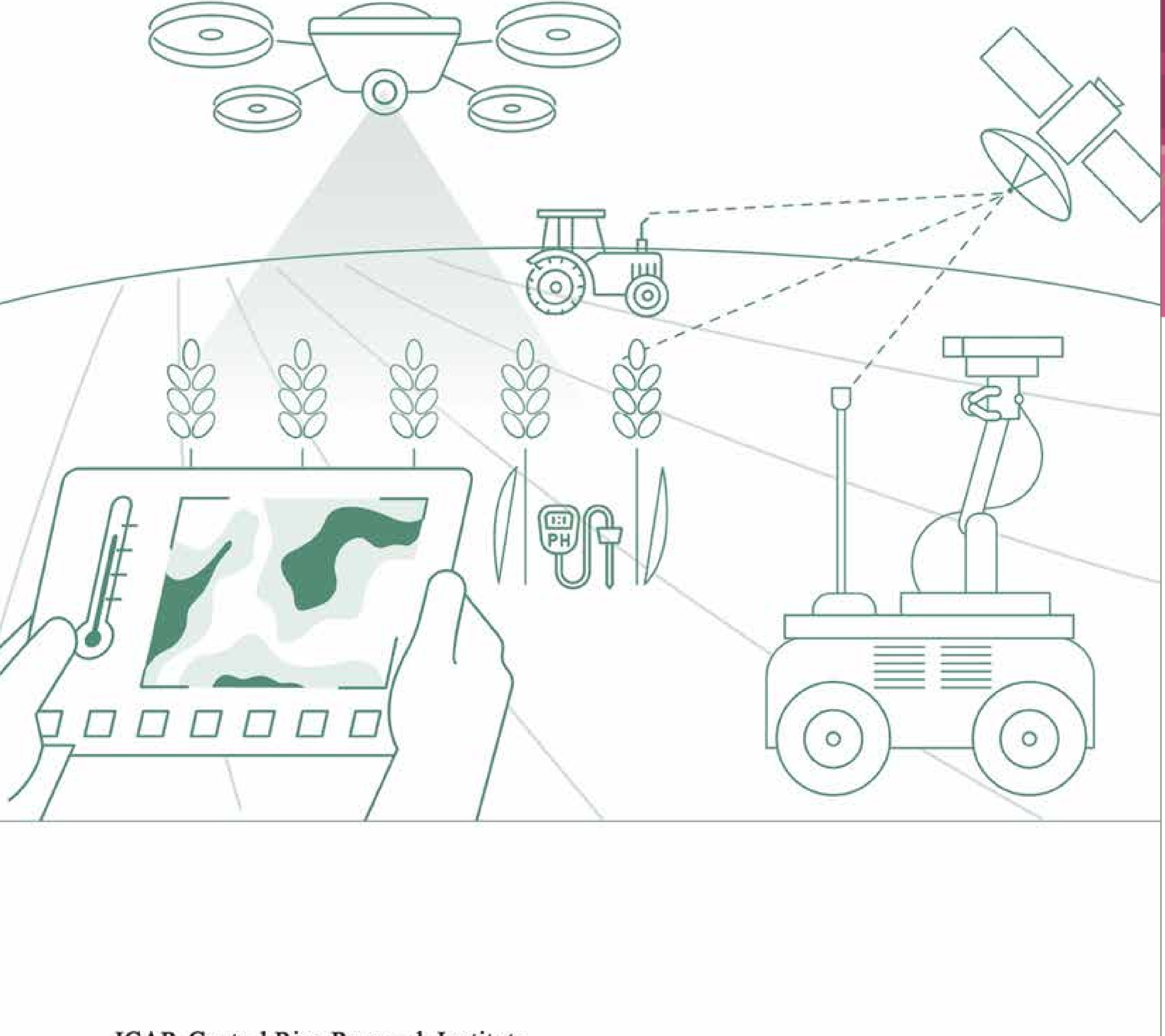

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