REVIEW ARTICLE **hppts://doi.org/10.58297/ LGUJ7885**

Sustainable DSR: Addressing Constraints through Advanced Breeding and Modern Technologies

Balaraju E [1], Aparanjitha Oggu[1], Ajay Bogati [1] , Venkateswarlu C[1] , Sai Prasad SV[2] , Kumar RM[2], Pronob J Paul[1] , Pallavi Sinha[1]* and Vikas K Singh[1]*

[1]International Rice Research Institute (IRRI), South Asia Hub, Hyderabad, Telangana, India

[2] ICAR-Indian Rice Research Institute, Rajendranagar, Hyderabad - 500030

*Corresponding author Email: p.sinha@cgiar.org; v.k.singh@cgiar.org

Received: 28th April, 2025, Accepted: 21st June, 2025

Abstract

As the global population is projected to surpass 9 billion by 2050, rice production must increase significantly to ensure food security, especially in developing countries that are most affected by climate change and the depletion of water and labour resources. Direct-seeded rice (DSR) emerges as a transformative solution, reducing water use and labour demands while achieving yields comparable to those of traditional transplanted rice systems. This article discusses the history of DSR, tracing its roots to ancient floodplains and its evolution into a modern, mechanized practice capable of yielding more tons per hectare in advanced systems. It discusses the latest breeding innovations that have shortened development timelines, utilizing genomic tools and precision technologies to develop resilient, weed-competitive varieties suited for diverse climates.

However, DSR's journey is not without hurdles-limited germplasm, complex trait demands, and persistent weed challenges threaten its scalability, with yields at risk without effective management. The article highlights efforts by global research institutes and the private sector, showcasing state-of-the-art facilities that accelerate variety development and mechanization-friendly designs poised to redesign the modern DSR breeding. Looking ahead, it discusses a future where sustainable weed control, climate-smart traits, and affordable machinery drive DSR breeding. When integrated with digital agriculture, these advancements promise a sustainable rice future, though equitable access to all rice researchers with a good understanding is needed. This review sheds light on current challenges and research innovations in DSR breeding, and further discusses future research directions, including the development of climate-resilient and future-proof DSR varieties, within a very short timeframe.

Keywords: Direct-seeded rice, sustainable rice farming, sustainable weed management, DSR breeding innovations

Introduction

With the global population projected to reach 9 billion by 2050, food production must increase manifold, especially in developing nations, to meet food security demands (Siegel *et al*., 2015). Accelerated climate change and resource scarcity, such as water and labour, are significant constraints on producing sufficient food with finite resources. Amidst these challenges, exploring solutions in rice cultivation that use less water while producing nearly the same quantity of food is essential for sustaining global food security. Direct-seeded rice (DSR), a cultivation method involving sowing seeds directly into the field rather than transplanting seedlings, has emerged as a sustainable alternative to the labour-and water-intensive traditional puddled transplanted rice (TPR) system. The history of DSR reflects a journey from ancient, rudimentary practices to a modern, mechanized approach, driven by the need for resource efficiency, labour savings, and environmental sustainability **(Figures 1 and 2).**

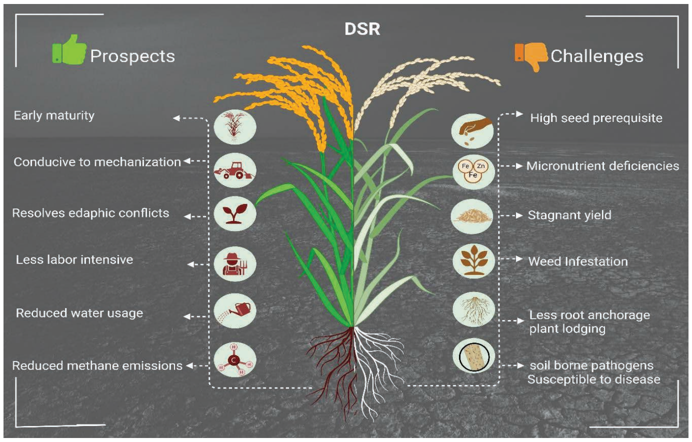

Figure 1: Prospects and Challenges of Direct-Seeded Rice

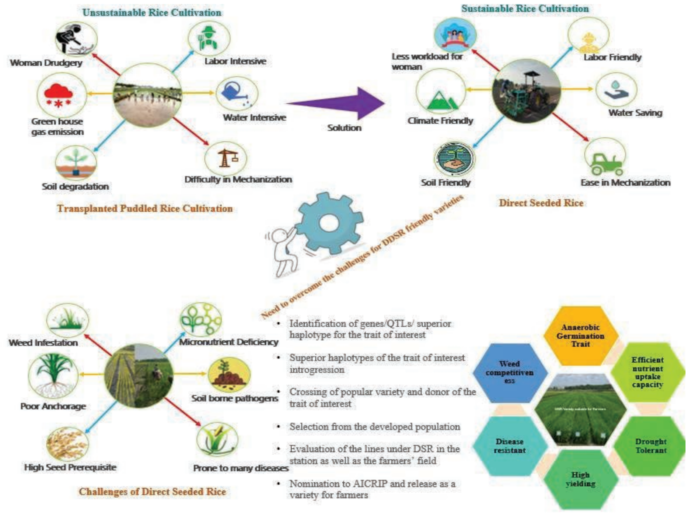

Figure 2: Transition from Unsustainable to Sustainable Rice Cultivation – Overcoming Key Challenges

Direct seeding is the oldest method of rice establishment by humankind for ages, but was gradually replaced by puddled transplanting for various reasons (Rao *et al.*, 2007). Early farmers broadcast seeds onto floodplains or rainfed soils, depending on natural moisture for germination (Bellwood, 2011). However, issues like uneven germination, weed competition, and inconsistent yields limited its use in irrigated systems **(Figure 2)**. In these systems, TPR's puddling provided better weed control and seedling establishment (Xu *et al.*, 2019).

By the early 20th century, the introduction of animal-drawn ploughs and basic seeders had begun to formalize DSR, particularly in the rainfed regions of India and Southeast Asia. The Green Revolution of the 1960s–1970s prioritized high-yielding varieties (HYVs) and irrigation, thereby reinforcing TPR's dominance in Asia, while DSR remained a secondary method in resource-constrained areas (Nelson *et al.*, 2019). In contrast, developed nations such as the USA and Australia adopted mechanized DSR in the 1950s, utilizing tractor-based drill-seeding to achieve uniform stands and reduce labour, as observed in California's water-seeded rice systems (Kumar and Ladha, 2011).

The late 20th century saw significant advancements in DSR through mechanization and breeding. Mechanized wet direct seeding with precision seeders reduced labour needs by 11 % to 75 % (Pandey *et al.*, 2002, Dawe *et al.*, 2005, Rashid *et al.*, 2009), while in India, tractor-drawn seed-cum-fertilizer drills boosted dry direct seeding adoption in Odisha and Punjab improving sowing efficiency by 30-55 % (Tiwari *et al.*, 2019). The development of herbicide-tolerant varieties in the 1990s, such as imidazolinone-tolerant rice in the United States, mitigated weed challenges - a historical barrier to DSR (Singh *et al.*, 2024). In the 21st century, breeding innovations have transformed DSR. IRRI's development of varieties like Sahod Ulan, with traits such as early vigour and drought tolerance, increased wet-DSR yields by 10-15 % (Kumar and Ladha, 2011). Genomic tools, including haplotype-based breeding and genomic-assisted breeding, have reduced breeding cycles by 30 %, identifying quantitative trait loci (QTLs) for DSR-specific traits (Sun *et al.*, 2019). High-throughput phenotyping (HTP) platforms, utilizing tools such as unmanned aerial vehicles (UAVs) and hyperspectral imaging, have reduced phenotyping time by 80 %, enabling faster screening of traits for thousands of lines (Wang *et al.*, 2022). CRISPR-Cas9 technology is now used to develop DSR varieties with improved weed competitiveness and nitrogen efficiency, tested in India and Vietnam (Lu *et al*., 2023a). Mechanized wet direct seeding (mDSR) systems, supported by automated seeders and laser levelling, have reduced seed rates by 61-83 % and decreased carbon footprints by 19-24 % (Van Hung *et al*., 2024).

Today, DSR is practiced on 20-30 % of the global rice areas, with high adoption in mechanized systems (USA, Australia: 80-90 %) compared to developing regions (India, Southeast Asia: 10-20 %) (Chakraborty *et al*., 2017). Policy support, such as subsidies for machinery and seeds in India and Bangladesh, and farmer training programs by the International Rice Research Institute (IRRI), have increased DSR adoption by 20 % in regions like Punjab (Tiwari *et al*., 2019). Looking forward, ongoing research focuses on climate-smart DSR varieties and digital tools, projecting 40 % adoption in Asia by 2030 (Singh *et al*., 2024). This paper examines the role of gaps in DSR breeding research, breeding innovations for addressing those gaps, and the future priorities of DSR research, providing a pathway to sustainable rice cultivation for smallholder farmers.

Roadblocks to DSR Breeding

Limited DSR-specific germplasm

One of the primary challenges in DSR breeding is the scarcity of germplasm specifically adapted to DSR conditions. Most existing rice varieties have been developed for TPR systems, which rely on puddling and transplanting to ensure weed control and uniform seedling establishment. These varieties often lack traits critical for DSR, such as early seedling vigour, weed competitiveness, and tolerance to abiotic stresses like drought or flooding (Sun *et al*., 2019). The lack of diverse DSR-adapted germplasm hinders the development of varieties suitable for mechanized DSR systems, particularly dry-DSR, where uniform germination and weed suppression are crucial. Without sufficient genetic diversity, breeders struggle to incorporate traits such as rapid root development or early canopy closure, which are essential for DSR success (Anjani *et al.,* 2024).

Complex trait requirements for DSR

DSR systems require varieties with a unique set of traits, including early seedling vigour, weed competitiveness, lodging resistance, anaerobic germination, deep sowing tolerance, uniform germination, and tolerance to abiotic stresses such as drought, flooding, and salinity (Negi *et al*., 2024). These traits are often controlled by multiple genes, making their combination in a single variety difficult (Singh *et al*., 2024). For instance, early vigour involves rapid seedling growth to outcompete weeds; however, this trait can reduce grain yield if not balanced with others, such as synchronized maturity for mechanical harvesting (Tiwari *et al*., 2019). The polygenic nature of DSR traits makes breeding more complex, as it involves precise selection and stacking of many QTLs. Traditional breeding methods are lengthy, often taking 10-12 years to develop a new variety, which delays the release of DSR-adapted cultivars (Kumar and Ladha, 2011).

Weed management

Weed competition is a significant challenge in DSR, as the absence of puddling and flooding- key weed control mechanisms in TPR-allows weeds to proliferate, resulting in yield reductions of 15-50 % in poorly managed DSR fields (Chakraborty *et al.,* 2017). Breeding for weed-competitive varieties is complex, as it requires traits such as rapid canopy closure and allelopathy, which are challenging to select for due to their complex environmental interactions and genetic complexity (Singh *et al*., 2024). The lack of effective weed-competitive varieties limits the adoption of DSR, particularly in dry-DSR systems, where manual weeding is labour-intensive and costly (Shekhawat *et al*., 2020). Developing herbicide-tolerant varieties is also challenging due to regulatory hurdles and the risk of herbicide resistance in weeds (Peerzada *et al*., 2019).

Resource constraints for breeding programs

Advanced breeding technologies, such as HTP platforms, genomic selection, and CRISPR, require significant financial and infrastructural investments, which are often inaccessible in developing countries where DSR is most needed. For example, establishing an HTP facility costs $ 1-2 million, making it unaffordable for many research institutions in South Asia and Sub-Saharan Africa (Kumar and Ladha, 2011). Additionally, limited access to high-quality seeds of DSR-adapted varieties hinders adoption, with only 20 % of Indian farmers able to access certified DSR seeds (Singh *et al*., 2024). Resource constraints limit the scale-up of breeding programs and the adoption of DSR varieties, particularly in regions with smallholding-dominated agriculture. The high cost of advanced technologies, such as automated seeders, phenotyping equipment, and tools, also poses barriers to field testing and validation of new varieties (Van Hung *et al*., 2024). The high cost of establishing and maintaining advanced breeding facilities restricts the development of DSR varieties in resource-poor regions. For instance, only a few institutions, such as IRRI, have access to high-throughput phenotyping (HTP) systems, which limits the scale of breeding programs in countries like India and Bangladesh (Kumar and Ladha, 2011). Additionally, the lack of robust seed production and distribution systems means that only 20 % of smallholding farmers in India have access to certified DSR seeds, which hampers their adoption (Singh *et al*., 2024).

Adaptation to diverse agro-climatic conditions

DSR is practiced across diverse agro-climatic zones, from rainfed uplands in India to irrigated lowlands in Vietnam, requiring varieties tailored to specific environmental conditions. Breeding for such diverse adaptations is challenging due to genotype-by-environment (G×E) interactions, which affect traits such as drought tolerance, flood resistance, and yield stability (Sun *et al.,* 2019). For example, dry-DSR varieties require strong root systems to uptake water and nutrients in rainfed conditions (Panda *et al*., 2021), whereas wet-DSR varieties need tolerance to anaerobic germination under flooded conditions. The need for region-specific varieties increases the complexity and cost of breeding programs, as multiple breeding pipelines are required. In Sub-Saharan Africa, for instance, the lack of locally adapted DSR varieties results in yield losses of 10-20 % due to poor environmental fit (African Development Bank, 2021).

Farmer knowledge and adoption barriers

Farmers' lack of knowledge about DSR-specific varieties and their management under mechanized systems poses a significant barrier to adoption. For example, improper seed rates and row spacing in DSR fields can reduce yields by 15–20 % due to poor stand establishment (Cheema *et al*., 2021). Additionally, smallholder farmers often lack training in the use of DSR-adapted varieties, resulting in suboptimal performance and a reluctance to transition from TPR (Singh *et al*., 2024). Limited farmer awareness and technical expertise lead to low adoption rates, particularly in developing regions, where only 10-20 % of rice areas utilize DSR (Chakraborty *et al*., 2017). This slows down the feedback loop needed to refine breeding programs based on field performance.

Integration with mechanization

Breeding DSR varieties compatible with mechanized systems, such as precision seeders and combine harvesters, is challenging due to the need for specific plant architecture traits, such as erect growth and uniform maturity. Many existing varieties are not optimized for mechanical sowing or harvesting, leading to losses of 10-15 % during harvesting due to lodging or asynchronous ripening (Tiwari *et al*., 2019). The mismatch between variety traits and mechanized systems reduces the efficiency of DSR adoption, particularly in regions transitioning to mechanized farming. For example, in India, only 5-10 % of rice varieties are suited for mechanized DSR, limiting scalability (Tiwari *et al*., 2019). Breeding mechanization-friendly traits, such as lodging resistance (20 % higher in IRRI's DSR varieties) and synchronous maturity, can enhance compatibility with machinery (Tiwari *et al*., 2019).

Automated plot seeders in breeding trials can ensure uniform testing conditions, improving variety performance by 15 % (Van Hung *et al*., 2024).

Breeding Innovations for Direct-Seeded Rice (DSR)

Dedicated DSR breeding programs and projects for accelerated variety development

Dedicated DSR breeding programs and projects speed up variety development by focusing specifically on traits of DSR and working towards developing DSR varieties. Recognizing the importance of DSR in current rice cultivation and the demand for DSR varieties, IRRI announced DSR as one of its flagship initiatives and established dedicated pipelines: DELS-I, targeting early maturing, long, slender, soft grain varieties for irrigated ecosystems in Punjab, Haryana, Western Uttar Pradesh, Cambodia, and Zambia, and DELS-R, focusing on similar varieties for upland rainfed areas like Bihar, Eastern Indo-Gangetic Plains, and Tanzania, developing hundreds of lines annually tested at over 10 locations in India for variety release (Bhosale *et al*., 2025).

IRRI's PlantDirect (funded by the Bill and Melinda Gates Foundation) and ScaleDirect (funded by USAID) projects promote DSR research and scaling in India's Eastern and Western Indo-Gangetic Plains. Moreover, Indian funding agencies, such as DBT, have supported IRRI in obtaining funding for DSR-specific projects aimed at incorporating several QTLs and genes into popular variety backgrounds and developing DSR-adapted lines. Many of these lines are currently being tested by the All India Coordinated Rice Improvement Project (AICRIP) (Paul *et al*., Unpublished). Recognizing the urgent need for dedicated testing pipelines to accelerate the development and adoption of direct-seeded rice (DSR) varieties, AICRIP has launched a specialized for the rainfed ecosystem and irrigated system. AICRIP has established two dry DSR trials, managed by ICAR-Indian Institute of Rice Research (IIRR), focusing on early, mid early, medium, and late duration varieties suitable for shallow, lowland environments. Similarly, for the irrigated ecosystem, two dry DSR trials, led by ICAR-National Rice Research Institute (NRRI), target the same range of variety durations, ensuring comprehensive testing and the delivery of DSR-ready lines across different agroecological conditions.

In the private sector, efforts like Bayer's Direct Acres program are a transformative initiative designed to help farmers seamlessly switch from traditional transplanted puddled rice to direct-seeded rice (DSR), providing maximum convenience and minimal risk while revolutionizing rice farming for a sustainable future. Bayer has developed an agricultural system for DSR that aims to reduce greenhouse gas emissions by up to 45 %, conserve water by up to 40 %, and lower labour costs by up to 50 % (Bayer, 2023). By 2030, Bayer plans to bring direct-seeded rice to one million hectares and support two million early-adopter smallholder farmers and their families in India.

Genomic tools for accelerated DSR variety development

Sequence-based trait mapping

Sequence-based mapping methods have rapidly advanced the discovery of DSR-specific QTLs and genes. For example, GWAS of 300 rice accessions identified four QTLs for mesocotyl length and two for deep sowing emergence, accounting for 6.9-8.5 % of the variation, including a major QTL (*qML3* on Chr3) with nine candidate genes; three of these genes carried allelic haplotypes with significant effects on ML (Xue *et al*., 2025). Concurrently, QTL-seq on multiple F_2 populations quickly localized 14 ML QTLs on chromosomes 1, 3, 4, 5, 6, 7, and 9 (Wang *et al*., 2021). Combining GWAS and QTL-*seq* revealed six QTLs that were consistent across populations, as well as eight high-confidence candidate genes for mesocotyl elongation. Similarly, GWAS conducted in an *aus* panel under low-N DSR identified approximately 97 QTLs for early root vigour traits; noteworthy candidates included root N-transporters

(PTR5/6) and phosphate transporters with advantageous alleles for nutrient acquisition (Anandan *et al*., 2022).

Integrative mapping has further refined these loci. For instance, Sandhu *et al*., (2023) combined GWAS, linkage mapping, and RNA-Seq to narrow down an approximately 881 kb interval on Chr7 associated with mesocotyl elongation, and they validated seven candidate genes through expression analysis. Overall, genome-wide association studies and bulked segregant analyses have identified numerous loci associated with DSR traits (early vigour, mesocotyl length, seedling emergence, and root development), providing breeder-friendly markers. Haplotype analysis and whole-genome resequencing have improved understanding of causal alleles. Xue *et al*., (2025) showed that three candidate genes under the *qML3* QTL contained distinct sequence haplotypes associated with mesocotyl length. Similarly, Yamasani *et al*., (2023) analyzed SSR haplotypes at known seedling vigour QTLs (*qSV-6a, qVI, qGP-6*) and identified allele combinations (*qVIHap-1, qGPHap-1*) that are significantly linked to better early vigour and germination. Anandan *et al*., (2022) highlighted "superior haplotypes" of nutrient transporter genes (for nitrogen and phosphorus uptake) that promote vigorous root growth under DSR.

At the population level, Liang *et al*., (2022) re-sequenced a RIL mapping population to construct a dense bin map (12,328 markers). They detected 50 QTLs related to coleoptile length, diameter, and volume under anaerobic germination stress. Even lodging resistance has been explored through sequence-based mapping: Yadav *et al*., (2017) mapped 12 lodging QTLs (culm length, diameter, strength) on chromosomes 1, 2, 6, and 7 and identified key loci *qCD1.1/qCS1.1* (~10-14 % PVE %) that co-locate with a gibberellin 3-beta-hydroxylase gene. In short, the use of GWAS, QTL-seq, haplotype analysis, and whole-genome resequencing is producing comprehensive maps of DSR trait genetics, covering anaerobic germination, nutrient uptake loci, and lodging resistance genes, and providing molecular targets for direct-seeded rice breeding.

Genomic selection (GS) based breeding program

GS utilizes genome-wide markers to predict breeding values, known as genomic estimated breeding values (GEBV), enabling the selection of superior lines without the need for extensive phenotypic evaluation. IRRI has already transformed its DSR breeding program through a genomic selection-based breeding program. In DSR breeding, GS has the potential to increase genetic gain for yield and stress tolerance, reducing breeding cycles from 10-12 years to 5-7 years (Bhosle, 2024). For instance, IRRI's GS pipeline has developed DSR varieties with considerable genetic gain over existing varieties, and several of these lines are included in the variety release programs of various countries, including India (AICRIP). GS enhances breeding efficiency, enabling rapid release of varieties tailored for mechanized DSR, such as those with uniform germination and lodging resistance.

Haplotype-based breeding

In direct-seeded rice (DSR), robust early seedling vigour and mesocotyl elongation are critical for uniform crop establishment under deep or adverse sowing. Recent studies have utilized high-density SNP genotyping and sequencing of diverse rice panels to identify multi-locus haplotypes controlling these traits (Singh *et al.,* 2022). For example, Menard *et al*., (2021) performed GWAS on 3K-RG accessions. They showed that haplotypes within a major QTL on chromosome 7 (controlling mesocotyl length, emergence rate, and biomass) predict seedling vigour in *indica* rice. Likewise, Yamasani *et al*., (2023) conducted haplotype analysis of known early-vigour QTL (*qSV-6a, qVI, qGP-6*) using flanking markers and identified specific haplotype alleles (e.g., 220/160 bp at *qVI*, 290/290 bp at *qGP-6*) associated with high vigour, genotypes carrying these "superior haplotypes" (e.g., BMF536, MM129) were proposed as DSR donors. Similarly, Anandan *et al*., (2022) mapped early root vigour under low-N DSR and reported that several candidate genes (e.g., phosphorus transporters PTR5/6, expansin genes) carry beneficial haplotypes; the novel QTL they found at 30 Mbp on chr4 harbors "expansin genes with superior haplotypes" linked to better root growth.

These studies demonstrate how high-resolution sequencing and haplotype mining can identify favourable alleles at multiple linked loci, resulting in high-value haplotype blocks suitable for selection.

Beyond early vigour, haplotype-based approaches are being applied to other key DSR traits. For anaerobic germination (AG), recent GWAS/NAM mapping identified major genomic regions (e.g., clusters on chr 3 and chr 6) associated with germination under flood (Verma and Sandhu, 2024), these loci can be further dissected into haplotypes or pyramided elite alleles for flood-tolerant DSR varieties. Traits for nutrient uptake and use efficiency (N, P, Fe) are likewise dissected by GWAS, and haplotype analysis of transporter or uptake genes can reveal adaptive alleles (as suggested by Anandan *et al*.,'s identification of PTR and phosphate-transporter haplotypes for improved root vigour). Lodging resistance has also benefited from haplotype analysis: Rashid *et al*., (2022) used high-coverage resequencing and GWAS to pinpoint *OsFBA2* as a lodging gene, then performed haplotype analysis of its alleles. They found that one haplotype (Hap3) with promoter variants confers significantly higher culm bending strength, suggesting breeders can introgress this superior allele to reduce lodging. In general, these efforts demonstrate the effectiveness of haplotype-based breeding. By sequencing diverse DSR germplasm (e.g., 3K panel, NAM populations) and defining multi-SNP haplotypes at key QTL, researchers can identify "stacked" allele combinations that maximize trait performance. As noted in recent reviews, combining superior haplotypes for DDSR traits via haplotype-based breeding is a promising strategy to accelerate genetic gains.

CRISPR-Cas9 gene editing

CRISPR enables the editing of specific loci related to agronomic performance under DSR conditions, such as anaerobic germination, lodging resistance, nitrogen use efficiency (NUE), and herbicide tolerance. One of the most impactful uses of CRISPR in DSR has been the targeted editing of the *OsALS* (acetolactate synthase) gene, which grants tolerance to imidazolinone herbicides (Zafar *et al*., 2023). This innovation, guided by agronomic priorities for better weed management, has significantly reduced weed pressure by up to 25 % and enabled early-stage weed control, a significant challenge in dry direct-seeded rice (DSR) systems. Similarly, editing OsPTR9, a gene involved in peptide transport, has improved NUE, grain yield, and growth, reducing fertilizer input needs while maintaining yield levels (Shobica *et al*., 2025). CRISPR also enables multiplex genome editing, allowing for the simultaneous improvement of multiple traits.

These edits, combined with agronomic validation through multi-location trials, ensure that the resulting lines are not only genetically enhanced but also suitable for field conditions.

High-throughput phenotyping (HTP) for precise trait screening

Drone phenotyping and hyperspectral imaging for faster trait screening

Unmanned Aerial Vehicles (UAVs) equipped with multispectral and hyperspectral cameras monitor traits, such as canopy cover, biomass, and stress responses, yield across large breeding plots (Shi *et al*., 2025). For example, Zhao *et al*., (2021) screened nearly 240 rice accessions for drought stress using UAV and performed GWAS. Although the technology is not yet widely used, the integration of UAVs (drone phenotyping for DSR traits) is accelerating the development of DSR varieties more quickly and accurately. Along with UAVs, hyperspectral imaging can be used to capture detailed spectral data for assessing traits such as grain chalkiness, protein content, and nitrogen uptake (Wang *et al.*, 2021). Hyperspectral imaging enhances selection precision, ensuring varieties meet both agronomic and consumer preferences.

Speed breeding facility

Speed breeding utilizes advanced automated chambers to optimize environmental conditions, including temperature, humidity, extended photoperiods, light intensity, CO_2 levels, irrigation, and pest management. This enables 4-5 rice generations per year, reducing breeding cycles from 6-7 years to 1.5 years while lowering operational costs by 30 % (Kabade *et al.*, 2024). This technology accelerates the development of direct-seeded rice (DSR) varieties by rapidly selecting traits such as early seedling vigour, anaerobic germination, deep sowing tolerance, and abiotic stress tolerance in early generations of line development. The SpeedBreed facility at the IRRI South Asia Regional Centre (ISARC) can accommodate 40,000 plants, making it suitable for early-generation DSR trait screening. Additionally, IRRI has validated its SpeedFlower protocol across 198 *Oryza sativa L.* accessions, confirming its applicability to both *indica* and *japonica* varieties. This work has inspired and supported at least 10 NARES (National Agricultural Research and Extension Systems) facilities across India, which can be further used for the fast-track development of DSR-suitable varieties.

Automated phenotyping facilities

Controlled automated DSR phenotyping facilities can be a valuable resource for screening large numbers of DSR advanced breeding lines (Dixit *et al.*, 2025). This facility can be useful for evaluating large mapping populations (biparental mapping populations, MAGIC population, NAM population, etc.) to identify traits of interest. These facilities are fully mechanized, equipped with automated drip irrigation and fertigation systems. Since the facility is automated and requires minimal external intervention, it can handle multiple lines simultaneously. Automation ensures consistent data collection, improves breeding efficiency, and enables rapid identification of elite lines. For example, IRRI has established such facilities in three locations around the world: IRRI in the Philippines, IRRI in Kenya, and IRRI in Hyderabad, India. At IRRI India, the DSR automated facility screens thousands of lines for mapping and identification of genes, QTLs, and haplotypes related to DSR traits, as well as for the development of final product lines that can be released as varieties. More such facilities are being established in collaboration with IRRI across Maharashtra, at various agricultural universities, to accelerate the development of DSR varieties tailored to regional needs.

Deep learning integration

The use of machine learning and deep learning algorithms for analyzing complex traits has significantly improved the accuracy of breeding value predictions (Sandhu *et al.*, 2021). This, in turn, can drive genomic selection initiatives for DSR. The prediction models developed at IRRI can predict the breeding values of lines and the potential breeding combinations of these lines that can achieve superior performance. This will help breeders in making the right cross combinations for desired traits. AI-powered deep learning models applied to high-throughput phenotyping (HTP) data enable the prediction of trait performance, resulting in a 50 % decrease in the time required for selection (Huang *et al.*, 2022).

Breeding for mechanization-friendly traits

DSR varieties must be engineered for compatibility with mechanized systems, such as precision seeders and combine harvesters, to boost efficiency and scalability while addressing labour shortages and minimizing losses. Breeding for mechanization-friendly traits ensures optimal performance during automated sowing, weeding, and harvesting, with lodging resistance being a critical factor, where weak culms cause 10-15 % yield losses in mechanized harvesting Additionally, early seedling vigour is vital, with breeding programs developing varieties that established itself very fast without showing any initial lag in the growth. Equally important is weed competitiveness, where breeding for rapid canopy closure and allelopathic traits - introgressed from wild rice (*Oryza rufipogon*) - results in new varieties with 30 % higher weed suppression due to taller plants and faster leaf expansion. These varieties reduce weed biomass by 25 % in field trials supporting sustainable DSR systems while enhancing mechanization compatibility. Moreover, uniform germination and synchronous maturity are essential for mechanized DSR systems, ensuring even stands for precision sowing and enabling single-time harvesting. IRRI's breeding lines achieve 90 % germination uniformity through selection for the *OsGA20ox* genes, leading to a 60 % reduction in seed rates when using precision seeders, while varieties like NSIC Rc222, with synchronous maturity, decrease harvesting losses by 8 % (Tiwari *et al*., 2019, Van Hung *et al*., 2024). These traits collectively improve planting and harvesting efficiency by 20-30 %, aligning DSR with automated equipment.

Integration of climate-smart traits

Breeding for climate-smart traits ensures DSR varieties are resilient to climate change challenges, such as drought, flooding, and heat stress, while minimizing environmental impact. These traits are crucial for sustaining DSR adoption in diverse and variable climates.

Drought tolerance

Dry-DSR systems face water scarcity, requiring varieties with deep root systems and efficient water uptake. Previous studies by IRR and other institutes have already identified major yield QTLs under drought, such as $qDTY_{12.1}$ and other *qDTY* QTLs, as well as *OsPIP1;2,* which contribute to drought tolerance. These QTLs have been incorporated into varieties like IR64-Drought. These varieties maintain an 80 % yield under moderate drought conditions (Kumar and Ladha, 2011). Traditional phenotyping methods are often labour-intensive and costly. HTP reduces these burdens by enabling rapid, non-destructive assessments, as shown by a method that processes panicle traits in under 10 seconds (Wang *et al*., 2023a)

Flood tolerance

Wet-DSR systems require anaerobic germination and submergence tolerance. The Sub1 gene, introgressed via MAS, enables varieties like Swarna-Sub1 to survive 14 days of submergence, boosting yields by 10 % in flood-prone areas (Kumar and Ladha, 2011). CRISPR editing of *OsERF922* further enhances flood tolerance, tested in Vietnam's Mekong Delta (Wang *et al*., 2023a). Flood-tolerant varieties expand the adoption of wet-DSR, ensuring resilience in low-lying areas.

Low-emission traits

Unlike puddled transplanted rice, DSR involves aerobic soil conditions, which significantly reduce CH_4 emissions but may increase N_2O emissions due to nitrogen dynamics. Breeding for traits such as improved nitrogen use efficiency (NUE), deeper root systems, and early vigour can optimize nutrient uptake and decrease greenhouse gas emissions under aerobic conditions (Chakraborty *et al*., 2017). For example, the development of elite rice varieties should target root traits enabling effective internal O_2 diffusion, via enlarged aerenchyma channels can reduce CH_4 emission (Jiménez and Pedersen, 2023). Additionally, varieties with synchronized phenology and efficient fertilizer response help minimize excess nitrogen (N) losses, resulting in a 20–30 % reduction in N_2O emissions (Rehman *et al*., 2022). Incorporating these low-emission traits into DSR breeding programs aligns with climate-smart agriculture goals and supports national efforts to cut greenhouse gas emissions in farming.

Future Research Priorities for DSR Breeding

Advancing CRISPR and genomic editing

The more effective use of CRISPR-Cas9 enables the development of DSR varieties with traits such as drought tolerance (*OsDREB1*), disease resistance

(*OsSWEET*), and herbicide tolerance (*OsALS*), potentially increasing yields by 15-20 % under stress (Zafar *et al*., 2023). For instance, OsERF922 editing enhanced flood tolerance in Vietnam's wet-DSR, increasing yields by 10 % (Linh *et al*., 2023). Research should focus on multi-trait stacking to create versatile varieties, reducing breeding cycles from 7 to 10 years to 2 to 3 years, with 50 % adoption projected by 2035. The effort involved stacking 3-5 genes for stress tolerance and grain quality (*OsGS3, OsBADH2*) using base editing to minimize off-target effects, followed by subsequent field trials across DSR systems to validate yield gains of 15 %. Develop harmonized global regulations to cut approval times by 2-3 years.

Sustainable weed management

Despite extensive ongoing research into herbicide-tolerant varieties, these solutions fall short of providing a sustainable approach to weed management in direct-seeded rice (DSR), as they inevitably leave a persistent chemical footprint in the environment. The reliance on herbicides, while cost-effective in the short term, poses long-term ecological risks, including soil degradation and water contamination, necessitating a shift toward more resilient alternatives **(Figure 2).** Future priorities should focus on breeding DSR lines with enhanced weed competitiveness, emphasizing traits such as enhanced seedling vigour, high absolute growth rate, extensive canopy coverage with maximum leaf expansion, and semi-erect plant architecture. These characteristics enable rice to naturally outpace weed growth, reducing the need for chemical interventions and promoting a more sustainable production system.

To further advance sustainable weed management, the introgression of allelopathic traits from wild relatives, such as *Oryza rufipogon,* presents a promising avenue for developing DSR varieties that suppress weed growth without the use of herbicides. Allelopathy, which involves the release of natural compounds that inhibit weed germination and growth, can reduce weed biomass by up to 15% in field trials, providing a chemical-free strategy that aligns with long-term environmental goals (Sun *et al*., 2019). By prioritizing these traits through advanced breeding techniques, such as marker-assisted selection and high-throughput phenotyping, researchers can create DSR lines that not only enhance yield stability by 10-15 % but also minimize ecological impact, ensuring a truly sustainable weed management system for the future (Singh *et al*., 2024).

Comprehensive DSR breeding facility for fast-track variety development

As the global demand for rice continues to grow with population increase, developing DSR varieties with a wide range of integrated traits becomes an urgent priority. Besides basic DSR traits such as early seedling vigour, weed competitiveness, and suitability for mechanized systems, there is a vital need to include climate-resilient traits, including drought, heat, and flood tolerance, from seedling emergence to ensure productivity amid increasingly unpredictable weather. Alongside resistance to major diseases like blast, bacterial leaf blight (BLB), and emerging diseases such as sheath blight, false smut, and brown spot, this strategy aims to maintain steady productivity. Achieving these goals requires a revolutionary breeding facility capable of addressing these complex challenges, providing an all-in-one solution to sustain rice production in the face of changing environmental and agricultural pressures.

To address this need, a state-of-the-art, comprehensive DSR breeding facility should be designed to streamline the evaluation process by screening for all these diverse traits within a single, integrated environment. Unlike traditional methods that require moving lines across multiple locations for different trait assessments, this innovative facility will enable the simultaneous testing of drought tolerance, heat stress resilience, flood adaptability, and disease resistance -all under one roof (Wang *et al*., 2022b). By leveraging advanced technologies like high-throughput phenotyping and marker-assisted selection, the facility will expedite the identification and validation of superior DSR lines, reducing the breeding cycle from the conventional 6-7 years to a remarkably shorter timeframe of 1.5–2 years (IRRI, 2024). With rapid and reliable results, this unique center will empower breeders to develop robust, multi-trait DSR varieties tailored to future needs, ensuring sustainable rice production and resilience against both climatic and biological stresses.

Integrating breeding with cross-disciplinary research

The success of DSR systems depends on a comprehensive integration of breeding with multiple disciplines, including agronomy, soil science, mechanization, weed science, water management, digital agriculture, and socioeconomics. Breeding alone cannot tackle the diverse and complex challenges of DSR-such as weed pressure, variable water availability, and labour shortages **(Figure 1 and Figure 2)** - without cross-disciplinary coordination that ensures varietal suitability under real-world field conditions. Agronomy-driven trait prioritization has allowed breeders to focus on key DSR traits such as early vigour, anaerobic germination, lodging resistance, and nutrient use efficiency. For example, incorporating agronomic feedback led to the development of Sahod Ulan varieties with increased yield and adaptability under wet direct-seeded rice (DSR) conditions (Kumar and Ladha 2011). Additionally, insights from soil science help breeders align with region-specific nutrient profiles, aiding in the development of varieties with improved phosphorus uptake or tolerance to low-fertility soils (Chakraborty *et al.,* 2017).

Mechanization and breeding co-evolve in DSR systems; calibrating seed drills to optimal sowing traits, such as seed size, uniformity, and emergence rate, requires close collaboration between breeders and agronomists (Tiwari *et al*., 2019). Lodging-resistant varieties with strong culms support combine harvesting, resulting in a 12 % reduction in losses (Nguyen Van Hung *et al*., 2024). Weed science guides breeding targets, including allelopathy and herbicide tolerance, and helps breeders develop weed-resistant varieties with proper knowledge of weeds. Meanwhile, integrating water management supports breeding for *qDTY* loci-linked drought tolerance, allowing synchronization of varietal maturity with irrigation schedules (Devi 2023; El-Razek *et al*., 2024). With the rise of digital agriculture, AI and UAV-based phenotyping are transforming selection decisions. Breeding programs now use high-throughput phenotyping in fields to evaluate stress responses and agronomic performance with 90-95 % predictive accuracy (Huang *et al.,* 2022; Yang and Zhai, 2022). Lastly, socioeconomic insights are critical to ensuring that developed varieties are economically viable and align with farmers' preferences. Participatory varietal selection and training modules based on agronomic management have increased adoption by 20-25 % (Bista 2018; Tiwari *et al*., 2019).

Integrating digital agriculture and artificial intelligence

The integration of machine learning and deep learning into direct-seeded rice (DSR) breeding has significantly enhanced the accuracy of predicting breeding values, thereby accelerating genomic selection (Sandhu *et al.*, 2021). At IRRI, deep learning models have been developed to forecast both the breeding values of individual lines and the performance of their potential cross combinations, facilitating informed decision-making for desirable trait pyramiding. Specifically, AI-powered models utilizing high-throughput phenotyping (HTP) data have reduced selection time by up to 50 %, while canopy closure and growth rate metrics have enabled the identification of DSR lines with 30 % higher weed competitiveness at IRRI's South Asia Hub (Huang *et al*., 2022). The convergence of artificial intelligence (AI), digital agriculture, and genomic prediction enables real-time monitoring, adaptive breeding strategies, and precision selection for complex DSR-specific traits such as early vigour, drought resilience, and weed competitiveness. Coupling AI-driven analytics with geospatial data, environmental sensing, and high-throughput platforms represents a paradigm shift, offering scalable and climate-resilient solutions for modern DSR breeding pipelines (Varshney *et al*., 2021; Singh *et al*., 2023).

Conclusion

As a new paradigm shift is occurring in rice cultivation to improve sustainability and address climate change and future issues, DSR is the most viable option; however, we do not have many varieties ready for diverse ecologies and different preferences. This review aims to address some of the pressing challenges of the breeding program, their mitigation through the current development of the breeding program for DSR, and further recommends future priorities for DSR breeding research, which should be cross-disciplinary. The DSR breeding program should not only focus on DSR key traits, but also on other climate-smart traits and the integration of AI and other innovative technologies to deliver products faster for the rice community.

References

Abbai R, Singh VK, Nachimuthu VV, Sinha P, Selvaraj R, Vipparla AK and Kumar A. 2019. Haplotype analysis of key genes governing grain yield and quality traits across 3K RG panel reveals scope for the development of tailor-made rice with enhanced genetic gains. *Plant biotechnology journal*, *17*(8), 1612-1622.

Anandan A, Panda S, Sabarinathan S, Travis AJ, Norton GJ and Price AH (2022). Superior haplotypes for early root vigour traits in rice under dry direct-seeded low nitrogen conditions through genome-wide association mapping. *Frontiers in Plant Science*. 13:911775.

Anjani K, Verma RL, Sah RP, Satapathy BS, Mohanty S, Tripathi R, Chattopadhyay K, Samantaray S and Nayak AK. 2024. Direct Seeded Rice: A Technology for Enhancing Climate Resilience (pp.7). *NRRI Research Bulletin No. 50*

Bellwood P. 2011. The checkered prehistory of rice movement southwards as a domesticated cereal-from the yangzi to the equator. *Rice* 4: 93–103.

Bhosale S, Prakash TP, Kadaru SB, Hussain W, Dixit S, Ali J, Platten JD, Islam MR, Singh VK, Murori, Ndayiragije A, Panchbhai A, Nayak S, Cruz PD, Demont M, Bartholome J, Pazaram GC, Cobb JN and Bhardwaj H. 2025. Onerice breeding framework: An end-to-end system to develop better varieties faster. *Crop Science*. 65(3):e70087.

Bista B. (2018). Direct seeded rice: A new technology for enhanced resource-use efficiency. *International Journal of Applied Sciences and Biotechnology*, 6(3): 181–198.

Chakraborty D, Ladha JK, Rana DS, Jat ML, Gathala MK, Yadav S, Rao AN, Mugadoli S, Ramesha MS and Raman A. 2017. A global analysis of alternative tillage and crop establishment practices for economically and environmentally efficient rice production. *Scientific Reports*, 7(1): 9342. DOI:10.1038/s41598-017-09742-9.

Cheema MJM, Nauman MH, Ghafoor A, Farooque AA, Haydar Z, Ashraf MU and Awais M. 2021. Direct seeding of basmati rice through improved drills: Potential and constraints in Pakistani farm settings. *Applied Engineering in Agriculture*, 37(1): 53-63. doi: 10.13031/aea.13372) @2021.

Dawe D. 2005. Increasing water productivity in rice-based systems in Asia: Past trends, current problems, and future prospects. *Plant Production Science,* 8(3): 221-230.

Dixit S, Ibabao X and Valenzuela M. 2025. Advancing Direct-Seeded Rice with Modern Phenotyping Facilities - Rice Today. https://ricetoday.irri.org/advancing-direct-seeded-rice-with-modernphenotyping-facilities/.

Gaihre YK, Singh U, Bible WD, Fugice Jr J and Sanabria J. 2020. Mitigating N_2O and NO emissions from direct-seeded rice with nitrification inhibitor and urea deep placement. *Rice science*, *27*(5), 434-444.

Huang C, Li W, Zhang Z, Hua X, Yang J, Ye J, Duan L, Liang XA and Yang W. 2022. An intelligent rice yield trait evaluation system based on threshed panicle compensation. *Frontiers in Plant Science*, 13: 900408. doi: 10.3389/fbls.2022.900408.

Jiang Z, Tu H, Bai B, Yang C, Zhao B, Guo Z, Liu Q, Zhao H, Yang W, Xiong L and Zhang J. 2021. Combining UAV-RGB high-throughput field phenotyping and genome-wide association study to reveal genetic variation of rice germplasms in dynamic response to drought stress. *New Phytologist*, 232(1): 440-455.

Jiménez JC and Pedersen O. 2023. Mitigation of greenhouse gas emissions from rice via manipulation of key root traits. *Rice*, 16: 24. doi. org/10.1186/s12284-023-00638-z.

Kabade PG, Dixit S, Singh UM, Alam S, Bhosale S, Kumar S, Singh SK, Badri J, Varma NRG, Chetia S, Singh R, Pradhan SK, Banerjee S, Deshmukh R, Singh SP, Kalia S, Sharma TR, Singh S, Bhardwaj H, Kohli A, Kumar A, Sinha P and Singh VK. 2024. Speed flower: a comprehensive speed breeding protocol for *indica* and *japonica* rice. *Plant Biotechnology Journal*, 22(5): 1051-1066.

Kaur D, Singh A, Sindhu VK. 2024. Growth and productivity of direct-seeded basmati rice (*Oryza sativa* L.) as influenced by sowing dates and irrigation schedules in north-western India. *Agricultural Water Management*. 302: 108994. doi. org/10.1016/j.agwat.2024.108994.

Kumar SS, Kumar HJM, Mourya S, Kumar A, Yadav S and Sah D. 2024. “Direct-Seeded Rice: Potential Benefits, Constraints and Prospective”. *Journal of Scientific Research and Reports*, 30(7): 272- 280. https://doi.org/10.9734/jsrr/2024/v30i72143.

Kumar V and Ladha JK. 2011. Direct sowing of rice: Recent developments and future research needs. *Advances in Agronomy*, 111: 297–413. doi. org/10.1016/B978-0-12-387689-8.00001-1.

Liang W, Du H, Pang B, Cheng J, He B, Hu F, Lv Y and Zhang Y. 2022. High-density genetic mapping identified QTLs for anaerobic germination tolerance in rice. *Frontier Plant Sciences*. 13:1076600. doi: 10.3389/fbls.2022.1076600.

Linh LK, Doai VN, Linh NT, Quyen P, Ha CH, Ngoc PB and Phat DT. 2023. Development of CRISPR/Cas9 systems to induce targeted mutations in the promoter region of the OsSRFP1 gene in rice. *Vietnam Journal of Biotechnology*. 21(3):463-475. https://doi.org/10.15625/1811-4989/19532.

Lu Y, Wang J, Fu L, Yu L and Liu Q. 2023a High-throughput and separating-free phenotyping method for on-panicle rice grains based on deep learning. Frontiers in Plant Science, 14, 1151480. doi:10.3389/fpls.2023.1219584.

Menard G, Sandhu N, Anderson D, Catolos M, Hassall KL, Eastmond PJ, Kumar A and Kurup S. 2021. Laboratory phenomics predicts field performance and identifies superior indica haplotypes for early seedling vigour in dry direct-seeded rice. *Genomics* 113(6):4227-4236.

Negi P, Rane J, Wagh RS, Bhor TJ, Godse DD, Jadhav P, Anilkumar C, Sreekanth D, Reddy KS, Gadakh SR, Boraih K, Harisha CB and Basavaraj PS. 2024. Direct-Seeded rice: Genetic Improvement of Game-Changing Traits for Better Adaption. *Rice Science*, 31(4): 417-433.

Nelson ARLE, Ravichandran K and Antony U. 2019. The impact of the Green revolution on indigenous crops of India. *Journal of Ethnic Food,* 6: 8.

Nguyễn VH, Thach NT, Hoang NN, Binh NCQ, Tam DM, Hau TT, Anh TTD, Khuong TQ, Chi VTB, Lien TTK, Goummert M, Rakotoson T, Saitol K and Kumar Virender. 2024. Mechanized wet direct seeding for increased rice production efficiency and reduced carbon footprint. Precision Agriculture. 25: 2226-2244. https://doi.org/10.1007/s11119-024-10163-8.

Panda S, Majhi PK, Anandan A, Mahender A, Veludandi S, Bastia D, Guttala SB, Singh SK, Saha S and Ali J. 2021. Proofing Direct-Seeded Rice with Better Root Plasticity and Architecture. *International Journal of Molecular Sciences,* 22: 6058. https://doi.org/10.3390/ijms22116058.

Pandey S and Velasco L. 2002. Economics of direct seeding in Asia: Patterns of adoption and research priorities. Direct Seeding: Research Strategies and Opportunities, International Rice Research Institute, Los Banos, the Philippines, pp. 3-14.

Peerzada AM, O'Donnell C and Adkins S. 2019. Optimizing herbicide use in herbicide-tolerant crops: Challenges, opportunities and recommendations. In: Hasanuzzaman M. (eds) *Agronomic Crops*. *Springer Singapore*. 283-316 pp. https://doi.org/10.1007/978-981-32-9783-8_15.

Ramasamy SP, Rathnasamy SA, Manickam S, Chellappan G, Natarajan B, Jaganathan D, Thiyagarajan K, Swaminathan M, Seshadri G, Muthurajan R. 2015. Targeted editing of rice genome for enhanced yield: Progress and prospects. Plant Sci. Today [Internet]. 2025 Apr. 30 [cited 2025 Jun. 27];12(sp1). Available from: https://horizonepublishing.com/journals/index.php/PST/article/view/7854.

Rao AN, Johnson DE, Sivaprasad B, Ladha JK, Mortimer AM. 2007. Weed management in direct-seeded rice. *Advances in Agronomy,* 93: 153-255. https://doi.org/10.1016/S0065-2113(06)93004-1.

Rashid MAR, Zhao Y, Azeem F, Zhao Y, Ahmed HGMD, Atif RM, Pan Y, Zhu X, Liang Y, Zhang H, Li D, Zhang Z and Li Z. 2022. Unveiling the genetic architecture for lodging resistance in rice (*Oryza sativa* L.) by genome-wide association analyses. *Frontier in Genetics,* 13:960007. doi: 10.3389/fgene.2022.960007.

Rashid MH, Alam MM, Khan MAH and Ladha JK. 2009. Productivity and resource use of direct(drum)-seeded and transplanted rice in puddled soils in rice-rice and rice-wheat ecosystems. *Field Crops Research*, 113(3): 274-281. https://doi.org/10.1016/ j.fcr.2009.06.004.

Sagare DB, Abbai R, Jain A, Jayadevappa PK, Dixit S, Singh AK, Challa V, Alam S, Singh UM, Yadav S, Sandhu N, Kabade PG, Singh VK and Kumar A. 2020. More and more of less and less: Is genomics-based breeding of dry direct seeded rice (DDSR) varieties the need of hour?. *Plant Biotechnology Journal*, 18(11): 2173-2186. https://doi.org/10.1111/pbi.13454.

Sandhu KS, Lozada DN, Zhang Z, Pumphrey MO and Carter AH. 2021. Deep learning for predicting complex traits in spring wheat breeding program. *Frontiers in plant science*, 11, 613325. Deep learning for predicting complex traits in spring wheat breeding program.

Sandhu N, Ankush AP, Singh J, Raigar OP, Bains S, Jindal T, Singh MP, Sethi M, Pruthi G, Augustine G, Verma VK, Goyal S, Kumar A and Kaur R. 2023. Integrating association mapping, linkage mapping, fine mapping with RNA sequencing conferring seedling vigor improvement for successful crop establishment in deep sown direct-seeded rice. *Rice* 16:46. https://doi.org/10.1186/s12284-023-00665-w.

Shekhawat K, Rathore SS and Chauhan BS. 2020. Weed Management in Dry Direct-Seeded Rice: A review on Challenges and Opportunities for Sustainable rice production. *Agronomy,* 10(9): 1264. https://doi.org/10.3390/agronomy10091264.

Shi Z, Wang L, Yang Z, Li J, Cai L, Huang Y, Zhang H and Han L. 2025. Unmanned Aerial Vehicle-Based Hyperspectral Imaging Integrated with a Data Cleaning Strategy for Detection of Corn Canopy Biomass, Chlorophyll, and Nitrogen Contents at Plant Scale. *Remote Sensing*, 17(5): 895. https://doi.org/10.3390/rs17050895.

Siegel FR 2015. Countering 21st-century social-environmental threats to growing global populations. Cham: Springer International Publishing. doi 10.1007/978-3-319-09686-5.

Singh H, Singh J, Ade PA, Raigar OP, Kaur R, Khanna R, Mangat GS and Sandhu N. 2022. Genetic evaluation of a diverse rice panel for direct-seeded-adapted traits using Kompetitive Allele-Specific PCR assay. *Agronomy* 12(9):2083.

Singh P, Sundaram KT, Vinukonda VP, Venkateshwarlu C, Paul PJ, Pahi B, Gurjar A, Singh UM, Kalia S, Kumar A, and Singh VK. 2024. Superior haplotypes of key drought-responsive genes reveal opportunities for the development of climate-resilient rice varieties. *Communications Biology*. 7(1):89. doi.org/10.1038/s42003-024-05769-7.

Sivabharathi RC, Rajagopalan VR, Suresh R, Sudha M, Karthikeyan G, Jayakanthan M and Raveendran M. 2024. Haplotype-based breeding: A new insight in crop improvement, *Plant Science*. 346: 112-129.

Stuart AM, Devkota KP, Sato T, Pame ARP, Balingbing C, Phung NTM, Kieu NT, Hieu PTM, Long TH, Beebout S and Singleton GR. 2018. On-farm assessment of different rice crop management practices in the Mekong Delta, Vietnam, using sustainability performance indicators. *Field Crops Research,* 229: 103-114. doi.org/10.1016/j.fcr.2018.10.001.

Sun D, Cen H, Haiyong W, Wan L, Abdalla A, El-Manawy AI, Zhu Y, Zhao N, Fu H, Tang J, Li X, Zheng H, Shu Q, Liu F and He Y. 2019. Using hyperspectral analysis as a potential high throughput phenotyping tool in GWAS for protein content of rice quality. *Plant Methods*, 15: 54. doi.org/10.1186/s13037-019-0432-x.

Tiwari PS, Singh KK, Sahni RK and Kumar V. 2019. Farm mechanization - trends and policy for its promotion in India. *The Indian Journal of Agricultural Sciences*, 89(10): 1555-1562.

Van Hung N, Thach TN, Hoang NN, Binh NCQ, Tâm DM, Hau TT, Anh DTT, Khuong TQ, Chi VTB, Lien TTK, Gummert M, Rakotoson T, Saito K and Kumar V. 2024. Mechanized wet direct seeding for increased rice production efficiency and reduced carbon footprint. *Precision Agriculture*, 25(5): 2226-2244.

Varshney RK. 2021. The plant genome special issue: Advances in genomic selection and application of machine learning in genomic prediction for crop improvement. *The Plant Genome*, 14(3): e20178. https://doi.org/10.1002/tpg2.20178.

Verma VK and Sandhu N. 2024. Understanding anaerobic germination in direct-seeded rice: a genomic mapping approach. *BMC Plant Biol*ogy. 24: 1194. https://doi.org/10.1186/s12870-024-05901-z.

Wang C, Caragea D, Kodadinne Narayana N, Hein NT, Bheemanahalli R, Somayanda IM and Jagadish SVK. 2022. Deep learning based high-throughput phenotyping of chalkiness in rice exposed to high night temperature. *Plant Methods*, 18(9): https://doi.org/10.1186/s 13007-022-00839-5.

Wang F, Yi Q, Hu J, Xie L, Yao X, Xu T and Zheng J. 2021. Combining spectral and textural information in UAV hyperspectral images to estimate rice grain yield. *International Journal of Applied Earth Observation and Geoinformation,* 102:102397. https://doi.org/10.1016/j.jag.2021.102397.

Wang L, Zhang Y, Luo D and Wang Q. 2024. Agricultural Mechanization, Productivity, and Factor Reallocation: Evidence from China. Available at SSRN: https://ssrn.com/abstract=4819903 or http://dx.doi.org/10.2139/ssrn.4819903.

Wang Y, Liu J, Meng Y, Liu H, Liu C and Ye G. (2021). Rapid identification of QTL for mesocotyl length in rice through combining QTL-seq and genome-wide association analysis. *Frontier in Genetics*, 12: 713446. https://doi.org/10.3389/fgene.2021.713446.

Xu L, Li X, Wang X, Xiong D, and Wang F. 2019). Comparing the grain yields of direct-seeded and transplanted rice: A meta-analysis. *Agronomy*, 9(11): 767. doi:10.3390/agronomy9110767.

Xue L, Wang S, Zhang Q, Han B, Cui D, Han L, Deng J and Ma X. 2025. Identification of key genes associated with mesocotyl length through a genome-wide association study in rice. *Frontiers in. Plant Science.* 16: 1546580. https://doi.org/10.3389/fpls.2025.1546580.

Yadav S, Singh UM, Naik SM, Venkateshwarlu C, Ramayya PJ, Raman KA, Sandhu N and Kumar A. 2017. Molecular mapping of QTLs associated with lodging resistance in dry direct-seeded rice (*Oryza sativa* L.). *Frontiers in Plant Science*, 8: 1431. https://doi.org/10.3389/fpls.2017.01431.

Yamasani MR, Pandu VR, Kalluru S, Bommaka RR, Bandela R, Duddu B, Komeri S, Kumbha D and Vemireddy LR. 2023. Haplotype analysis of QTLs governing early seedling vigour-related traits under dry-direct-seeded rice (*Oryza sativa* L.) conditions. *Molecular Biology Reports,* 50(10): 8177–8188. doi: 10.1007/s11033-023-08714-9.

Zafar K, Khan MZ, Amin I, Mukhtar Z, Zafar M and Mansoor S. 2023. Employing template-directed CRISPR-based editing of the *OsALS* gene to create herbicide tolerance in Basmati rice. *AoB Plants*, 15(2): plac059. doi: 10.1093/aobpla/plac059.