CRRI Research Bulletin No. 58

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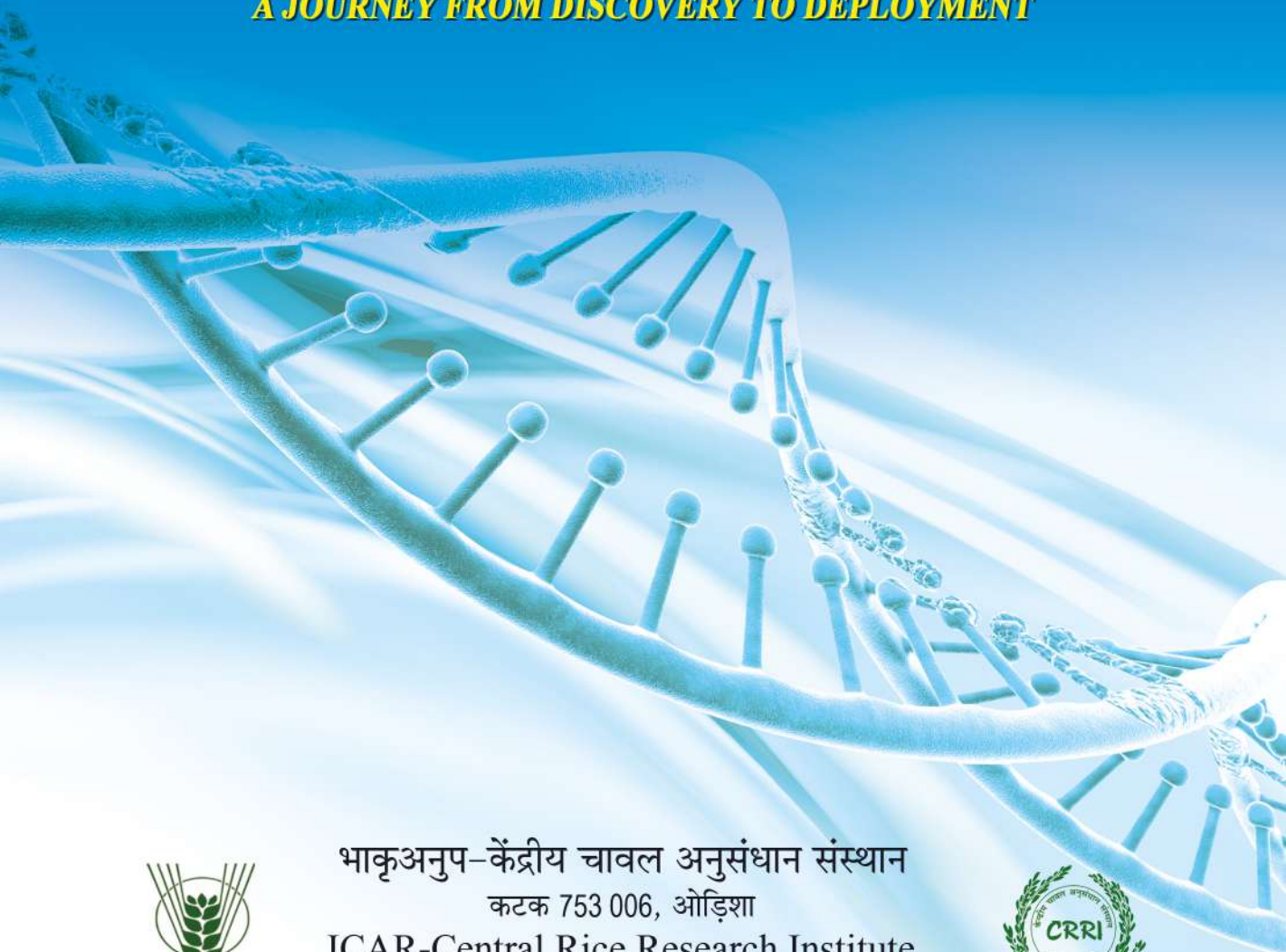
## *A JOURNEY FROM DISCOVERY TO DEPLOYMENT*



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# PREFACE

Rice (*Oryza sativa* L.) is one of the most important cereal crops globally, serving as the primary food source for nearly half of the world's population. In India, rice contributes 30-50% of agricultural income and is a staple food for over 65% of its people. Conventional breeding approaches have achieved significant success, leading to a doubling of rice production over the past six decades. Efforts by rice scientists have resulted in the development of improved varieties with shorter growth durations, higher yield potential, and enhanced resistance or tolerance to various biotic and abiotic stresses. By 2050, global rice demand is projected to rise by 65%, requiring the production of 858 million tons of unmilled rice compared to the current output of 643 million tons. However, challenges such as population growth, diminishing arable land, water scarcity, emerging biotypes of pests and diseases, and the potential impacts of climate change create significant obstacles. Addressing these challenges necessitates increasing production and productivity while developing varieties with multi-stress tolerance/resistance. Although traditional breeding methods remain important tool, they offer limited solutions for the evolving challenges. Advancements in biotechnology and omics have opened new avenues for more precise and time-efficient breeding strategies. These technologies focus on enhancing resistance and/or tolerance to various stresses, improving input use efficiency, and stabilizing rice yield while adding value to the crop.

The ICAR-Central Rice Research Institute (ICAR-CRRI), Cuttack, Odisha, India, is a premier institute dedicated to basic, strategic, and applied research to develop high-yielding varieties and technologies, with a greater focus on rainfed ecosystems. Recognizing the potential of the biotechnology, ICAR-CRRI initiated research in this field during the 1990s, focusing on tissue culture, genetic engineering, DNA marker technologies, and functional genomics. These efforts have enabled the transfer of beneficial traits from wild rice to elite cultivars and the identification of genes and QTLs associated with tolerance to abiotic stresses such as salinity, submergence, stagnant water, drought, temperature extremes, iron toxicity, and phosphorus deficiency. Research has also targeted resistance to biotic stresses, including sheath blight, gall midge, and brown planthopper, along with agro-morphological and yield-related traits like seed vigor, tiller number, plant height, panicle architecture, spikelet fertility, grain weight, and yield. Additionally, nutritional qualities, including protein, iron, zinc, starch, and antioxidant properties, have been emphasized. Hence, ICAR-CRRI has made efforts to compile this publication, highlighting the significant achievements in QTL/gene identification for different traits and their use for varietal development. We hope this publication serves as a helpful reference material for students, plant breeders, biotechnologists, and rice scientists from various disciplines to understand and appreciate the potential and realize the benefits of biotechnology and omics technologies. The progress and achievements made so far are briefly presented in this research bulletin.

Cuttack
March, 2025

**Authors**

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# CHAPTER 1: INTRODUCTION

Rice (*Oryza sativa* L.) is cultivated on approximately 160 million hectares worldwide, producing 493 million tons of milled rice. With over 100 countries engaged in its cultivation, rice ranks as the third highest globally produced crop, yielding 740 million tons of rough rice annually, following sugarcane and maize. It provides 35-75% of the calorie intake for more than 3 billion people in Asia and contributes 27% of global dietary energy, 20% of dietary protein, and 3% of dietary fat. Covering vast areas, rice is the third-largest cereal crop and a critical food source for the world's poorest populations. In India, rice occupies the largest share of about 141 million hectares of net cultivated land, covering about 43 million hectares. Over the past four decades, significant advancements have been made in rice production, primarily due to the introduction of high-yielding varieties and intensive input-based management practices. However, in recent years, increasing rice production has become more challenging due to the degradation of natural resources like soil, water, and air, coupled with labour shortages and the adverse impacts of climate change. Looking ahead, rice must be cultivated using less land, water, and labour, adopting efficient and environmentally sustainable production systems. These systems must be resilient to climate change while minimizing greenhouse gas emissions. Additionally, the focus on production growth has overshadowed the importance of profitability. A shift towards a profit-driven approach is now essential. In the pursuit of higher yields, the vital role of natural resources such as soil, water, and air has been overlooked in many instances, treating them as passive elements in crop production. To improve productivity, profitability, climate resilience, and sustainability in rice farming, a comprehensive strategy is required. These include technological innovations, enhancing infrastructure, and implementing policy reforms to transition from the current production-oriented rice-based cropping systems to profit-oriented rice-based farming systems. Agricultural research must adopt participatory approaches that actively involve farmers to address poverty, reduce labour-intensive practices, and meet the needs of resource-limited smallholder rice farmers.

Rice exhibits extensive genetic diversity across thousands of landraces, elite breeding lines, high-yielding varieties, and 22 wild species. These genetic resources vary significantly in grain yield, quality, input use efficiency, and resistance to biotic and abiotic stresses, making rice an invaluable reservoir of naturally occurring alleles for trait enhancement, including yield improvement. Environmental factors and field management practices strongly affect the yield performance of rice varieties, with notable genotype-environment interactions leading to the adaptation of specific varieties to distinct conditions. Leveraging the diverse gene pools within rice germplasm is now widely regarded as the most efficient and sustainable strategy for achieving both high productivity and adaptability. The development of high-yielding varieties is driven by the integration of beneficial and superior alleles from germplasm. Over 120,000 rice germplasm accessions, including traditional varieties, landraces, genetic stocks, breeding lines, and wild relatives, are conserved in gene banks across India and globally. Identifying quantitative trait loci (QTLs) and genes linked to yield, quality traits, input use efficiency, and stress tolerance is crucial for their incorporation into popular high-yielding rice varieties using marker-assisted selection (MAS). This approach not only accelerates marker-assisted breeding but also facilitates gene discovery, contributing to sustainable agriculture and enhancing rice yield potential. To address the

challenges of climate change, focused efforts are needed to harness the capabilities of OMICS technologies for yield improvement.

Since the Green Revolution of the 1960s, sustained efforts have more than doubled global rice production. However, the annual growth rate of rice production has steadily declined, even as the population in rice-consuming nations continues to grow at an annual rate of 1.8%. This discrepancy poses a significant challenge to ensuring food security. Over the past decade, rice production has struggled to keep up with population growth due to factors such as diminishing cultivable land, water scarcity, declining soil fertility, climate change, and the emergence of new biotypes of insect pests and pathogens. Addressing these challenges requires the integration of innovative tools with traditional methods to boost rice production and meet the growing demand. The availability of the complete rice genome sequence, combined with advancements in genomics, has paved the way for accelerated breeding programs aimed at enhancing yields and reducing production risks. High-throughput OMICS technologies provide a comprehensive platform for identifying QTLs and genes associated with important traits. Additionally, gene prospecting and allele mining complement breeding efforts through marker-assisted selection (MAS).

This research bulletin highlights significant progress made by ICAR-CRRI, Cuttack, Odisha, India in identifying QTLs and genes related to key traits, including tolerance to abiotic stresses, resistance to biotic stresses, seed and early seedling vigor, agro-morphological and yield-related traits, and grain nutritional qualities. Various markers such as SSR, cgSSR, SNP, STS, etc. have been effectively used to pinpoint QTLs and potential candidate genes for these traits. Genetic dissection of these traits has been achieved through genotyping and phenotyping bi-parental populations, including doubled haploids, recombinant inbred lines, backcross inbred lines, inter-cross lines, segregation populations, and association mapping panels. The mapping of QTLs and genes offers critical benefits, such as precise identification and quantification of loci linked to specific traits and insights into their contribution to phenotypic variation. Moreover, cloning QTLs and genes for target traits provides an in-depth understanding of underlying molecular mechanisms. These advancements have significant potential for application in marker-assisted selection, genomic selection, and forward breeding, enabling targeted improvement of desired traits in rice.

# CHAPTER 2. ABIOTIC STRESS TOLERANCE

## 2.1. Salinity tolerance

Rice is highly sensitive to salt stress during critical growth stages, including seed germination, seedling development, and reproduction (Zeng et al. 2001). The issue of salinity is exacerbated by poor-quality irrigation water and irregular climatic conditions that result in inadequate water supply. However, rice can adapt and thrive in saline environments due to soil flooding, which dilutes salt concentrations in the root zone. Globally, around 100 million hectares of land are affected by salinity, with a significant proportion located in South and Southeast Asia. In India, about 6.73 Mha of land is salinity-affected by salts encompassing sodicity, inland salinity, and coastal salinity. Salinity poses a significant challenge in coastal areas where rice is cultivated using irrigation systems with poor drainage.Rice production decrease up to 1 t $ha^{-1}$for every unit increase in irrigation water electrical conductivity (EC) beyond 2 dS $m^{-1}$ in a rice variety whose normal yield is 8 t $ha^{-1}$ under floodwater with EC < 2.0 dS $m^{-1}$ (Reddy et al. 2017). Improving riceproductivity in a saline environment is therefore essential to enhance profitability and ensure a consistent food supply. More than 638 QTLs related to salinity tolerance have been identified (Yang et al. 2020). Among them, *Saltol*,a major QTL associated with seedling-stage tolerance, explains about 40% of the phenotypic variance. This QTL was detected on chromosome 1 in the salt-tolerant landrace, Pokkali (Bonilla et al. 2002). Using this QTL, a few high-yielding varieties with seedling-stage salt tolerance have been developed and released for commercial cultivation in a saline environment (Thomson et al. 2010; Islam et al. 2012; Rahman et al. 2017). However, while *Saltol* and most of the reported QTLs are effective at the seedling stage, few significant QTLs have been identified for the reproductive stage tolerance. Hence, there is scope to explore and utilize other QTLs with greater potential, especially for reproductive stage tolerance (Jaisal et al. 2019). Chattopadhyay et al. (2018) developed, standardized, authenticated, and and validated a novel screening protocol to assess the tolerant donor, AC41585, and conducted precise phenotyping of the $BC_3F_5$ population derived from IR64 × AC41585.

Rice is sensitive to salinity stress especially at early seedling and reproductive stages (Zeng et al. 2001). Poor-quality irrigation water as well as intrusion of saline water due to sea level rise aggravate the salinity problem. Approximately 100 million ha of global land is affected by salinity in the south and southeast. In India, about 6.73 Mha of land is affected by salts encompassing sodicity, inland salinity, and coastal salinity. It is a significant problem in coastal areas where rice is cultivated using irrigation with lousy drainage systems. Rice production decreases up to 1 t $ha^{-1}$ per unit increase of irrigation water EC beyond 2 dS $m^{-1}$ in a rice variety whose normal yield is 8 t $ha^{-1}$ at flood water of EC < 2.0 dS m–1 (Reddy et al. 2017). Hence, improving rice productivity in a saline environment is a prerequisite for improving profitability and ensuring a regular food supply. More than 638 QTLs related to salinity tolerance have been identified (Yang et al. 2020). Initially, a major QTL, *Saltol*, associated with seedling stage tolerance and explaining about 40% of the phenotypic variance, was detected on chromosome 1 in the salt-tolerant landrace, Pokkali (Bonilla et al. 2002). Using this QTL, a few high-yielding varieties showing salt tolerance at the seedling stage have also been developed and released for commercial cultivation in a saline environment (Thomson et al. 2010; Islam et al. 2012; Rahman et al. 2017). Though *Saltol*

and most of the reported QTLs are effective at the seedling stage, hardly any significant QTLs have been identified for the reproductive stage tolerance. Hence, there is a scope to explore and utilize other QTLs with better potential, especially for reproductive stage tolerance (Jaisal et al. 2019). Chattopadhyay et al. (2018) standardized, authenticated, and employed a novel screening protocol to validate tolerant donor, AC41585, and precise phenotyping of the $BC_3F_5$ population derived from IR64 × AC41585.

### 2.1.1. Chlorophyll fluorescence traits influencing salt tolerance at the seedling stage

Pokalli is tolerant to both seedling and reproductive stage salinity and is used as a donor for developing high-yielding salt-tolerant varieties in Southeast Asian countries (Chattopadhyay et al. 2014**)**. To identify QTLs for traits related to salinity tolerance, Chattopadhyay et al. (2020a) developed 180 $BC_3F_4$ lines of the cross salinity-tolerant donor Pokalli (AC41585) and salinity-susceptible recurrent variety IR64 and evaluated them at the seedling stage in both salinized and non-salinized conditions in the wet seasons of 2015 and 2016. Salinity stress with the exact constituents of Yoshida culture solution in Styrofoam at EC 12 dS $m^{-1}$ was maintained till the experiment was over. Around 120 hypervariable SSRs out of 762 SSRs and gene-based markers were found to be polymorphic between parents, AC41585 and IR64, which were used for genotyping 180 $BC_3F_4$ lines. Thirty main effect additive QTLs along with more than 500 digenic epistatic QTLs were detected for Chl fluorescence/JIP-test parameters in rice. (Table 1a). These M-QTLs were located in almost all the chromosomes except chromosomes 6 and 8 and explained 2.66% to 21.53% PVE. Twenty-three main QTLs explained >10.0% PVE. The positional similarity of overlapping additive and additive × additive interaction QTLs indicated the substantial resemblance of the genetic basis of many JIP-test parameters, substantially a salinity tolerance in rice at the seedling stage. Twenty-three potential functional genes were identified inside these additive QTL regions and would be helpful for imparting greater photosynthetic potential in rice under salt stress (Table 1a).

### 2.1.2. Salinity tolerance at the reproductive stage

About 180 backcross-derived lines ($BC_3F_5$) using Pokkali (AC41585), a salt-tolerant donor for seedling and reproductive stages, and IR 64 as the recurrent parent were developed (Chattopadhyay et al. 2021a). These lines were evaluated in saline (EC = 8 dSm−1) and non-saline conditions during the wet seasons of 2014 and 2015. The evaluation began 14 days before booting and continued until 7 days before grain maturity, utilizing a modified phenotypic platform. Data were collected for eight yield-related traits. A total of 100 hyper-variable SSRs and 700 type I and II SSR markers were screened for polymorphism between the parents, of which 117 markers were polymorphic and subsequently used for genotyping of this population. Linkage analysis identified nine QTLs consistent across multiple environments for traits such as spikelet degeneration, potassium concentration in flag leaves, stress susceptibility index for grain yield (SSI-Grain), and spikelet sterility (SSI-STE). These QTLs were located on chromosomes 1, 2, 3, 4, and 11 explaining 17-42% PVE (Fig. 1). One digenic epistatic interaction was linked to the main effect QTL (*qSSI-STE-11-1*) over the environments (Table 1a). Additionally, genotype × environment interactions involving two additive QTLs, *qDEG-S-2-2* and *qSSI-STE-2-1*, positively influenced the phenotype during the reproductive stage. Probable functional genes encoding calmodulin-binding protein and

potassium transporter were predicted within the identified QTLs. The stable QTLs, associated markers, predicted candidate genes, and derived introgression lines offer valuable resources for future breeding programs aimed at enhancing salt tolerance at reproductive stage.

### 2.1.3. Salinity tolerance at the germination stage

Seed germination is the most sensitive stage to salinity. Toidentify markers associated with salt tolerance at the germination stage, 117 doubled haploid (DH) lines were derived from the $F_1$s of the cross between the salinity-tolerant donor Pokkali and the susceptible variety Savitri **(**Ngangkham et al. 2021). The117 DH lines, along with the parents, were evaluated in a 16 $dsm^{-1}$ NaCl solution, which exhibited variations in germination %, shoot length, and root length. The mean germination % of DHs varied from 3.3 to 90.0% with a mean of 53.29%. Bulked segregant analysis (BSA) of extreme bulks, containing 10 genotypes each, along with parents, was screened with 79 polymorphic markers. Three markers, RM283 (chromosome 1, 4.88 Mb), RM324 (chromosome 2, 11.38 Mb), and RM247 (chromosome 12, 3.18 Mb), were identified and found to be linked to salt tolerance at the germination stage (Fig. 2, Table 1a). Further, four prospective candidate genes, LOC_Os12g06560, LOC_Os12g06570, LOC_Os01g009550, and LOC_Os01g09560, were identified in the identified marker regions.These genes need further characterisation and validation to understand their role in tolerance to salinity at the germination stage.

## 2.2. Stagnant flooding tolerance

In lowland rice ecosystems, stagnant flooding or partial submergence severely affects key yield-related traits, leading to significant grain yield losses. The genetic mechanisms underlying this stress have not been extensively investigated. While a few studies have examined the agrophysiological responses of rice to stagnant flooding (e.g., Kato et al. 2014; Kuanar et al. 2017), reports on QTLs or genes linked to high yield under stagnant flooding conditions are scarce, with Singh et al. (2017) being a notable exception. Currently, the genetic basis of tolerance to stagnant flooding stress remains largely unknown. Rashpanjor (IC 575321), an Indian landrace, has been identified and utilized as a donor for tolerance to this stress.

Stagnant flooding harms grain yield and related traits, causing substantial yield reduction in lowland rice ecosystems. The rice landrace, Rashpanjor (IC 575321), from coastal areas of India, is tolerant to stagnant flooding and salinity. To identify QTLs associated with stagnant flooding tolerance, Chattopadhyay et al. (2021b) used the tolerant donor Rashpanjor and susceptible high-yielding variety Swarna to develop the RIL population. During the wet season of 2018, 180 recombinant inbred lines (RILs) were evaluated for yield and yield-related traits under rainfed, non-stressed, and stressed conditions (stagnant flooding with 45 ± 5 cm of standing water). Elongation ability (EL) was determined by measuring the difference in plant height before and after exposure to stress. Six agro-morphological and yield traits were recorded under both stress (S) and non-stress (NS) conditions. Additionally, elongation ability (EL), stress tolerance index (STI), and stress susceptibility index (SSI) were calculated for all traits. The RIL population and their parental lines were genotyped using genotyping-by-sequencing (GBS), which identified 1 million polymorphic SNPs between the parents. Of these, 153 high-quality homo-polymorphic SNPs were selected for mapping, leading to the identification of 17 putative

QTLs related to plant height, shoot elongation, panicle number, grain weight, and panicle length under both stress and non-stress conditions. Tolerance and susceptibility indexes for these traits were mapped to chromosomes 1, 3, 4, 5, 6, 10, 11, and 12, with phenotypic variance explained (PVE) ranging from 6.53% to 57.89% (Fig. 3, Table 1a). Two major QTL clusters were identified: one associated with the SSI for grain and panicle weight on chromosome 1, and another linked to plant height under non-stress conditions and the SSI for elongation ability on chromosome 3. Functional genes associated with non-synonymous SNPs or located within the QTL regions were predicted. These included genes involved in ethylene biosynthesis and auxin-responsive factors that facilitate adaptation to stagnant flooding. Other genes encoded transcription factors such as NAC domain-binding proteins, WRKY family genes, and MYB class factors, known for their roles in reactive oxygen species (ROS) scavenging and the production of metabolites that enhance tolerance to stagnant flooding.

## 2.3. Combined stress tolerance in Rashpunjar (IC 575321)

Two RILs and eight backcross-derived mapping populations were developed to identify robust QTLs for multi-environment and multi-background tolerance to combined stresses of salinity and waterlogging. Donors used for this purpose include Rashpunjar(IC 575321), AC39416a, Luna Suvarna, and Patnai,.Rashpunjar (IC 575321), a rice landrace tolerant to both salinity and waterlogging, was used to develop a recombinant inbred line (RIL) population from the cross Swarna/Rashpunjar. This population was evaluated for combined stress tolerance under conditions of stagnant flooding with saline water (EC = 4 dSm−1) (Chattopadhyay et al. 2020b). High-throughput DNA sequencing of 150 RILs and their parental lines was performed using the Illumina HiSeq platform, resulting in the identification of an average of 2.8 million SNPs in the parents and RILs. Approximately 150 high-quality polymorphic SNPs were selected for linkage mapping, covering a genetic map distance of 2134.9 cM across 12 rice chromosomes. Seven additive QTLs were identified for traits including Fv/Fm (maximum quantum yield of primary PSII photochemistry), Y-NO (quantum yield of non-regulated energy dissipation), and qL (coefficient of photochemical quenching), with phenotypic variance explained (PVE) ranging from 11.32% to 34.49% and LOD scores between 2.9 and 8.42 (Table 1a). Two pleiotropic QTLs associated with Fv/Fm and Y-NO were mapped to chromosomes 1 and 11.

## 2.4. Drought tolerance

Drought is one of the major limiting abiotic stresses for rice production in both rain-fed upland and lowland areas worldwide. More than half of the global rice area suffers from droughts of various intensities (Urmi. et al 2023). Drought tolerance traits are controlled by multiple QTLs. More than 1200 QTLs related to morphological, root, physiological, biochemical, and yield-related traits associated with drought tolerance have been identified (Du et al. 2023; Chen et al. 2023). However, several major QTLs (*qDTY1.1*, *qDTY1.2*, *qDTY1.3*, *qDTY2.1*, *qDTY2.2*, *qDTY2.3*, *qDTHI2.3*, *qDTY3.1*, *qDTY3.2*, *qDTY4.1*, *qDTY6.1*, *qDTY6.2*, *qDTY9.1*, *qDTY9.1A*, *qDTY10.1*, *qDTY10.2*, *qDTY12.1*, and *qPDL1.2*) associated with grain yield under the reproductive-stage drought stress have been reported, and some of them have been extensively utilized in molecular breeding programs (Dixit et al. 2014; Swamy et al 2017). Hence, the identification of QTLs/genes controlling reproductive stage drought tolerance in different rice genotypes and their deployment in rainfed rice improvement programs are very important.

### 2.4.1. Morpho-physiological and yield-related traits at the reproductive stage under drought conditions

To identify QTLs for morpho-physiological and grain yield-related traits at the reproductive stage under drought stress conditions, a RIL mapping population was developed from the cross between CR143-2-2 (drought-tolerant) and Krishnahamsa (drought-susceptible). CR143-2-2 is tolerant to both vegetative and reproductive stage drought stress conditions and was registered by the PGRC. The RIL population was evaluated for morpho-physiological traits such as leaf drying, leaf rolling, relative water content, cell membrane stability, proline content, biomass, and grain yield under reproductive stage drought stress conditions in a rain-out shelter during the *kharif* season of 2014 (Barik et al. 2018a). Seventy-seven out of 201 SSR markers showed polymorphism between parents (CR143-2-2 and Krishnahamsa). Twenty-one out of these 77 were found to be polymorphic between high and low bulks and used to genotype 190 RILs. Linkage analysis led to the identification of two QTLs, *qDFF1.1* and *qDFF6.1*, for days to 50% flowering on chromosomes 1 and 6, respectively. These QTLs are linked to RM3825 and RM527 and explained phenotypic variations of 8.80% and 4.77%, respectively (Fig. 4, Table1a). Only the phenotypic trait, days to 50% flowering (DFF) at reproductive stage stress, showed an association with chromosomes 1 and 6, and *qDFF1.1* was found to be novel against drought.

The same RIL mapping population was assessed for relative water content (RWC) under drought stress in a rain-out shelter during the *kharif* seasons of 2014 and 2015. Significant variation in RWC was observed among the RILs and their parent lines (Barik et al. 2018b). Genotyping of 190 RILs using 77 polymorphic markers, followed by linkage analysis through CIM, identified a QTL named *qRWC9.1*. This QTL, located within the RM316–RM257 marker interval on chromosome 9, exhibited a LOD score of 4.27 and explained 60.87% of the phenotypic variation (PVE) across both seasons under reproductive stage drought conditions (Fig. 5, Table 1a). This makes *qRWC9.1* a promising target for marker-assisted breeding to enhance drought tolerance at the reproductive stage in rice.

A total of 190 recombinant inbred lines (RILs) derived from the drought-tolerant parent CR 143-2-2 and the drought-susceptible parent Krishnahamsa (DRR Dhan 20) were evaluated for eleven morpho-physiological traits under reproductive stage drought stress during the *kharif* seasons of 2014 and 2015 (Barik et al. 2019). These traits included plant height (PH), leaf rolling (LR), leaf drying (LD), relative water content (RWC), cell membrane stability, percentage of panicle emergence, panicle length, spikelet fertility percentage, harvest index, 1000-grain weight, and grain yield. Out of 401 SSR markers, 77 were polymorphic between the parental lines and were further used to assess polymorphism between contrasting bulks. These polymorphic markers were then utilized to genotype the 190 RILs. Linkage analysis through CIM identified five consistent QTLs associated with leaf rolling (*qLR9.1*), leaf drying (*qLD9.1*), harvest index (*qHI9.1*), spikelet fertility (*qSF9.1*), and relative water content (*qRWC9.1*) (Fig. 6, Table 1a). Additionally, two non-allelic QTLs controlling leaf rolling (*qLR8.1*) and leaf drying (*qLD12.1*) were detected. Among these, four QTLs *qLR9.1*, *qLD9.1*, *qHI9.1*, and *qRWC9.1* were identified as novel and hold potential for marker-assisted breeding to enhance drought tolerance at the reproductive stage in rice.

A set of 190 RILs, derived from a cross between the drought-tolerant donor CR 143-2-2 and the drought-susceptible variety Krishnahamsa, were evaluated for ten physiological traits during the *kharif* seasons of 2014 and 2015 under reproductive stage drought stress

(Barik et al. 2020). The evaluated traits included flag leaf length, flag leaf width, relative chlorophyll content, chlorophyll a, chlorophyll b, chlorophyll a/b ratio, total chlorophyll, cell membrane stability, proline content, biomass, and grain yield (g/plant). A wide range of variation was observed across these traits.The RIL population was genotyped using the bulk-segregant analysis (BSA) approach. Out of 401 markers screened, 77 were polymorphic between the parents, and three showed polymorphism between contrasting bulks. Linkage analysis identified three novel QTLs*: *), *qCHLa1.1* (for chlorophyll a), *qRCC1.1* (for relative chlorophyll content, and *qPRO3.1* (for proline content), associated with the markers RM3825, RM6703, and RM517, respectively. These QTLs explained phenotypic variances of 12.47%, 64.5%, and 78.19%, respectively.Among these, *qPRO3.1* emerged as a highly significant QTL, with a LOD value of 13.93 and a phenotypic variance of 78.19%. It was located within the RM22–RM517 marker interval on chromosome 3. The QTL *qRCC1.1*, controlling relative chlorophyll content, was mapped to chromosome 1 under terminal drought stress conditions. Another QTL, *qCHLa1.1*, associated with chlorophyll a content, was positioned on chromosome 1, accounting for 64.5% of phenotypic variation (Fig. 7, Table 1a).These three novel QTLs *qRCC1.1*, *qCHLa1.1*, *and qPRO3.1*hold great potential for improving terminal drought stress tolerance in rice through marker-assisted breeding strategies.

## 2.5. High temperature stress tolerance

Heat stress is a significant challenge to rice production, impacting both vegetative growth and the reproductive stage. It disrupts normal pollination; leading to poor seed set and reduced grain quality during the reproductive phase (Krishnan et al. 2011). A projected global temperature rise of 1.5–2°C could increase food insecurity, leaving more people hungry by 2050 (Fujimori et al. 2018). Regions where temperatures exceed 37°C between mid-April and May are particularly vulnerable to heat stress, as this period often coincides with the crop's reproductive stage (Jha et al. 2014). Research on the effects of high-temperature stress on grain yield indicates a 10% reduction in rice grain yield for every 1°C increase in temperature. Among the various growth stages, the flowering stage is the most sensitive to heat stress (Jagadish et al., 2015). Temperatures above 35°C during flowering adversely impact anther dehiscence, pollination, and pollen germination, resulting in spikelet sterility and yield losses. Even brief exposure of spikelets to temperatures as low as 33.7°C during anthesis can cause sterility (Jagadish et al. 2007). Genotypes capable of maintaining high spikelet fertility under elevated temperatures provide valuable resources for developing heat-tolerant rice varieties. This can be achieved by associating phenotypes with the chromosomal regions responsible for tolerance. Over 175 QTLs have been identified for heat tolerance at various stages of rice growth, including the seedling and reproductive stages, using diverse mapping populations. However, the phenotypic effects of alleles associated with spikelet fertility under heat stress remain underexplored. Moreover, only a limited number of QTLs have been used in molecular breeding programs for enhancing heat tolerance in elite rice cultivars grown during the rabi season.

### 2.5.1. High temperature stress tolerance at the reproductive stage

A set of 240 breeding lines and landraces was evaluated for spikelet fertility under field conditions during the *rabi* season of 2014. To synchronize flowering with high-temperature stress during April-May 2014, four staggered sowings were conducted at 7-day intervals, starting in mid-January. Twenty-five-day-old seedlings were transplanted accordingly, with a

7-day gap between each planting. Spikelet fertility was recorded across all staggered plantings to measure tolerance to high-temperature stress. Based on spikelet fertility percentages under heat stress, the genotypes were broadly classified into four tolerance categories. From these 240 genotypes, an association panel of 59 germplasm lines was selected based on their spikelet fertility (SF) during the peak heat stress period of April-May in the 2014 dry season and screened under controlled conditions (Pradhan et al. 2016). Spikelet fertility among the tested genotypes ranged from 7.6% (AC11209) to 88.6% (N22), with susceptible lines averaging 15.3%. The selected genotypes were genotyped using two INDEL markers and 18 linked SSR markers. The population was divided into three sub-populations based on STRUCTURE analysis, suggesting that majority of landraces in each group shared a common primary ancestor, with a few showing admixture. AMOVA revealed genetic variation distributed as 25% between populations, 61% among individuals, and 14% within individuals. Association analysis using GLM and MLM models identified RM547 as significantly associated with spikelet fertility under high-temperature stress. Additional markers, including RM228, RM205, RM247, RM242, INDEL3, and RM314, were linked to traits indirectly influencing heat stress tolerance (Table 1b). All these markers could be valuable tools for marker-assisted breeding programs for improving high-temperature stress tolerance in rice.

### 2.5.2. Spikelet fertility under high-temperature stress conditions

An association panel consisting of 198 rice varieties was evaluated for heat stress-related traits, including days to 50% flowering (DFF), plant height, tiller number, panicle length, flag leaf dimensions (length and width), spikelet number, and heat stress susceptibility index during the 2016 dry season (Parameswaran et al. 2021). Of these, 67 selected varieties were further validated for heat tolerance through staggered sowing during the 2017 dry season to align flowering with high-temperature conditions. The genetic analysis revealed average spikelet sterility rates of 21.82% and 33.81% for the first and second sowings, respectively. A spikelet sterility increase of 7.93% was observed for every unit rise in maximum temperature during the flowering stage. All these 67 varieties were genotyped using nine markers linked to heat stress tolerance. Phylogenetic and substructure analysis based on a neighbour-joining approach identified four subpopulations. Marker-trait association analysis identified two SSR markers, RM205 and RM242, as significantly associated with spikelet sterility, explaining phenotypic variances of 7.7% and 6.0%, respectively (Table 1b). The presence of favourable alleles at these markers reduced spikelet sterility by 14.49% compared to the average sterility of 33.81%. Additionally, four rice varieties demonstrated spikelet sterility rates of less than 15%. The favorable alleles at RM205 (130 bp) and RM242 (180 bp) hold potential for enhancing heat stress tolerance in rice breeding programs.

## 2.6. Low temperature stress tolerance

Rice crops are highly sensitive to cold stress, particularly during the seedling and reproductive stages, leading to annual yield losses of 5-10%, which can occasionally rise to 20-40%. Globally, approximately 15 million hectares of rice fields across 24 countries are affected by cold weather. In India, about 4 million hectares, including *boro* and parts of the dry-season rice-growing areas, are severely affected by cold stress at the seedling stage. This stress delays plant growth, which is further aggravated by high temperatures during the flowering stage (Pradhan et al. 2016). The optimal temperature for rice germination and seedling development is 25-35°C, and temperatures below 15°C can disrupt various

physiological processes (Nakagahra et al. 1997). During the early vegetative stage, rice plants are particularly vulnerable to cold stress, leading to poor germination, slow initial growth, yellowing, withering, reduced tillering, stunted development, and ultimately lower yields (Zhang et al. 2005; Andaya and Tai 2006; Lou et al. 2007; Suh et al. 2010; Pradhan et al. 2015). The intensification of cold and heat stress due to global climate change has caused the affected regions in Asia to expand (Pradhan et al. 2015, 2016).

To address these challenges, it is essential to incorporate QTLs for enhancing tolerance to both low- and high-temperature stresses into high-yielding rice varieties suitable for specific environments. Over 490 QTLs were identified for cold tolerance at various growth stages, including germination, seedling, and reproductive phases (Sun et al. 2019; Gopinath 2020; Yang et al. 2020). However, pyramiding these QTLs is challenging due to the limited availability of robust molecular markers and highly tolerant donor varieties with multiple QTLs, which complicates marker-assisted breeding efforts.

### 2.6.1. Chilling stress tolerance at the seedling stage in *indica rice*

A panel of 304 *indica* rice germplasm accessions was selected and evaluated for chilling stress tolerance at the seedling stage under field conditions in December 2014. Various traits associated with cold tolerance were recorded. Sixty-six genotypes representing all six phenotypic classes were subjected to six low-temperature stress regimes for varying durations in a controlled phenotyping facility. These genotypes were genotyped using 58 SSR markers and 2 trait-linked markers. The analysis revealed 30% variation among populations and 70% among individuals (Pandit et al. 2017). STRUCTURE analysis categorized the genotypes into three sub-populations. A total of 130 marker-trait associations (MTAs) were identified through GLM, while 8 MTAs were detected using MLM across different temperature treatments (25°C, 15°C, 8°C, and 40°C) over 7, 14, and 21 days. Nineteen SSR markers (RM9, RM50, RM104, RM152, RM245, RM282, RM328, RM341, RM493, RM1211, RM1335, RM1347, RM2634, RM4112, RM3701, RM3602, RM5310, RM5704, and RM7179,) showed significant associations with chilling stress tolerance across the temperature range of 8°C to 40°C for durations of 7 to 21 days (Table 1b). The study revealed that among previously reported QTLs, only nine (*qSCT1a, qSCT2, qCTS-1b, qCTS-2, qCTS-3.1, qCTS6-1, qCTS9, qCTS11.1,* and *qCTS12.1*) demonstrated significant contributions to enhance cold tolerance at the seedling stage. These key QTLs need to be further validated and used in molecular breeding programs for the development of a chilling-tolerant variety.

## 2.7. Low phosphorous stress tolerance

Low phosphorus (P) availability poses a significant challenge to rice production. Only 20-30% of the applied phosphorus is accessible to plants, with the remainder converting into forms that are unavailable, contributing to water eutrophication. Phosphorus plays a vital role in plant growth and productivity, but its availability is restricted despite its abundance in the soil. This is because phosphorus primarily exists in organic, carbonate (alkaline), or oxide (acidic) forms, which are less accessible to plants. Given that rice is a major consumer of phosphorus, improving phosphorus-use efficiency (PUE) is essential for sustainable cultivation.

Globally, about 20 million hectares of rice-growing areas are affected by phosphorus deficiency, and 61.02% of Indian soils are low in phosphorus. Furthermore, global

commercial phosphate reserves are expected to be exhausted in 300 to 400 years. In India, approximately 90% of the phosphorus-based fertilizers and raw materials are imported, while the remaining 10% from domestic rock deposits is insufficient to meet the demand. Since the introduction of high-yielding varieties (HYVs), the use of phosphate fertilizers has increased significantly, rising from less than 1 million metric tonnes (0.132 million MT) in 1965-1966 to 6.86 million metric tonnes in 2017-2018 (https://www.faidelhi.org/statistics/statistical-database). This trend underscores the urgency of developing rice varieties that can efficiently utilize phosphorus to reduce dependency on phosphate fertilizers and ensure sustainable rice production.

### 2.7.1. Low phosphorus stress tolerance in cultivated and its wild relatives

A study involving 155 rice accessions, including 41 wild species, 37 landraces, and 77 elite cultivars collected from various Indian states, was conducted to examine phenotypic variability in morphometric and geometric traits under phosphorus (P) deficiency (Anandan et al. 2022). Based on phenotypic data and tolerance levels, a subset of 120 accessions was selected for an association panel. These accessions were genotyped using 78 low-P QTL-linked markers, including 13 specific to *Pup1*, to identify QTLs associated with traits under low-P conditions. Additionally, the symbiotic interaction of arbuscular mycorrhizal (AM) fungal colonization in *Oryza sativa*, *O. nivara*, and *O. rufipogon* was studied. A positive correlation was observed between the geometric trait of the top-view area and root traits, indicating the potential for non-destructive screening of genotypes under low-P conditions. Total root surface area emerged as a crucial trait for P uptake, with up to a 33% higher uptake attributed to root traits compared to mycorrhizal colonization. Phenotypic analysis of morphometric and geometric trait variations and their interactions highlighted the potential of these traits for selecting donor lines to enhance P-use efficiency. AMOVA results showed greater variability among individuals due to their representation across different *Oryza* species, with an NM value of 2.0, suggesting possible gene flow between populations. Cluster and population structure analyses grouped the 120 accessions into three primary clusters. A sub-cluster with superior-performing accessions contained a higher proportion of landraces (42.85%), while four *Pup1*-specific markers distinguished *O. rufipogon* accessions (33.3%). Nineteen QTLs were identified across four chromosomes (1, 8, 11, and 12). On chromosome 8, five QTLs (*qARD8.1*, *qLL8.1*, *qSL8.1*, *qTRP8.1*, and *qTSA8.1*) were linked to traits such as average root diameter, leaf length, shoot length, total root projected area, and total surface area. Similarly, five QTLs on chromosome 11 (*qNT11.1*, *qRDW11.3*, *qRV11.3*, *qSDW11.2*, and *qTDW11.2*) were associated with tiller number, root dry weight, root volume, shoot dry weight, and total dry weight. Additional QTLs included five on chromosome 12, four on chromosome 1, three on chromosome 3, and two (*qRL6.1* and *qTRL6.1*) on chromosome 6 (Table 1b). AM fungal root colonization (C%) was linked to two markers on chromosomes 2 and 4, with phenotypic variability ranging from 8.0% to 10.0%. Seven markers (RM259, RM297, RM30, RM6966, RM242, RM184, and PAP1) and six promising genotypes (IC459373, Chakhao Aumbi, AC100219, AC100062, Sekri, and Kumbhi Phou) were identified as valuable for improving rice in P-deficient conditions. These candidate genes and markers provide significant insights into the molecular and physiological mechanisms of P-use efficiency and offer opportunities for enhancing grain yield under low-P conditions.

### 2.7.2. Combined low phosphorus and nitrogen deficient conditions at the seedling stage

Rice adapts to nitrogen (N) and phosphorus (P) deficiencies by modifying root traits and exhibiting specific starvation responses. A panel of 142 rice genotypes was evaluated for nine root and shoot traits at the seedling stage (21 days after sowing) under low-N and low-P soil conditions in tank experiments conducted in the last week of July 2022. The panel was genotyped using the GBS approach, resulting in the identification of 22,000 high-quality SNPs, which were subsequently used for association analysis. A total of 24 statistically significant marker-trait associations were identified, explaining 10% to 79% of the phenotypic variation (Parameswaran et al. 2024). Under N- and P-deficient conditions, while root length increased by 10%, traits such as shoot length, number of leaves, shoot area, shoot dry weight, and root dry weight were reduced by 45%, 15%, 60%, 24%, and 45%, respectively. Candidate genes linked to root architecture remodeling (*Dro1* and *Sor1*), P and N uptake (*PTF1* and *PEPC*), and amino acid transport and homeostasis (*AAP7* and BCAT2) were identified within genomic regions associated with combined tolerance to low P and N conditions (Fig. 8, Table 1b). Additionally, three superior genotypes were identified for their ability to regulate multiple traits under nutrient-deficient conditions: ENT-62 (root area, shoot area, and shoot dry weight), ENT-303 (shoot dry weight and root dry weight), and ENT-32 (number of leaves and shoot area). This study provides a comprehensive characterization of seedling-stage trait responses in rice genotypes under low-N and low-P conditions, highlighting key genomic regions and QTLs associated with these traits. These findings offer valuable resources for breeding programs aimed at enhancing nitrogen and phosphorus use efficiency in nutrient-deficient soils.

## 2.8. Iron toxicity tolerance

Iron (Fe) toxicity is a major abiotic stress that severely affects rice production in numerous countries worldwide. Rice germplasm exhibits substantial genetic diversity in its tolerance to this stress. Pinpointing and mapping QTLs and genes linked to stress tolerance and integrating these traits into high-yielding rice varieties are essential steps for improving resilience to this challenge.

A panel of 352 germplasm lines, comprising landraces and released rice varieties, was assessed for tolerance to iron (Fe) toxicity in a Fe-toxicity plot during the 2016 wet season at the experimental fields of OUAT, Bhubaneswar, and CRRI, Cuttack, Odisha (Pawar et al. 2021). The landrace Dhusura and the variety Sebati served as the tolerant and susceptible checks, respectively. Soil Fe levels ranged between 225 and 250 ppm. From this panel, 119 genotypes representing different phenotypic groups based on Fe-toxicity tolerance were selected for *in vitro* evaluation under Fe-toxicity conditions, where leaf browning was measured. Substantial genetic variation for stress tolerance was observed among the genotypes in the panel. The population was classified into three genetic structure groups. Marker-trait association analysis using GLM and MLM models revealed significant associations of the leaf-browning index (LBI) with markers RM3, RM471, RM243, and RM590. Three novel QTLs related to Fe-toxicity tolerance *qFeTox4.3*, *qFeTox6.1*, and *qFeTox10.1* were identified. Additionally, a previously reported QTL within the marker interval C955-C885 on chromosome 1 was validated. The QTL *qFeTox6.1* was co-localized with grain Fe-biofortification QTLs, *qFe6.1* and *qFe6.2*, suggesting a shared pathway for Fe-

toxicity tolerance and Fe accumulation in rice grains. Similarly, *qFeTox10.1* was co-localized with *qFe10.1* (Table 1b). These Fe-toxicity tolerance QTLs identified in this study hold significant potential for marker-assisted breeding programs.

## 2.9. Herbicide tolerance

Weeds are a significant stress factor in both irrigated and upland ecosystems, leading to yield losses ranging from 18% to 48% (Rao et al. 2007). This stress not only reduces productivity but also escalates production costs due to increased labour requirements for weed management. In India, weed control expenses can constitute up to 30% of the total cultivation cost (Rao et al. 2015). Additionally, the issue of weedy rice has become increasingly prevalent in direct-seeded rice (DSR) areas in India. Herbicide-tolerant rice varieties offer an effective and sustainable solution to this challenge (Rathore et al. 2013). Herbicides primarily function by targeting and disrupting critical enzymes and proteins essential for the metabolic and physiological processes involved in plant growth and development. Common herbicides, such as sulfonylureas, glyphosate, synthetic auxins, imidazolinones, glufosinate, and phenylpyrazolines, exploit well-established herbicide tolerance (HT) mechanisms, which are widely utilized for developing herbicide-tolerant crops (Endo and Toki 2013).

### 2.9.1. Herbicide (Imazethapyr) tolerance in N22 mutant line, HTM-N22

About 100,000 EMS-mutagenized M2 plants of an upland rice variety, Nagina 22, were evaluated for herbicide tolerance under the DBT-funded network project, ‘Generation, Characterization, and use of EMS induced mutants of upland variety Nagina22 for functional genomics of rice”. A stable mutant, HTM-N22 (HTM), tolerant to the herbicide Imazethapyr, was identified (Shoba et al. 2017). Inheritance analysis of herbicide tolerance in a cross between Pusa 1656-10-61 and HTM showed that a single dominant gene governs this trait. To identify the causal gene for Imazethapyr tolerance, bulked segregant analysis (BSA) was followed using microsatellite markers flanking the three putative candidate genes, viz., an Acetolactate Synthase (ALS) on chromosome 6 and two Acetohydroxy Acid Synthase (AHAS) genes, one on chromosome 2 and another on chromosome 4. RM 6844 on chromosome 2 located 0.16 Mbp upstream of AHAS (LOC_Os02g30630), co-segregated with herbicide tolerance (Table 2a).Cloning and sequencing of AHAS (LOC_Os02g30630) from the wild type, N22, and the mutant HTM and their comparison with reference The Nipponbare sequence revealed several single nucleotide polymorphisms (SNPs) in the mutant.Eight SNPs resulted in non-synonymous mutations. The mutation, S627D, was a previously reported as conferringimidazolinone tolerance in rice. Of the novel ones, G152E was found to alter the hydrophobicity and abolish an N myristoylation site in the HTM compared to the WT, which is useful for MAS breeding programs.

# CHAPTER 3. BIOTIC STRESS RESISTANCE

## 3.1. Sheath blight disease resistance

Sheath blight disease of rice causes substantial crop losses; causing yield losses ranging from 5% to 69% (Singh et al. 2004). Most of the rice varieties are susceptible to the ShB disease. Only a limited number of moderate-resistant sources are available. Significant resistance genes have not been identified in rice varieties. However, QTLs with minor and significant effects have been identified in various rice germplasms. More than 200 QTLs associated with sheath blight resistance have been identified using different mapping populations (Zarbafi and Ham 2019). QTLs, namely, *qSM9-2* and *qSB12-2*, have been introgressed from Teqing into Lemont through the MAS approach (Wang et al. 2012). Similarly, three ShB resistance QTLs (*qSBR11-1TE*, *qSBR11-2TE*, and *qSBR7-1TE*) have been transferred into Pusa 6B, the maintainer line of aromatic hybrid rice Pusa RH10. In addition, *qSBR11-1TE* has been transferred into Improved Pusa Basmati1 from Tetep through MABC. Due to the unavailability of any major QTL or gene governing ShB resistance, multiple QTLs from different backgrounds are required to be pyramided, which can also additionally show positive QTL and QTL interaction.

### 3.1.1. Sheath blight disease resistance in CR 1014

To identify QTLs and candidate genes in the sheath blight-resistant genotype, CR 1014, Bal et al. (2020) developed 654 F2 progenies from the cross between Swarna-Sub1(susceptible) and CR 1014 (resistant) and phenotyped them under field conditions during the Kharif seasons of 2015–2018 against sheath blight. 216 $F_2$ plants were genotyped using 120 polymorphic SSR markers. Linkage analysis identified three QTLs (*qShB-1.1*, *qShB-1.2*, and *qShB-1.3*) on chromosome1 in the moderately resistant genotype CR 1014. Only the major QTL *qShB-1.1* was recorded consistently in the $F_5$ generation of the same cross and the $F_4$ generation of an alternative mapping population of Tapaswini (susceptible) and CR 1014(Fig. 9). Two putative candidate genes,a leucine-rich repeat (LRR) motif-containing gene (LOC_Os01g65650) and a chitin-inducible gibberellin-responsive protein-coding non-LRR gene (LOC_Os01g65900), located within the *qShB-1.1* QTL region,were identified (Table 2a). A 27.8% reduction in relative lesion height was observed in near-isogenic lines (NILs) of Swarna-Sub1 carrying the QTL region from CR 1014.

To identify QTLs and candidate genes in the sheath blight-resistant genotype, CR 1014, Bal et al. (2020) developed 654 $F_2$ progenies from the cross between Swarna-Sub1(susceptible) and CR 1014 (resistant) and phenotyped them under field conditions during the *Kharif* seasons of 2015–2018 against sheath blight. 216 $F_2$ plants were genotyped using 120 polymorphic SSR markers. Linkage analysis identified three QTLs (*qShB-1.1*, *qShB-1.2*, and *qShB-1.3*) on chromosome1 in CR 1014. Only the major QTL *qShB-1.1* was recorded consistently in the $F_5$generation of the same cross and the $F_4$ generation of an another mapping population derived from Tapaswini (susceptible) and CR 1014 (Fig. 9). Two putative candidate genes, a leucine-rich repeat (LRR) motif-containing gene (*LOC_Os01g65650*) and a chitin-inducible gibberellin-responsive protein-coding non-LRR gene (*LOC_Os01g65900*), located within the *qShB-1.1* QTL region, were identified (Table 2a). A reduction of 27.8% in relative lesion height was observed in a near-isogenic lines (NILs) of Swarna-Sub1 carrying the QTL region from CR 1014.

## 3.2. Bakanae disease resistance in Thavalakannan

Bakanae disease caused by *Fusarium fujikuroi*is an emerging seed-borne disease in northeastern India. It also causes significant yield losses in basmati rice in northwestern states. The disease causes poor tillering in seedlings, lanky and elongated seedlings, stunted growth, seedling mortality, and poor grain-filling. A few QTLs have been identified in *japonica* and basmati rice cultivars (Volante et al. 2017). None of the QTLs has been identified in non-basmati *indica* rice cultivars.

To identify QTLs for bakanae disease resistance, a bi-parental RIL population was developed between a resistant *indica* cultivar, Thavalakannan, and a susceptible variety, Pooja (Khan et al. 2024). The population was evaluated against a highly virulent Gerua F3 strain of the *Fusarium fujikuroi* pathogen, which showed wide variations. Genotyping of 148 RILs with 103 polymorphic SSR markers and linkage analysis identified a main QTL, *qBK5.1*, on chromosome 5 between RM249 and RM289, explaining 8.97% of the phenotypic variation (Fig. 10). Three genes associated with gibberellic acid biosynthesis pathways were identified, indicating the significance of the QTL identified. One among three genes *Os05g0518800* is known for its function of biotic stress tolerance (Table 2a). Furthermore, seven pairs of QTLs interactions favouring resistance were identified on different chromosomes. Identified QTLs in the study could be useful in molecular breeding programs aimed at developing bakanae-resistant rice varieties.

## 3.3. Gall midge resistance

The Asian rice gall midge, *Orseolia oryzae* Wood-Mason, is a major pest of irrigated and shallow-water rice ecosystems in South and Southeast Asia, causing an annual yield loss of 28-35%. In India, gall midge has been a significant due to the presence of five distinct biotypes across various regions. Chemical and cultural control measures are in effective because of the internal feeding habits of the pest. Many resistant varieties have been developed using resistant gall midge donors of gall midge and cultivated extensively. The cultivated germplasm has ample sources of resistance; however, constant change in the virulence of the insect has resulted in the breakdown of resistance in cultivars. Pyramiding two or more non-allelic resistance genes in a single cultivar can increase the durability of resistance. Initially, five significant gall midge resistance genes (*Gm1, Gm2, gm3, Gm4, Gm5)* was identified which wasfollowed by the identification of another seven resistance genes (*Gm6, Gm7, Gm8, Gm9, Gm10, Gm11*, and *Gm12) (*Bentur et al. 2016; Leelagud et al. 2020). However, some of these markers are genotype-specific and fail to generate polymorphism for selecting desired genotypes in a segregating progeny, limiting their use in molecular breeding programs. Therefore, a study was designed for identifying new resistance sources and more robust markers for use in marker-assisted breeding programs.

### 3.3.1. Gall midge resistance in ARC5984 and PTB10

At ICAR-CRRI, Cuttack several germplasm were collected from different parts of India and screened for gall midge resistance. Some of these resistant germplasms were used to develop gall midge-resistant varieties using conventional breeding approaches. To identify the gall midge resistance gene/linked marker**,** ARC5984, a collection from Assam, known to harbour a dominant gall midge resistance gene, *Gm5*, against biotypes 1, 2, and 5, a RIL mapping population was developed from the cross between the resistant donor ARC 5984 and the

susceptible cultivar, TN1 (Lima et al. 2007)**.** Phenotyping of 120 RILs against gall midge biotype 2 identified 58 resistant, 56 susceptible, and 6 segregating lines, confirming the presence of a single dominant gene in ARC5984. The bulked segregant analysis (BSA) approach was used to identify markers linked to gene-controlling gall midge resistance in the resistant rice cultivar ARC5984. Homozygous resistant and susceptible bulks of 15 RILs each and parents were screened with 120 RAPD markers. Five RAPD primers (OPB14, OPE1, OPP9, OPQ, and OPR19) amplified polymorphic fragments between the bulks and the parents. Amplification of individual RILs with these primers, followed by segregation analysis, indicated that $OPQ_{1150}$ was linked to susceptibility at a distance of 30 cM (Table 2a).

PTB10, a landrace from Kerala, harbours a single dominant gall midge resistance gene (*Gm4*), which provides resistance against gall midge biotypes 1, 2, 3, and 4 (Sahu et al. 2004). Abhaya, a derivative of PTB10, was found to contain the gall midge resistance gene, *Gm4* (Srivastava et al. 1994). *Gm4* was mapped on chromosome 8 in Abhaya using AFLP and RFLP markers (Mohan et al. 1997; Nair et al. 1996). However, the linked markers were not useful for the MAS breeding program. Hence, to fine map *Gm4*, a recombinant inbred line (RIL) population was developed from the cross TN1 (susceptible) and resistant donor PTB10 (Nanda et al. 2010)**.** The BSA followed by a co-segregation approach to identify closer flanking markers linked to *Gm4*. Out of 75, two closer flanking microsatellite markers, RM22550 and RM547, were found to be linked to the gall midge resistance gene in PTB10 on the short arm of rice chromosome 8 and were identified at a distance of 0.9 and 1.9 cM, respectively (Fig. 11, Table 2a). These markers were evaluated for allelic diversity and their potential application in MAS breeding programs involving a set of gall midge donors and elite rice cultivars. The amplification of these markers in gall midge-resistant and susceptible cultivars demonstrated their utility in MAS for developing gall midge-resistant varieties. A MAS kit that aids in selecting appropriate combinations of markers depending on the donors and recipient elite lines has been developed. *Gm4* from Abhaya was introgressed into high-yielding varieties, Kavya, Lalat, and Tapaswini, using these microsatellite markers.

### 3.3.2. Gall midge resistance in association-mapping population

An association panel of 200 diverse rice genotypes, along with a resistant check (Abhaya) and a susceptible check (TN1), was screened against GM biotype-2 and genotyped using 13 reported markers linked to gall midge resistance genes (Sahu et al. 2023). Positive skewness and a platykurtic distribution of gall midge response scores suggested the inheritance of gall midge resistance within the population. Among the markers gm3del3 explained the most genetic variation, followed by RM28574, while RM22709 explained the least variation. Marker-trait association analysis, using a single marker-trait linear regression approach, was performed to identify markers associated with previously reported gall midge resistance genes. Only one marker, RM17480, located on chromosome 4 was found to be significantly associated with the *gm3* gene (Table 2b). The 200 bp allele of this marker was associated with susceptibility, whereas the 250 bp allele was linked to resistance. The allelic effects of the markers showed a significant correlation with the phenotypic variation of gall midge resistance. Four prospective candidate genes (*LOC_Os04g02640*, *LOC _Os04g30760*, *LOC _Os04g40570*, *LOC _Os04g34600*, and *LOC _Os04g04230*) were identified in the marker region, which contributes to stress response mechanisms in rice plants. The gene locus *LOC _Os04g30760* is involved in fatty acid synthesis, while *LOC_Os04g40570* and *LOC*

_*Os04g02640* are implicated in various metabolic processes, epicuticular wax secretions, and ATP-binding cassette (ABC) transportation. The gene *Loc_Os04g34600* is involved in abscisic acid stress, and the up-regulation of these genes may contribute to susceptibility to GM attack. In contrast, *LOC _Os04g04230* is involved in ABA biosynthesis, regulating multi-abiotic stress tolerance in rice. $RM17480_{200\text{-}250}$ marker would be useful in molecular breeding programs aimed at developing all midge-resistant varieties.

## 3.4. Brown planthopper resistance

The brown planthopper (*Nilaparvata lugens* Stål) is a highly destructive pest in rice-growing areas of Asia and Southeast Asia. Both the adult and nymph stages feed on rice sheaths by extracting sap from the phloem. Mild infestations lead to yellowing of leaves, stunted growth, reduced plant height, lower vigour, fewer productive tillers, and poor grain filling. Severe infestations can result in complete plant drying and death, a condition known as "hopperburn." In addition to direct damage, the brown planthopper also transmits rice tungro, grassy stunt, and rugged stunt viruses, causing further harm to rice crops. The frequency and severity of outbreaks have risen since the 1990s, mainly due to year-round rice cultivation and increased use of fertilizers and insecticides. One of the most effective strategies to mitigate brown planthopper damage is the use of resistant rice varieties. Systematic screening of germplasm has led to the identification of several donor varieties, which have been used to develop BPH-resistant varieties and to pinpoint genes/QTLs associated with resistance. Over 46 genes and numerous QTLs for brown planthopper resistance have been identified through different mapping populations in both cultivated and wild rice species. Several major QTLs/genes have been introduced into elite susceptible cultivars, resulting in the release of resistant varieties. Additionally, 17 QTLs/genes have been cloned to better understand the molecular mechanisms behind resistance. Identifying QTLs with different resistance mechanisms and incorporating them into elite cultivars is essential for preventing the breakdown of resistance and ensuring sustainable rice production.

### 3.4.1. BPH resistance in the rice landrace, Salkathi

Salkathi, a rice landrace from Western Odisha, demonstrates strong resistance to brown planthopper (BPH), as confirmed by trials at CRRI, Cuttack, and AICRIP Planthopper Screening in 2003 and 2004. To identify QTLs for BPH resistance, a recombinant inbred line (RIL) mapping population was created by crossing Salkathi (resistant) with TN1 (susceptible) and screening for BPH resistance. The segregation pattern suggested the involvement of two major epistatic QTLs in Salkathi. Through microsatellite markers and linkage analysis, two BPH resistance QTLs, *qBph4.3* and *qBph4.4*, were mapped to the short arm of chromosome 4, with LOD scores of 34.2 and 4.61, respectively, located between the markers RM551-RM518 and RM335-RM5633 (Mohanty et al. 2017). These QTLs explained 37.02% and 7.1% of the phenotypic variance, while their epistatic interaction accounted for an additional 69.01% with an LOD score of 6.93 (Table 2a). High-density SNP genotyping using the 40K Affymetrix SNP chip further refined the localization of these QTLs to the regions 0.62-1.39 Mb and 18.63-23.85 Mb on chromosome 4 (Fig. 12). Salkathi has been successfully utilized to transfer BPH resistance into two elite rice cultivars, Pusa 44 and Samba Mahsuri, through conventional breeding methods.The presence of *qBph4.3* and *qBph4.4* was validated in resistant breeding lines, CR3008-2 (Pusa 44/Salkathi) and CR3005-230-5 (Samba Mahsuri/Salkathi) and the $IC_1F_5$ population derived from Naveen (susceptible) and CR3006-8-2 (resistant). Ten putative candidate genes were identified

within these QTL regions. Expression analysis conducted on resistant (Salkathi and CR3006-8-2), susceptible (TN1 and Naveen) parents, and $IC_1F_5$ lines with varying levels of resistance highlighted seven potential candidate genes: NBS-LRR, ZOS4-01-C2H2 zinc finger protein, leucine-rich repeat family protein, disease resistance protein RPM1, leucine-rich repeat family protein, serine/threonine-protein kinase receptor, and serine-threonine protein kinase. Validation of these genes in NILs containing one or both QTLs was taken further.

### 3.4.2. BPH resistance in the farmers' varieties of Odisha

A total of 600 farmer's varieties (FVs) from various regions of Odisha were screened for resistance to brown planthopper (BPH). From these, 104 varieties were selected and genotyped with 87 markers linked to 34 BPH-resistance genes (Anant et al. 2021**).**Genetic diversity and population structure analysis grouped these varieties into three main clusters. Principal Component Analysis (PCA)revealed distinct distribution patterns for resistant and moderately resistant varieties. The analysis of molecular variance indicated that most of the genetic diversity (83%) was found within populations, while only(17%) was found between populations. Association analysis identified eight markers (RM222, RM6997, RM17006, RM6308, RM463, RM28561, RM586, RM309, RM5479) linked to nine BPH resistance genes (*BPH30, BPH6, BPH33, bph19, bph2, BPH21, bph4, BPH26, BPH25)* that were consistently associated with four phenotypic traits: honeydew excretion, nymphal survival, percent damage, and feeding marks (Table 2b). The BPH-resistant varieties carrying single BPH resistance gene often became susceptible within a few years of release. Therefore, the BPH-resistance genes identified in farmers' varieties hold the potential for introgression into elite susceptible varieties, enabling durable resistance against BPH.

### 3.4.3. BPH resistance in the pigmented and indigenous rice

An association panel of 268 rice landraces, comprising 208 pigmented rice genotypes, 27 indigenous lines, 22 known differentials, popular varieties, and one each of resistant and susceptible checks, was screened for resistance against brown planthopper (BPH). Four pigmented rice genotypes (Kakharua, Chadaiguda Uttarbang local-3, and Manipuri black) and 8 indigenous lines (IC-426148, IC-426139, IC-256515, IC-426149, IC-273558, IC-256545, IC-346890, and IC-426126), exhibited a strong resistance against BPH (Babu et al. 2022). Based on the screening results, 96 landraces were selected for genotyping using 93 molecular markers linked to 26 different BPH resistance genes. Cluster and population structure analyses grouped the genotypes into three major clusters, with the resistant genotypes forming separate groups. Principal coordinate analysis supported the findings of the cluster analysis. Marker-trait association identified five markers RM7 (*Qbph*3), RM5633 (*Qbph4.4*), RM28449 (*Bph17*), RM28472 (*Bph18*), and RM19291 (*Bph30*) as significantly associated with phenotypic traits such as nymphal survival, feeding marks, percent damage, and honeydew excretion (Table 2b). *Qbph3, Bph30,* and *Bph18* were strongly linked to all four traits. Three markers RM28449 (*Bph17*), RM28472 (*Bph18*), and RM19291 (*Bph30*) were common in both GLM and MLM analyses. These identified resistance genes in rice landraces will serve as valuable sources for developing durable BPH-resistant varieties. Manipuri black rice, known for its high nutritional value, with higher vitamin and mineral content than white and brown rice, could be particularly useful for transferring both BPH resistance genes and nutritional qualities into elite rice cultivars.

### 3.4.4. BPH resistance in *indica* rice

An association panel of 191 rice cultivars was screened for resistance against BPH during the wet season of 2021 and the *rabi* season of 2022. These cultivars were further genotyped with 23 SSR markers specific to BPH resistance genes (Meher et al. 2024**)**. Cluster and population structure analysis grouped the cultivars into three clusters, with resistant cultivars forming a distinct group. Principal coordinate analysis further supported the same categorization of resistant genotypes, moderately resistant genotypes, and susceptible genotypes. Genetic variation analysis revealed 90% variation within populations and 10% between populations. Marker-trait association identified six SSR markers, RM7102 (*Bph1*), RM401 (*bph4*), RM314 (*Bph6*), RM16999 (*Bph6*), RM6732 (*Bph15*), and RM7 (*QBph3*). These markers were strongly associated with key phenotypic parameters, including honeydew excretion, percent damage, feeding mark, and nymphal survival (Table 2b). The resistance genes and QTLs identified in these cultivars could help in the marker-assisted rice variety development against BPH.

## 3.5. Resistance to stored grain pest, angoumois grain moth

The Angoumois grain moth (*Sitotroga cerealella* Olivier) is a rapidly spreading pest of stored cereals in India, also affecting other cereal crops like sorghum, maize, and wheat. The moth causes grain weight loss, reduced nutritional quality, increased contamination, and renders the product unsafe for consumption. Kajal et al. (2024) conducted association mapping to identify QTLs for resistance to the Angoumois grain moth in an association panel of 80 rice varieties released between 1970 and 2010, using gene 39-derived SSR markers. The screening revealed that 38 varieties exhibited moderate resistance, with a susceptibility index between 3 and 7. In contrast, 37 varieties were found to be susceptible, with a susceptibility index ranging from 7 to 10, while the remaining 5 varieties were highly susceptible, with a susceptibility index greater than 10. Three major subpopulations were identified, and principal component analysis (PCA) explained 16%, 9%, and 6% of the total variation. Two cgSSR markers, M8 and M16, associated with genes SDG725 and FLO2 on chromosomes 2 and 4, respectively, were linked to resistance traits against S. cerealella infestation (Table 2b). These two marker-trait associations (MTAs) explained 18% and 13% of the phenotypic variation, respectively, and are novel. This is the first report of such an association, which could help in the development of rice cultivars resistant to the Angoumois grain moth.

# CHAPTER 4: SEED AND EARLY SEEDLING VIGOUR TRAITS

Seed vigour is one of the essential traits of good seed quality, which directly influences crop productivity by ensuring uniformity in seed germination, seedling growth, establishment of seedlings in the field, and the ability to withstand unfavourable environmental conditions (Raijou et al. 2012; Ventura et al. 2014). It is also equally crucial for direct seeding, as it enhances early crop establishment and produces vigorous seedlings that can compete with weeds (Yamauchi et al. 1996; Mahender et al. 2015). Improving seed vigour in rice remains a breeding challenge, as it is essential for enhancing yield and improving crop resilience against adverse effects of climate change and biotic impediments to crop yields (Daniel OI 2017). Seed vigour is governed by different physiological and biochemical parameters controlled by many quantitative trait loci. Early seedling vigour (ESV) is a critical trait for direct seeding, particularly in competing with weeds, and is vital in both upland and lowland rice ecosystems. While irrigated rice varieties are high-yielding, they generally exhibit lower early vigour compared to rainfed and upland varieties. In rice-growing regions of South and Southeast Asia, the ESV traits have been utilized in the development of rainfed upland cultivars, but its application in rainfed lowland and irrigated systems has been limited, primarily due to the focus on selecting traits for higher grain yields, resulting in a narrow genetic base. Enhancing ESV, which contributes to quicker establishment, stress tolerance, and competitiveness against weeds, presents a promising approach for improving direct-seeded rice (DSR) systems, which are increasingly favored for their reduced water and labour requirements compared to traditional transplanting methods. To improve ESV in rice, it is essential to explore the existing genetic variation, examine trait correlations, and identify QTLs and genes from diverse genetic backgrounds.

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methods. To improve ESV in rice, it is essential to explore the existing genetic variation, examine trait correlations, and identify QTLs and genes from diverse genetic backgrounds.

## 4.1. Early seedling vigour (ESV) traits

A panel of 629 rice genotypes, consisting of 25 tropical *japonica*, 57 *indica* landraces, 127 breeding lines, and 427 ARC, was selected and grown during the dry season of 2013 in an upland environment. Observations on early seedling vigour traits, including root length and weight, shoot length and weight, leaf length and width, number of leaves, and vigour index, were recorded on the 14$^{th}$, 28$^{th}$, and 56$^{th}$ days after sowing (DAS) under direct-seeded aerobic conditions. From the 629 genotypes, 96 were selected using principal component (PCA) and discriminant function analyses (Anandan et al. 2016). These 96 rice lines were genotyped using 39 polymorphic SSR markers. Population structure analysis grouped the accessions into two distinct populations, while the unrooted tree classified the genotypes into three clusters. Both model-based and structure-based methods successfully differentiated early vigour genotypes from non-early vigour ones. Association analysis revealed 16 and 10 marker-trait associations (MTAs) with ESV traits using GLM and MLM approaches, respectively, explaining phenotypic variances ranging from 4-10% (Table 3). The marker RM341 on chromosome 2 was associated with multiple traits, including shoot dry weight at 28 DAS and vigour index at both 14 and 28 DAS.

The early seedling vigour (ESV) diversity in rice can be explored by screening natural populations and conducting genome-wide association studies (GWAS) to identify the genomic loci involved. Previous GWAS studies for seedling vigour have been carried out using various rice diversity panels, such as the 744 accessions from the 3000 Rice Genome Panel (3K-RGP), Rice Diversity Panels 1 and 2, and 200 *indica* accessions from China. The *aus* varietal group, which includes aus, boro, ashina, and rayada ecotypes, is known for its unique stress tolerance traits and is valuable for rice breeding. However, the agro-morphological diversity and genetic control of yield traits in *aus* rice are not well understood. In a study by Basha et al. (2024), genetic variation in seven ESV traits, days to 50% flowering, and grain yield was examined in a panel of 181 *aus* accessions under field conditions. Significant variations were observed for the traits studied, with vegetative vigour showing strong correlations with most traits, including grain yield, indicating its influence on overall plant performance. Using 918,863 single nucleotide polymorphism (SNP) markers for GWAS, 14 significant QTLs were identified, including seven novel ones, associated with vegetative vigour, average growth rate, and seedling biomass. Potential candidate genes, such as *NCKAP1*, *OsPDR1*, and *OsSAUR10*, involved in jasmonic acid biosynthesis, ABA signalling, and brassinosteroid pathways, were found to be linked to ESV regulation (Table 3).

## 4.2. Physio-biochemical traits related to seed vigour

An association panel of 120 diverse rice genotypes, collected from Assam, Madhya Pradesh, Kerala, Odisha, and Manipur, was selected and grown during the wet season of 2018 and 2019. The seeds were harvested, dried, stored for three months, and then evaluated for 18 physio-biochemical traits, including chlorophyll a, chlorophyll b, total chlorophyll, carotenoids, total anthocyanin content, gamma-oryzanols, total phenolic content, superoxide dismutase, catalase, peroxidase, total soluble sugar, total protein, seed vigour index-I (SVI-I), seed vigour index-II (SVI-II), moisture content, starch, amylose, and total flavonoid content.

A mini-core set of 48 genotypes was selected from the 120, representing all phenotypic groups for each of the 18 traits studied, and genotyped using 50 SSR markers (Sahoo et al. 2020). Significant genetic variation was observed in traits such as chlorophyll a, chlorophyll b, total chlorophyll, carotenoids, total anthocyanin content, gamma-oryzanols, total phenolic content, superoxide dismutase, catalase, guaiacol peroxidase, total soluble sugar, total protein, seed vigour index-I, and seed vigour index-II. A strong positive correlation was found between seed vigour index-II and amylose, total anthocyanin, catalase, phenolic, and total flavonoid content, while a negative correlation was observed with gamma-oryzanol content. The panel population exhibited three genetic structure groups. Markers RM222, RM225, and RM547 were associated with total phenolic content, while RM582, RM337, RM223, RM3701, RM7364, RM547, and RM229 were linked to total flavonoid content, showing high phenotypic variation explained (PVE) values (Table 3). The association of total flavonoids with marker RM7364, located on chromosome 8, was previously reported. The other associated markers are novel and could be useful for enhancing seed vigour in rice.

A panel of 48 genotypes were selected from 120 diverse rice accessions collected from Assam, Madhya Pradesh, Kerala, Odisha, and Manipur (Sanghamitra et al. 2021). These genotypes were grown during the wet seasons of 2018 and 2019 and assessed for 11 seed vigour physiological traits: rate of imbibition (RI), seed germination (SG), germination index (GI), seedling dry weight (SDW), vigour index I (SVI-I), seed vigour index II (SVI-II), rate of root growth (RRG), rate of shoot growth (RSG), absolute growth rate (AGR), relative growth rate (RGR), and mean germination time (MGT). Significant variation was observed among the accessions for these traits. The accessions were genotyped using 50 microsatellite markers. STRUCTURE analysis classified these genotypes into two sub-groups. Both GLM and MLM analyses identified strong associations between the markers RM256, RM25181, RM6547, RM328, and RM201 with rate of root growth, RM440 and RM223 with seedling dry weight, RM20, RM13335, and RM216 with rate of shoot growth, RM20A and RM201 with absolute growth rate, RM167 with seed vigour index-I, and RM7364 and RM235 with seed vigour index-II (Table 3). These associated markers explained up to 34.84% of the phenotypic variance, offering valuable insights for improving seed vigour in rice.

## 4.3. Seed vigour index, root growth parameters and germination percentage

A panel of 274 rice landraces from five states, Assam, Madhya Pradesh, Kerala, Odisha, and Manipur, was selected and grown during the wet season of 2018. After harvesting, the seeds were stored for three months to overcome seed dormancy before being evaluated for six seedling growth parameters: rate of root growth, rate of plumule elongation, root-shoot ratio, germination percentage, seed vigour index I, and seed vigour index II (Barik et al. 2022). Based on these parameters, a panel of 120 landraces representing all six phenotypic groups was developed, grown during the wet seasons of 2019 and 2020, and evaluated for the same traits. The population exhibited wide variations for these traits. The landraces were classified into three subpopulations, with each subpopulation corresponding to the six physiological traits. Five previously reported QTLs were identified: *qGP8.1* for germination percentage (GP), *qRSR11.1* for root-shoot ratio (RSR), and *qSVII2.1*, *qSVII6.1*, and *qSVII6.2* for seed vigour index II (SVII). Additionally, 13 novel QTLs were discovered: *qGP6.2* and *qGP6.3* for germination percentage, *qSVI11.1* for seed vigour index I, *qSVI11.1* and *qSVI12.1* for seed vigour index II, *qRRG10.1*, *qRRG8.1*, *qRRG8.2*, *qRRG6.1*, and *qRRG4.1* for rate of root

growth (RRG), and *qRSR2.1*, *qRSR3.1*, and *qRSR5.1* for root-shoot ratio. Co-localization of QTLs, such as *qGP8.1* and *qSVI8.1* for GP and SVI-I, *qGP6.2* and *qRRG6.1* for GP and RRG, and *qSVI11.1* and *qRSR11.1* for SVI and RSR, was also detected (Fig. 13, Table 3). The identified QTLs could be valuable for improving seed vigour traits in rice.

## 4.4. Germination rate and early seedling growth traits

A panel of 278 germplasm lines, collected from the states of Assam, Madhya Pradesh (MP, Kerala, Odisha, and Manipur, was selected and raised during the wet season of 2019. The freshly harvested seeds were dried and stored for three months to overcome seed dormancy and then used for estimation of germination rate and early seedling growth parameters such as mean germination rate (MGR), shoot growth (RSG), absolute growth rate (AGR), and relative growth rate (RGR). The frequency distributions of the 278 germplasm lines based on the mean phenotypic values, were broadly classified into five groups. An association panel of 124 genotypes was shortlisted from all five groups foreach studied trait and raised during the wet season in 2020 (Mohanty et al. 2023). Observations on the above traits were recorded. A wide variation was observed in these traits. The panel was genotyped with 143 SSR markers. STRUCTURE analysis identified four sub-populations, while Analysis of Molecular Variance (AMOVA) showed 67% among individuals, 20% within individuals, and 14% among the populations. Marker-trait association analysis identified eight novel QTLs: *qRSG8.1* for relative shoot growth (RSG); *qAGR4.1*, *qAGR6.1*, *qAGR6.2*, and *qAGR8.1* for absolute growth rate (AGR); *qRSG6.1*, *qRSG7.1*, and*qRGR11.1* for relative growth rate (RGR) (Table 3). The reported QTL for germination rate (GR), *qGR4-1*, was identified. Further, QTLs present on chromosome 6 controlling RSG and AGR on chromosome 8 at 27 cM, and RSG and AGR at 221 cM were detected as genetic hotspots for these traits. The QTLs identified in the study would be useful for improving the seed vigour trait in rice.

## 4.5. Seed vigour traits

A panel of 278 germplasm lines collected from Assam, Madhya Pradesh, Kerala, Odisha, and Manipur was selected and grown during the wet season of 2019. The freshly harvested seeds were dried and stored for three months to break seed dormancy, after which they were used to estimate germination rate and early seedling growth parameters such as shoot growth (RSG), absolute growth rate (AGR), mean germination rate (MGR), and relative growth rate (RGR). Based on the mean phenotypic values, the 278 germplasm lines were broadly classified into five groups. From these, 124 lines were chosen for each trait and raised during the wet season of 2020 (Mohanty et al. 2024). Observations for these traits revealed a wide variation. The panel was genotyped with 143 SSR markers. STRUCTURE analysis identified four subpopulations, and Analysis of Molecular Variance showed that 67% of the variation was among individuals, 20% within individuals, and 14% among populations. Marker-trait association analysis identified eight novel QTLs: *qRSG6.1*, *qRSG7.1*, and *qRSG8.1* for relative shoot growth (RSG); and *qRGR11.1* for relative growth rate (RGR), and *qAGR4.1*, *qAGR6.1*, *qAGR6.2*, and *qAGR8.1* for absolute growth rate (AGR) (Fig. 14, Table 3). Additionally, the previously reported QTL for germination rate (GR), *qGR4-1*, was identified. Furthermore, genetic hotspots were detected on chromosomes 6 and 8, where QTLs controlling RSG and AGR at 221 cM and 27 cM, respectively, were found. These identified QTLs will be valuable for improving seed vigour traits in rice.

# CHAPTER 5: AGRO-MORPHOLOGICAL AND YIELD-RELATED TRAITS

To enhance rice yields, breeding programs have prioritized increasing the yield sink capacity of rice varieties, primarily by boosting the number of spikelets per panicle. This approach has led to the successful development of high-yield varieties, such as the New Plant Type (NPT) lines by the International Rice Research Institute (IRRI) and China's 'super' rice or 'super' hybrid rice varieties. However, these varieties often face challenges in realizing their full grain yield potential due to poor grain filling, particularly in basal spikelets. Plant architecture significantly influences photosynthesis, which directly affects yield production (Peng et al. 2004; Dah et al. 2015). Yet, an excessive leaf area can result in mutual shading, reduced light penetration, and lower canopy photosynthesis. Several bottlenecks hinder optimal yield, including spikelet sterility, short panicle length, limited grain numbers, and susceptibility to lodging. While a higher grain number is positively associated with yield, dense panicles with numerous spikelets often experience poor filling in the basal spikelets.

Grain size is another critical factor, as it affects not only yield but also consumer preferences, driving efforts to improve grain size characteristics. The quantitative inheritance of these traits presents a challenge, as multiple alleles are involved in their expression. Achieving higher production efficiency requires accumulating positive alleles for yield-related traits in a single elite genetic background. Higher rice yields result from the combined contribution of various yield-related traits, especially panicle characteristics such as length, the number of primary branches, grain number per panicle, and panicle weight. These attributes collectively play a significant role in determining the total yield per hill.

In recent years, significant advances in molecular breeding have been achieved to enhance rice productivity and improve various agro-morphological traits. The identification of QTLs and marker-trait associations has been central focus of rice genetic research, as these markers are essential for understanding the genetic basis of traits such as yield, plant height, spikelet fertility, grain size, and resistance to biotic and abiotic stresses. Despite considerable progress in mapping QTL mapping, challenges persist, particularly in achieving stable and high yields under diverse environmental conditions. The application of Genome-Wide Association Studies (GWAS) and biparental mapping approaches has led to the discovery of numerous QTLs associated with key traits. GWAS, which harnesses the natural variation within populations, has been especially valuable for identifying marker-trait associations linked to complex traits influenced by multiple genes. Similarly, biparental mapping methods, which track the inheritance of traits in controlled crosses, have provided a more refined understanding of the genetic architecture of rice traits. However, despite identifying numerous QTLs, translating these findings into practical breeding applications remains challenging due to issues such as the environment-specific expression of traits, pleiotropy, and epistasis. Additionally, the genetic diversity of rice germplasm is vast, and a comprehensive understanding of the relationship between genotype and phenotype across different genetic backgrounds is still limited. This gap in knowledge has led to the continued need for extensive QTL mapping, despite numerous previous studies. The complexity of traits like yield, influenced by multiple genetic and environmental factors, means that no single QTL or marker can consistently predict performance. At ICAR-CRRI, significant efforts have been directed to identifying QTLs and MTAs associated with agro-

morphological and yield-related traits using both GWAS and biparental approaches. This study seeks to bridge existing gaps by utilizing diverse rice genotypes, emphasizing economically significant traits, and creating high-resolution maps for marker-assisted selection (MAS). Although progress has been made in this area, the complexity and polygenic nature of many rice traits underscore the ongoing need for research to enhance QTL identification and increase the precision of marker-assisted breeding programs. Such efforts are essential for expediting the development of high-yielding rice varieties that are better equipped to withstand environmental stresses.

## 5.1. Plant type characters and grain yield

An association mapping panel of 88 elite rice breeding lines from diverse ecologies was selected to identify the marker-trait associations (MTAs) with traits such as grain yield per plant (GY), plant height (PH), effective bearing tillers (EBT), and number of leaves (NL) by using 142 candidate gene-based SSR (cgSSR) markers (Azharudheen et al. 2022a). This panel was evaluated across three seasons for these plant-type traits and grain yield. Seventeen MTAs were identified across six chromosomes: 2, 3, 4, 5, 7, and 8. cgSSR markers linked to the genes *OsMADS18, RePRP2.1, OS-PYDK, PIL16, OsGID1*, and OsSUT1 were associated with plant height, while markers derived from *OsBAK1*, *OsBBS1*, *YGL98*, *RePRP2.1*, *OsbHLH107*, and *EP3* showed associations with the number of leaves. For grain yield, two cgSSR markers, Sd17 and M60, developed from the genes *IDEF1* and *OsGID1,* respectively, were identified (Table 4b). Additionally, three markers derived from *OsGID1, OsFBK12,* and *OsMADS18* were associated with other traits previously reported to be influenced by these genes. Notably, several novel associations were detected, including three markers linked to two traits each. Trait-associated cgSSR markers derived from specific or related genes can be directly utilized for allele selection, while linked markers can indirectly modify the phenotype of interest, providing valuable tools for targeted breeding efforts.

## 5.2. Agro-morphological traits in *aus* rice germplasm

The *aus* varietal group, which includes the aus, boro, ashina, and rayada seasonal and field ecotypes, is known for its unique stress tolerance traits, making it a valuable resource for rice breeding. To fill knowledge gaps, Sar et al. (2024) examined the genetic structure of 181 *aus* accessions using 399,115 SNP markers and evaluated 11 morpho-agronomic traits during the wet season (June-November) of 2020. Genome-wide association studies (GWAS) were conducted to identify key loci associated with yield and plant architecture traits. Population STRUCTURE analysis identified six distinct subpopulations with strong geographical clustering. Subpopulation-specific differences were evident for most phenotypic traits. Principal component analysis (PCA) of the 11 agronomic traits showed that the first three components (PC1 to PC3) accounted for 24.4%, 16.8%, and 13.9% of trait variance, respectively. PC1 was primarily associated with panicle traits, plant height, and heading date, while PC2 and PC3 were linked to primary grain yield traits. GWAS using PC1 identified *OsSAC1* on chromosome 7 as a significant gene influencing multiple agronomic traits. PC2-based GWAS highlighted *OsGLT1 and OsPUP4/Big Grain 3* as key genes affecting grain yield (Table 4b). Several significant marker-trait associations (MTAs) overlapped with previously cloned genes, including: *OsGI* (GIGANTEA), regulating days to heading; *OsGPX1* (Plant Glutathione Peroxidases 1), affecting plant height, spikelet number, and root development; *OsMADS15*, influencing flowering time and plant architecture; and *WFP/IPA1*

(WEALTHY FARMERS PANICLE/IDEAL PLANT ARCHITECTURE 1), which governs yield and plant architecture. For PC2, key genes coinciding with significant SNPs included: *OsGLT1* (NADH-glutamate synthase 1), controlling yield; *dep2/SRS1* (DENSE AND ERECT PANICLE 2), regulating panicle size; *fzp* (frizzy panicle), influencing panicle and yield traits; and *SP1* (*Os11g0235200*, SHORT PANICLE 1), linked to panicle traits. For PC3, important genes identified included*: OsDOS* (DELAY OF SENESCENCE), regulating crop maturity; *SE13* (PHOTOSENSITIVITY 13), affecting heading date and yield; *GS3* and *qGL3*, influencing grain traits; and *OsIPT7* (Adenosine phosphate isopentenyl transferase 7), affecting yield traits. Notably, prominent peaks were detected on chromosome 4 at position ~3.540 Mb for both PC1 and PC3, corresponding to the QTLs *qSNP-4a* and *spp4-2*, previously reported for spikelets per panicle. Another prominent peak on chromosome 6 at position ~10.116 Mb aligned with a QTL hotspot containing *qSNP6*, *gp6* (spikelet number), *gw6* (1000-grain weight), *qTN2-6-1* (tiller number at maturity), *qPH2-6-1*, *Ph6* (plant height at maturity), *qGY6.1* (grain yield), and *qHD6-1* (heading date). The key gene in this region, *Hd1*, regulates photoperiodic flowering in rice. Haplotype analysis of these genes in the 3,000 Rice Genome Panel revealed distinct genetic variations in *aus* rice (Fig. 15).

## 5.3. Agro-morphological traits and yield traits in New Plant Types

An association panel of 60 genotypes, including New Plant Types (NPTs) along with *indica*, tropical, and temperate *japonica* genotypes, was evaluated phenotypically across four seasons under irrigated conditions for grain yield and its component traits. Among these, 20 NPT genotypes showed promise, with average grain yields ranging from 5.45 to 8.8 t/ha. A set of 85 SSR markers was utilized to identify QTLs linked to grain yield and related traits (Donde et al. 2020). Of these markers, 66 (77.65%) were found to be polymorphic. Genetic variation was distributed as 8% within genotypes, 68% among genotypes within the population, and 24% among populations. Association analysis using GLM and MLM models identified 30 and 10 SSR markers associated with 70 and 16 QTLs, respectively (Table 4b). Thirty novel QTLs linked with 16 SSRs were identified to be associated with eleven traits: tiller number (*qTL-6.1*, *qTL-11.1*, *qTL-4.1*), panicle length (*qPL-1.1*, *qPL-5.1*, *qPL-7.1*, *qPL-8.1*), flag leaf length (*qFLL-8.1*, *qFLL-9.1*), flag leaf width (*qFLW-6.2*, *qFLW-5.1*, *qFLW-8.1*, *qFLW-7.1*), the total number of grains (*qTG-2.2*, *qTG-a7.1*), thousand-grain weight (*qTGW-a1.1*, *qTGW-a9.2*, *qTGW-5.1*, *qTGW-8.1*), fertile grains (*qFG-7.1*), seed length-breadth ratio (*qSlb-3.1*), plant height (*qPHT-6.1*, *qPHT-9.1)*, days to 50% flowering (*qFD-1.1*), and grain yield per se (*qYLD-5.1*, *qYLD-6.1a*, *qYLD-11.1*). Several SSR markers were found to be associated with more than two traits. The highest co-localization was observed with RM5709, linked to nine traits, followed by RM297, associated with five traits. Similarly, markers such as RM112, RM168, RM204, RM5575, RM22899, and RM26499 were co-localized with multiple traits. These markers hold significant potential for marker-assisted backcross breeding programs aimed at pyramiding QTLs for critical yield-related traits. Utilizing these markers could aid in developing next-generation rice varieties with enhanced yield potential, addressing yield ceilings effectively.

## 5.4. Grain fertility and related traits in dense panicle rice variety, PDK Shriram

Low spikelet fertility is a significant challenge in enhancing grain yield in high-yielding rice varieties. While grain number is positively correlated with yield, low grain filling in the basal spikelets of dense panicles often limits this potential. To identify QTLs and genes influencing spikelet fertility in dense-panicle rice variety, PDK Shriram, Sekhar et al. (2021) developed recombinant inbred lines (RILs) from a cross between two *indica* rice cultivars: PDK Shriram (compact, high spikelet number) and Heera (lax, low spikelet number) (Fig. 16, Table 4a).The RILs, along with the parent varieties, were phenotyped for grain and panicle traits during the *kharif* seasons of 2017 and 2018. Genotyping using microsatellite and SNP markers, combined with linkage analysis, led to the identification of 20 QTLs associated with spikelet fertility and related traits such as panicle compactness and ethylene production, both of which significantly affect grain filling. Novel QTLs consistently identified in both seasons included *qETH1.2*, *qETH3.1*, and *qETH4.1* for ethylene production; *qSFP1.1*, *qSFP3.1*, and *qSFP6.1* for spikelet fertility percentage; and *qIGS3.2* and *qIGS4.1* for panicle compactness. Comparative expression analysis of candidate genes associated with these QTLs, such as *ERF3*, *AP2*-like ethylene-responsive transcription factor, *EREBP*, *GBSS1*, *E3* ubiquitin-protein ligase *GW2*, and *LRR* receptor-like serine/threonine-protein kinase *ERL1*, highlighted their roles in the poor grain filling of basal spikelets in dense panicles. These candidate genes represent promising targets for improving grain filling in compact-panicle rice varieties through biotechnological approaches.

## 5.5. Grain size traits

Grain size plays an important role in grain yield and consumer preferences. To identify QTLs associated with grain size characters, Nayak et al. (2022a) selected an association panel of88 rice genotypes and cultivated them during the wet seasons of 2018, 2019, and 2020. Seeds were harvested, dried, and evaluated for grain size-related characters (GL, GW, LWR, and TGW). The thousand-grain weight (TGW) varied from 10.6 to 31.9 g, with an average of 21.50 g, while grain length (GL) ranged from 5.21 to 10.59 mm, with a mean of 8.39 mm. Grain width (GW) ranged from 1.65 to 3.26 mm, averaging 2.62 mm, and the length-to-width ratio (LWR) ranged from 2.01 to 5.59, with an average of 3.31. The panel was genotyped using 142 candidate gene-based SSR (cgSSR) markers derived from yield-related genes. STRUCTURE and PCA analyses revealed three subpopulations among the genotypes. Using the efficient mixed-model association (EMMA) approach in the GAPIT package, 10 significant associations were identified for four grain size-related traits (grain weight, grain length, grain width, and length-to-width ratio), explaining 6.34% to 13.25% of the phenotypic variance. The markers M69, Sd14, M55, and Sdi21, derived from the genes *OsBC1L4*, *OsC1*, *SHO1*, and *RSR1*, respectively, were associated with TGW. Markers M35, Sd1, M99, and M69, linked to the genes *NPP1*, *OsD2*, *Rd*, and *OsBC1L4*, were associated with grain weight (Table 4b). Markers M69, M55, and Sd1 demonstrated associations with multiple traits, indicating that the corresponding genes influence the development of more than one trait through the interaction of gene products. Among the identified associations, seven marker-trait pairs explained over 10% of the phenotypic variance, suggesting they represent major putative QTLs for the respective traits. For example, allelic variations at the genes *SHO1*, *OsBC1L4*, and *OsD2* showed associations between TGW and grain width, TGW and grain length, and grain width and LWR, respectively. The cgSSR markers linked

to specific traits can be directly employed for allelic selection, while other significantly associated markers may be utilized for allelic accumulation in breeding programs to improve grain size. These newly identified cgSSR markers for grain size-related traits have significant potential in practical rice breeding, enabling marker-assisted programs to increase the number of beneficial alleles for these traits and enhance grain yield.

## 5.6. Panicle architecture and grain yield

Panicle traits like length, number of primary branches, grain number, and panicle weight are the key factors for grain yield. To identify QTLs and genes, Sah et al. (2023) selected an association panel of 88 rice varieties released for different ecologies over the last three decades, along with some germplasm accessions. The association panel was evaluated over three years during the wet seasons of 2018, 2019, and 2020 for various panicle traits, including panicle length (PL), number of primary branches per panicle (NPB), number of grains per panicle (NG), panicle weight (PW), and grain yield per hill (GY). Panicle length varied from 14.33 cm to 32.20 cm, with an average of 23.78 cm, while panicle weight ranged from 0.37 g to 7.70 g, with a mean of 2.90 g. The number of primary branches per panicle spanned from 5.00 to 14.33, with an average of 10.35 branches. The number of grains per panicle ranged from 35.00 to 284.33, with a mean of 133.83 grains. Grain yield per hill varied between 6.97 g and 18.94 g, averaging 12.92 g. The panel was genotyped with 114 cgSSR markers. Population structure and PCA analysis identified the subpopulations. Seventeen marker-trait associations on six chromosomes were identified for five traits, including several novel QTLs. These QTLs explained a phenotypic variance ranging from 4.0 to 13.0%. Markers M17 (*EP2*) and M81 (*YGL98*) for PL; M91 (*OsbHLH107*), M78 (*OsSUT1*), M88 (BLS1), and *Sdi21* (*RSR1*) for NPG; M82 (*Osgl1-2*), M34 (*OsAHP1*), and M36 (*COE1*) for NG; M92 (*GH2*), M34 (*OsAHP1*), M82 (*Osgl1-2*), M91 (*OsbHLH107*), M57 (*D11*), and M36 (*COE1*) for PW; *Sd17* (*IDEF1*) and M60 (*OsGID1*) for GY were identified (Table 4b).Trait-associated cgSSR markers, derived from specific or related genes, are valuable for direct allele selection, while other linked markers support indirect allele selection by influencing the target phenotype. These marker-trait associations can be effectively utilized in marker-assisted breeding programs.

# CHAPTER 6: GRAIN NUTRITIONAL QUALITY TRAITS

Rice is an important source of daily calories, especially for millions of poor families who depend on it as their main staple food. It is high in carbohydrates, with over 80% of its kernel consisting of starch, but has relatively low protein content (7-8%). However, rice protein is considered of the highest quality among cereals, due to its digestibility and amino acid composition, making it highly favored in the food and feed industries. The protein content also affects rice's cooking and eating qualities (Wang et al. 2017). Total soluble sugars (TSS) are important for seed quality and contribute to the development of fresh, sweet flavors. Many high-yielding rice varieties tend to be low in grain iron (Fe) and zinc (Zn), two essential micronutrients involved in various enzymatic processes. A deficiency of these micronutrients can cause numerous health issues. The lack of protein and these micronutrients leads to malnutrition, which is responsible for around 24,000 deaths daily worldwide. Antioxidants in rice offer notable health benefits, such as reducing oxidative stress, cholesterol levels, and the risks of type II diabetes, obesity, and cancer. Consuming whole-grain rice, enriched with antioxidants, can improve human health by lowering the risk of chronic diseases (Shao et al. 2015; Mbanjo et al. 2020). Since rice is rich in antioxidant compounds, it provides many health advantages. Biofortification is a cost-effective and accessible method to increase the levels of protein, micronutrients, and antioxidants in rice grains. Thus, identifying QTLs/genes that regulate these components, along with developing reliable markers, is crucial for enhancing these traits through molecular breeding techniques.

## 6.1. High grain protein content in ARC10075

About 190 backcross-inbred lines (BILs, $BC_3F_4$) by crossing the high-protein donor ARC10075 with the high-yielding variety Naveen (Chattopadhyay et al. 2019). These BILs were grown in the *kharif* season of 2013, the *rabi* season of 2014, and the *kharif* season of 2014, with seeds harvested each time. Grain protein content (GPC) in the BILs was measured using the standard micro-Kjeldahl method. The BILs were genotyped with a 40K Affymetrix custom SNP array. Three QTLs for GPC and 11 QTLs for single grain protein content (SGPC) were identified. Among these, *qGPC1.1* for GPC and *qSGPC2.1* and *qSGPC7.1* for SGPC were found to be stable across environments, explaining 13%, 14%, and 7.8% of the phenotypic variance, respectively (Fig. 17, Table 5a). Additionally, an epistatic QTL independent of the main effect QTL was detected for SGPC across environments. Several functional genes related to seed storage proteins were also postulated within the QTL regions. High-protein lines, CR Dhan 310, CR Dhan 311 carrying the introgressed *qGPC1.1* in the telomeric region of the short arm of chromosome 1 exhibited higher glutelin content. This result was supported by the identification of a potential candidate gene within this QTL region, encoding glutelin family proteins.

## 6.2. High grain protein content in association-mapping panel

A set of 305 genotypes, comprising mainly landraces, cultivars, and protein-biofortified genotypes, was selected and evaluated for grain protein content during the dry season of 2015 using near-infrared spectroscopy (NIRS) (Pradhan et al. 2019). The genotypes were categorized into three groups: high protein content (> 9.5 ppm), medium (8.0–9.5 ppm), and

low (< 8.0 ppm). An association panel of 105 genotypes was shortlisted from these 305 genotypes. They were grown during the wet seasons of 2016 and 2017 and phenotyped for grain protein content. A wide variation in grain protein content was observed. STRUCTURE analysis identified three subpopulations. AMOVA analysis showed that 15% of the variation was among populations, while 73% was among individuals. Seven QTLs strongly associated with grain protein content (PC) were detected. Among these, three novel QTLs, *qPC3.1*, *qPC5.1*, and *qPC9.1*, were identified. Additionally, four previously reported QTLs (*qPC3, qPC8, qPC6.1, and qPC12.1*) were validated for use in breeding programs (Table 5b). The reported QTLs *qPC6, qPC6.1*, and *qPC6.2* might represent the same QTL controlling grain protein content in rice. A closely associated marker, RM407, was found near the protein-controlling QTLs *qProt8* and *qPC8*. The markers strongly linked to grain protein content, *qPC3, qPC3.1, qPC5.1, qPC6.1, qPC8, qPC9.1*, and *qPC12.1*, could be useful for pyramiding these traits to develop protein-rich, high-yielding rice varieties.

## 6.3. High grain Fe and Zn contents

Most rice genotypes have low levels of iron (Fe) and zinc (Zn) in their grains. Polished rice, a staple food in India, loses a significant amount of Fe and Zn during milling. However, some landraces, such as CR Dan 311 and Chhattisgarh Rice 1, are high-yielding varieties that contain higher levels of Zn. To improve Fe and Zn content in high-yielding varieties, it is essential to identify the QTLs and genes associated with these micronutrients. In a study by Pradhan et al. (2020), 485 germplasm lines, including landraces, cultivars, and biofortified varieties, were evaluated for Fe and Zn content in milled rice from 2013 to 2015. A panel of 102 genotypes representing three distinct phenotypic classes for grain Fe and Zn content, along with three check varieties, was grown during the wet seasons of 2016 and 2017. Significant variation in grain Fe and Zn content was observed. The genotypes were genotyped with 25 gene-specific and 75 SSR markers. STRUCTURE analysis identified seven sub-populations, while AMOVA analysis revealed that 39% of the variation was among populations, 51% among individuals, and 10% within individuals. The study detected two novel QTLs for grain Fe content, *qFe3.3* and *qFe7.3*, and three novel QTLs for grain Zn content, *qZn2.2*, *qZn8.3*, and *qZn12.3*. Additionally, four QTLs for Fe content, *qFe3.3*, *qFe7.3*, *qFe8.1*, and *qFe12.2*, were found to be co-localized with QTLs for Zn content, including *qZn3.1*, *qZn7*, *qZn8.3*, and *qZn12.3*. Fe-Zn-controlling QTLs were also co-localized with yield component QTLs, such as *qTBGW*, *OsSPL14*, and *qPN*. Several previously reported QTLs for Fe and Zn content were also detected, including *qFe1.1*, *qFe3.1*, *qFe5.1*, *qFe7.1*, *qFe8.1*, *qZn6*, *qZn7*, and *gRMm9-1* (Table 5b). The identified QTLs, including *qZn6, qZn7, qZn2.2, qZn8.3, qZn12.3, qFe1.1, qFe3.1, qFe5.*1, *qFe7.1, qFe8.1, qFe3.3*, and *qFe7.3*, could be valuable for biofortification of rice using molecular breeding approaches to improve micronutrient content.

## 6.4. Antioxidant enzymes, phenolic content, and antioxidant activity

Antioxidants protect cells from damage and influences seed viability, vigour, and longevity. Additionally, antioxidants present in rice grains offer several health benefits. Enhancing the antioxidant content of rice grain is one of the best options for health benefits for human beings. To identify QTL for antioxidants in rice grain, Sanghamitra et al. (2022) shortlisted 270 diverse genotypes of India and raised them during the wet season of 2018. The seeds were harvested, dried, and evaluated for six antioxidants (CAT, PEROX, TPC, DPPH, FRAP, and CUPRAC). A panel of 117 genotypes, consisting of 64 white and 53 coloured

rice grain varieties, was selected based on six phytochemical traits and grown during the wet seasons of 2019 for evaluation of these six antioxidants. These traits exhibited wide variations. A strong positive correlation was observed between DPPH and TPC, FRAP, and CUPRAC. The panel was genotyped with 131 SSR markers. STRUCTURE analysis identified three sub-populations within the panel. AMOVA analysis revealed that 1% of the genetic variation was among populations, 4% among individuals, and 95% within individuals in the panel. The panel exhibited moderate to high mean gene diversity. Eleven significant marker-trait associations for antioxidant traits were identified: *qCAT8.1* and *qCAT11.1* for catalase; *qACD2.1, qACD11.1*, and *qACD12.2* for DPPH (2, 2'-diphenyl picryl hydrazyl); *qCUPRAC3.1, qCUPRAC11.1*, and *qCUPRA12.1* for CUPRAC (cupric reducing antioxidant capacity); and *qFRAP11.1, qFRAP12.1,* and *qFRAP12.2* for FRAP (ferric reducing antioxidant power) (Fig. 18, Table 5b). Co-localization of the QTLs *qACD11.1, qCUPRAC11.1,* and *qFRAP11.1* was detected, suggesting they may serve as antioxidant hotspots for regulating DPPH, CUPRAC, and FRAP activities, respectively, while *qFRAP12.1* and *qACD12.2* were located close to each other on chromosome 12. These identified QTLs will be valuable for improving antioxidant content in rice grains.

## 6.5. Superoxide dismutase, flavonoids, anthocyanins, carotenoids, γ-Oryzanol and antioxidant activity

The majority of rice consumers suffer from malnutrition, including deficiencies in protein, Fe, and Zn, as well as health issues related to oxidative stress, such as cancer, diabetes, and obesity. Therefore, the consuming biofortified rice, rich in protein, Fe, Zn, and antioxidants is one of the best and cheapest options to combat malnutrition and stress-related health problems. To identify QTLs associated with antioxidants, Bastia et al. (2022) shortlisted a set of 120 rice genotypes representing the landraces and cultivars (67 white and 53 red grain) from an original population of 270 germplasm lines and raised during the wet seasons of 2019 and 2020. The seeds were harvested, stored for three months to break dormancy, and then used to measure five antioxidant traits: superoxide dismutase, flavonoids, anthocyanins, carotenoids, γ-oryzanol, and ABTS antioxidant activity. Significant genetic variation was observed across these traits in the germplasm lines. STRUCTURE analysis revealed four sub-populations, while AMOVA showed 6% genetic variation between populations, no variation among individuals, and 94% variation within individuals of the panel. Fourteen significant marker-trait associations were identified for these antioxidant traits (Fig. 19, Table 5b). Known QTLs for anthocyanin content (*qANC3, qPAC12-2*) and ABTS activity (*qAC12*) were detected, along with eleven novel QTLs: *qOZ8.1* and *qOZ11.1* for γ-oryzanol (OZ); *qSOD1.1, qSOD5.1*, and *qSOD10.1* for superoxide dismutase (SOD); *qTAC1.1* and *qTAC5.1* for anthocyanin content; *qAC11.1* for ABTS activity*;* and *qTFC6.1*, *qTFC11.1*, and *qTFC12.1* for total flavonoid content (TFC). Antioxidant hotspots were identified on chromosome 11 at 45.3 cM for GO, TFC, and TAC, and on chromosome 12 at 101.8 cM for TAC and ABTS activity, which could aid in molecular breeding programs.

## 6.6. Protein, total soluble sugars, starch, amylose and chlorophyll content in association mapping panel

An association panel of 120 germplasm lines was selected from an initial group of 274 lines collected from Assam, Madhya Pradesh, Kerala, Odisha, and Manipur to map six biochemical traits: total protein, starch, amylose, total soluble sugars, chlorophyll a, and

chlorophyll b content (Nayak et al. 2022b). The seeds were harvested and stored for three months before estimating the biochemical traits. Significant genetic variation was observed for these traits in the population. The panel was genotyped with 136 microsatellite markers, revealing three sub-populations. AMOVA showed 8% genetic variation among populations, no variation among individuals, and 92% variation within individuals of the panel. Previously reported QTLs for amylose content (*qAC1.2*), total soluble sugar (*qTSS8.1*), protein content (*qProt1, qPC6.2*, *qPC8.2*), chlorophyll a (*qCH2* and *qSLCHH*), and chlorophyll b *(qChl5D)* were identified in this population. Additionally, novel QTLs were detected: *qAC11.1, qAC11.2*, and *qAC11.3* for amylose content; *qTSS7.1, qTSS8.2*, and *qTSS12.1* for total soluble sugars; *qSC2.1, qSC2.2, qSC6.1,* and *qSC11.1* for starch content; *qPC1.2* for protein content; *qChla8.1* for chlorophyll a content; and *qChlb7.1* and *qChlb8.1* for chlorophyll b (Fig. 20, Table 5b). Genetic hotspots for these traits were found on chromosome 8 at 234 cM for grain protein content, at 363 cM for total soluble sugars, and at 48 cM on chromosome 11 for starch and amylose content. The validated and novel QTLs identified in this study would be valuable for improving protein, starch, amylose, total soluble sugars, and chlorophyll content.

## 6.7. Grain phytic acid content

Most of the phosphorus in rice grains is stored as phytic acids, which reduces the bioavailability of essential minerals like Fe, Zn, K, Ca, Mg, etc., causing malnutrition among rice consumers. Hence, rice with low to moderate phytic acid content in rice grains is desirable. To identify QTLs and develop markers for low phytic acid (PA) contents, Azharudheen et al. (2022b) selected an association panel of 94 rice varieties raised during the wet seasons of 2020 and 2021. These varieties were developed over 50 years (1971–2020). Seeds were collected from each variety and evaluated for grain phytic acid content. A substantial and significant variation in grain PA content (ranging from 0.3% to 2.8%) was observed among rice varieties, with differences based on decade and ecological factors. The significant genotype × environment interaction suggested that multiple genes control the trait. Fourteen novel candidate gene-based markers were used to genotype 94 varieties, detecting 43 alleles. These new markers proved to be highly informative, as shown by their PIC values (ranging from 0.11 to 0.65, with an average of 0.34) and their ability to cover a broad range of diversity. Marker alleles derived from two potential transporter genes, SPDT and *OsPT8*, were significantly associated with grain PA variation. A 201 bp allele in the 3' UTR of the SPDT gene was negatively correlated with grain PA content, explaining 7.84% of the phenotypic variation (Table 5b). A rare allele in the coding region of the *OsPT8* gene was positively associated with grain PA content, explaining 18.49% of the phenotypic variation.

## 6.8. Nutritional traits in brown and pigmented rice

A panel of 96 high-yielding rice genotypes were selected from a pool of 300 accessions, comprising 36 landraces, 39 released varieties, and 21 breeding lines from both indigenous and exotic germplasm (Chattopadhyay et al. 2023). These genotypes were cultivated during the *kharif* season of 2018, and after drying, the harvested seeds were evaluated for 17 grain nutritional and physicochemical traits. Significant variation was observed in all nutritional traits, including grain protein content (GPC) (3.81-14.88%), zinc (Zn) content (14.18-129.09 ppm), and iron (Fe) content (10.46-73.42 ppm). Antioxidant traits, such as anthocyanin (ANTH) (2.50-96.14 mg), γ-oryzanol (GORY) (27.69-82.25), total phenolic content (TPC)

(15.63-664.20), total flavonoid content (TFC) (65.78-428.56), and DPPH activity (2.16-99.87%), also exhibited wide variation. Amylose content ranged from 5.4% in Kala Birohin to 27.4% in Sahabhagidhan. Initially, 250 Type I and II SSR markers were tested using five randomly selected genotypes, and 122 markers with good amplification and even distribution across all 12 rice chromosomes were chosen for genotyping the association panel. Population structure and PCA confirmed the presence of three subpopulations within the panel. A total of 78 significant marker-trait associations were identified across all chromosomes, explaining phenotypic variation from 4% to 27% (Table 5b). SSR marker RM 467 was co-localized with the previously identified QTL *qPC10.1* and the gene *OsGluA2*. Grain protein and metal content were associated with cooking quality, and marker-trait associations supported this. Two QTLs for grain protein and amylose content (AC), with markers RM 17600 and RM 1272, were found to be co-localized with an additive effect in opposite directions. RM 162 was linked to both zinc content and cooking time (alkali spreading value). Iron content showed a significant association with grain size, with RM 8050 co-localized with both iron content and kernel length/breadth ratio. Pigmented rice varieties were associated with low amylose content, and a genetic locus for anthocyanin (*qANTH5.1*) was found to co-localize with a QTL for amylose content (*qAC5.1*), showing an additive effect in the opposite direction. These co-localized loci for nutritional, cooking, and eating quality could guide biofortification programs aimed at improving rice's nutritional traits without affecting consumer preference.

# CHAPTER 7: USE OF QTLS AND GENES FOR DEVELOPMENT OF RICE VARITIES/GENOTYPES

## 7.1. BPH-resistant rice varieties

Salkathi, a landrace, was found to be highly resistant to brown planthopper (BPH) for three consecutive years (2000-2002) and was subsequently evaluated at various locations in the Planthopper Screening (PHS) trial of AICRIP in 2003 and 2004. It showed promising resistance across multiple years of testing in AICRIP (DRR Annual Progress Report, vol. 2; 2003 and 2004). Salkathi was widely used in the breeding program at CRRI, Cuttack, Odisha. Four cultures developed from crosses using Salkathi as a donor were screened at CRRI, Cuttack resulting in the identification of three resistant cultures: CR 3005-230-5 (Samba Mahsuri/Salkathi), CR 3005-77-2 (Samba Mahsuri/Salkathi), and CR 3006-8-2 (Pusa 44/Salkathi). These resistant cultures were further evaluated under the Multiple Resistant Screening Trial (MRST) of AICRIP in 2011 and 2012 (DRR Annual Progress Report, vol. 2; 2011, 2012) and were reported to be resistant to BPH.

Two QTLs, *qBph 4.3* and *qBph 4.4*, associated with resistance to brown planthopper (BPH) in Salkathi on chromosome 4, were identified at ICAR-CRRI, Cuttack, Odisha (Mohanty et al. 2017). A resistant pre-breeding line, CR 3006-8-2, exhibited resistance across India in AICRIP trials and was found to carry both of these QTLs from Salkathi. This resistant line was then utilized in a marker-assisted backcross breeding (MABC) program to transfer the two QTLs into elite rice backgrounds. Initially, two popular varieties, Naveen and Pooja, were selected for QTL introgression from Salkathi. Later, two additional varieties, Swarna and CR Dhan 312, were chosen, and the work is still ongoing. Three STMS markers linked to the BPH resistance QTLs *qBph4.3* and *qBph4.4* were used for foreground selection of the QTLs. Additional polymorphic markers (SSRs and Indels) were identified in that interval and nearby regions of chromosome 4 by screening 25 more reported markers. Background selection was conducted using a reduction-based approach with 107 polymorphic markers identified between Naveen and CR 3006-8-2. The flanking markers for *qBph4.3* and *qBph4.4* (Mohanty et al. 2017) were employed for foreground selection as progeny lines advanced from $BC_1F_1$ to $BC_2F_1$ in the Naveen/CR-3006-8-2 cross. Only lines carrying both QTLs were selected up to $BC_1F_1$ and backcrossed with the recurrent parent. In $BC_2F_1$, recombinants within the QTL intervals were also selected. By $BC_2F_2$, homozygous near-isogenic lines (NILs) for both QTLs and recombinants within and between QTLs were identified and advanced. Rigorous phenotypic selection for recurrent parent traits continued until $BC_2F_5$, and seeds were bulked in $BC_2F_6$.

## 7.2. Promising NILs and subsequent release of BPH resistant rice varieties

Three resistant NILs (CR 4331-74-2-2-1, CR-4331-84-3-2-1, and CR 4331-85-1-2-1) in the background of Naveen were identified and evaluated in AICRIP trials. The entry CR 4331-85-1-2-1-2 (IET 29203) showed superior performance only in Odisha and comparable yield level with Naveen. As a result, it was officially released as the variety CR Dhan 805 exclusively for Odisha state in 2023 (Fig. 21).

Among the entries, CR Dhan 809 (IET 30282), a MAS-derived NIL entry from the cross Naveen*3 / CR 3006-8-2, introgressed with BPH resistance QTLs *qBph4.3* and *qBPH4.4.* (Fig. 22), demonstrated superior performance in AICRP trials across all six states (Odisha, Bihar, Jharkhand, West Bengal, Assam, and Tripura), where Naveen is widely cultivated. Based on the superior performance, CR Dhan 809 was identified for release in these six states by the Varietal Identification Committee (VIC) of AICRIP in April 2024 and subsequently released and notified by the Central Sub-Committee on Crop Standards, Notification and Release of varieties.CR Dhan 809 performed at par or better than Naveen in grain yield in all the zones where Naveen is popularly grown. The grain quality, phenological traits and morphological attributes of CR Dhan 809 are also similar to Naveen. It has shown enhanced resistance to BPH compared to its recurrent parent, Naveen. Over three years of natural and artificial screening for BPH in multi-location trials under AICRIP, IET 30282 consistently outperformed Naveen in terms of damage score and hopper burn percentage. In the agronomic trials in areas of adaptation of Naveen, the nutrient response (Kg grain/Kg Nutrient) of IET 30282 (11.99 Kg grain/Kg Nutrient) was higher than Naveen (6.79 Kg grain/Kg Nutrient). At the optimum fertilizer level in Zone-III, the yield of IET 30282 was 4.62 t /ha as compared to 3.89 t /ha of Naveen. Genotyping with 1K RiCASNP markers indicated 91.99% background genome recovery in IET 30282 compared to the recurrent parent.

## 7.3. BPH-resistant NILs of Pooja

The same marker-assisted backcross breeding (MABC) approach used for Naveen was also applied to Pooja. However, because of the variety's photosensitive nature, only one generation could be advanced per year. Currently, ten BPH-resistant near-isogenic lines (NILs) of Pooja have been developed at CRRI, Cuttack, Odisha. Among these, one NIL (CR 4696-2-15-32-82), which closely resembles the recurrent parent in terms of morphology, yield, and grain quality, has been nominated for the AICRP trial (Fig. 23).

## 7.4. Herbicide (Imazethapyr) tolerant rice variety

CR Dhan 807 (CR 4333-35-2-2-1, IET 30438), a non-GM herbicide (Imazethapyr) tolerant near-isogenic line (NIL) of popular variety, Sahbhagidhan, was developed using the mutant line Robin as a donor through a marker-assisted backcross breeding (MABB) strategy (Fig. 24). It was released for six states, namely, Jharkhand, Odisha, Chhattisgarh, Gujarat, Andhra Pradesh, and Tamil Nadu. Three backcrosses were performed with recurrent parent Sahbhagidhan were performed to recover over 95% of its genome. CR Dhan 807 matures within 110-115 days and is suitable for growing under rainfed direct-seeded upland conditions and zero tillage-DSR cultivation, where weed and weedy rice management are major challenges. Under rainfed direct seeded trials, the variety demonstrated an average yield potential of 4.4 t/ha under normal rainfall across all test locations of the country and 2.8 t/ha under moderate drought situations. Yield potential up to 6.8/ha was recorded under normal rainfall in AICRIP trials. Imazethapyr application (10% SL) does not cause any phytotoxicity in CR Dhan 807 but effectively controls the weeds when applied at the appropriate stage. Besides herbicide tolerance, the variety also possesses better weed competitive ability due to its higher early seedling vigour. The variety CR Dhan 807 is also tolerant to drought and is efficient in nutrient use, providing a significant advantage in rainfed conditions.

# CHAPTER 8: TIMELINE FOR QTLS, MOLECULAR MARKERS, AND PROSPECTIVE GENES IDENTIFIED FOR DIFFERENT TRAITS IN RICE

Several QTLs, molecular markers, and potential candidate genes have been identified at ICAR-CRRI, Cuttack, Odisha, and some have been successfully integrated into molecular breeding programs to develop climate-smart rice varieties. The first molecular marker ($OPQ05_{1150}$) was identified in ARC5984 for gall midge resistance/susceptibility in 2007, followed by the identification of closer flanking markers to the gall midge resistance gene (*Gm4*) in PTB10 in 2010. After that, several QTLs, molecular markers and prospective candidate genes have been identified for different traits in rice. Table 7 gives an overview of QTLs, molecular markers, and prospective candidate genes that have been identified for different traits in rice, chronologically.

# 9. WAY AHEAD

Significant progress has been made in identifying QTLs for many traits in rice, including resistance to biotic and abiotic stresses, seed and seedling vigour, agro-morphological characteristics, yield-related traits, and grain quality. However, advancements in areas such as input use efficiency (water, nitrogen, and phosphorus), metal toxicity tolerance, direct-seeding rice (DSR)-related traits, lodging resistance, viviparous germination, straw quality, and nutraceutical properties (e.g., glycemic index, protein, and micronutrient content, medicinal and antioxidant properties) remain limited. Additionally, QTLs for traits like high photosynthetic efficiency, resistance to diseases (e.g., false smut, brown spot, grain discoloration), and insect pests (e.g., gundhi bug, leaf folder, stored grain pests) require further exploration. Although some QTLs have been validated in alternative rice populations and incorporated into elite cultivars, there is a clear need for increased focus on validating and fine-mapping existing QTLs and genes. Such efforts are crucial for advancing molecular breeding programs aimed at improving high-yielding, climate-resilient rice varieties. Future research should prioritize the identification and fine-mapping novel QTLs/genes for different traits, utilizing both established and new donor sources. The identification of superior alleles for these traits, coupled with the application of gene-editing technologies, will help to validate the functions of these novel QTLs/genes. Additionally, incorporating multiple superior haplotypes of effective QTLs/genes into widely grown susceptible varieties could greatly enhance rice performance. Cloning these QTLs/genes is crucial for understanding their molecular functions and unlocking their potential for practical breeding applications.

To enhance the breeding process, whole-genome resequencing of key donor varieties is essential to identify SNPs and INDELs. This will facilitate the understanding of the structure, function of critical genes linked to important traits, and allow for the development of markers for more efficient utilization in breeding programs. Additionally, scaling up seed production and distribution, conducting large-scale trials, and promoting awareness programs for already released varieties are key steps toward broader adoption. Establishing

comprehensive databases, creating seed banks, and ensuring the long-term storage of donor materials for various traits are vital to sustaining and advancing rice improvement efforts.

# 10. REFERENCES


Anandan A, Anumalla M, Pradhan SK, Ali J (2016). Population structure, diversity and trait association analysis in rice (*Oryza sativa* L.) germplasm for early seedling vigor (ESV) using trait linked SSR markers. PLoS One 11(3): e0152406.

Anandan A, Nagireddy R, Sabarinathan S, Bhatta BB, Mahender A, Vinothkumar M,Parameswaran C, P Panneerselvam P, Subudhi H, Meher J, Bose LK, Ali J (2022). Multi-trait association study identifies loci associated with tolerance of low phosphorus in *Oryza sativa* and its wild relatives. Scientific Reports 12: 4089.

Anant AK, Pandi Govindharaj GP, Jena M, Chandrakar G, Chidambaranathan P, Raghu S, Basana Gowda G, Annamalai M, Patil N, Adak T, Ramasamy N, Rath PC (2021). Genetic dissection and identification of candidate genes for brown planthopper, *Nilaparvata lugens* (Delphacidae: Hemiptera) resistance in farmers' varieties of rice in Odisha. Crop Protection 144: 105600.

Azharudheen TPM, Nayak AK, Behera S, Anilkumar C, Marndi BC, Moharana D, Singh LK, Upadhyay S, Sah RP (2022a). Genome-wide association analysis for plant type characters and yield using cgSSR markers in rice (*Oryza sativa* L.). Euphytica 218: 69.

Azharudheen TPM, Kumar A, Anilkumar C, Sah RP, Behera S, Marndi BC (2022b). Understanding natural genetic variation for grain phytic acid content and functional marker development for phytic acid-related genes in rice. BMC Plant Biology 22: 446**.**

Babu SB, Pandi Govindharaj GP, Parameswaran C, Anant AK, Padhi J, Bansal R, Priyadarsini S, Patra BC, Gowda GB, Mahendiran A, Patil NK, Rath PC (2022). Genomic analysis and finding of candidate genes for *Nilaparvata lugens* (stål) resistance in Indian pigmented and other indigenous rice genotypes. Crop Protection 156: 105959.

Bal A, Samal P, Chakraborthi M, Mukherjee AK, Ray S, Molla KA, Behera L, Samal R, Sarangi S, Sahoo P, Behera M, Lenka S, Azharudheen TPM, Khandual A, Kar MK (2020). Stable quantitative trait locus (QTL) for sheath blight resistance from rice cultivar CR 1014. Euphytica 216:182.

Barik SR, Pandit E, Mohanty SP, Pradhan SK (2018a). QTL mapping for traits at reproductive stage drought stress in rice using single marker analysis. Oryza 55(1): 134-140.

Barik SR. Pandit E, Pradhan SK, Singh S, Swain P, Mohapatra T (2018b). QTL mapping for relative water content trait at reproductive stage drought stress in rice. Indian Journal of Genetics and Plant Breeding 78(04): 401-408.

Barik SR, Pandit E, Pradhan SK, Mohanty SP, Mohapatra T (2019). Genetic mapping of morpho-physiological traits involved during reproductive stage drought tolerance in rice. PLoS One 14(12): e0214979.

Barik SR, Pandit E, Mohanty SP, Nayak DK, Pradhan SK (2020). Genetic mapping of physiological traits associated with terminal stage drought tolerance in rice. BMC Genetics 21(1): 1-12.

Barik SR, Pandit E, Sanghamitra P, Mohanty SP, Behera A, Mishra J, Pradhan SK (2022). Unravelling the genomic regions controlling the seed vigour index, root growth parameters and germination percent in rice. PLoS One 17(7): e0267303.

Basha FTM, Sar P, Bhowmick PK, Mahato A, Bisht DS, Iquebal MA, Chakraborty K, Banerjee A, Verma BC, Bhaduri D, Kumar J, Ngangkham U, Saha S, Priyamedha, Mandal NP, Roy S (2024) Genome-wide association study identified QTLs and genes underlying early seedling vigour in *aus* rice (*Oryza sativa* L.). Molecular Genetics and Genomics 299:112.

Bastia R, Pandit E, Sanghamitra P, Barik SR, Nayak DK, Sahoo A, ... , Pradhan SK (2022). Association mapping for quantitative trait loci controlling superoxide dismutase, flavonoids, anthocyanins, carotenoids, γ-Oryzanol and antioxidant activity in rice. Agronomy 12(12): 3036.

Chattopadhyay K, Behera L, Bagchi TB, Sardar, SS, Moharana N, Patra NR, Chakraborty M, Das A, Marndi BC, Sarkar A, Ngangkham U, Chakrborty K, Bose LK, Sarkar S, Roy S, Sharma S (2019). Detection of stable QTLs for grain protein content in rice (*Oryzasativa* L. employing high throughput phenotyping and genotyping platforms. Scientific Reports 9: 3196.

Chattopadhyay K, Vijayan J, Ray A, Chakraborty K, Sarkar RK (2020a). Additive main effect and digenic epistatic quantitative trait loci for chlorophyll fluorescence traits influencing salt tolerance at seedling stage in rice. Photosynthetica 58 (S1): 410-422.

Chattopadhyay et al. (2020b). ICAR-NRRI Annual Report 2020, 24-25.

Chattopadhyay K, Mohanty SK, Vijayan J, Marndi BC, Sarkar A, Molla KA, Chakraborty K, Ray S, Sarkar RK (2021a). Genetic dissection of component traits for salinity tolerance at reproductive stage in rice. Plant Molecular Biology Reporter 39: 386-402.

Chattopadhyay K, Chakraborty K, Samal P, Sarkar RK (2021b). Identification of QTLs for stagnant flooding tolerance in rice employing genotyping by sequencing of a RIL population derived from Swarna x Rashpanjor. Physiology and Molecular Biology of Plants 27(12): 2893–2909.

Chattopadhyay K, Bagchi TB, Sanghamitra P, Sarkar S, Anilkumar C, Marndi BC, Kumar A, Moharana N, Mohapatra SS, S. K. Sahoo SK (2023). Mapping genetic determinants for grain physicochemical and nutritional traits in brown and pigmented rice using genome-wide association analysis. Euphytica 219: 57.

Donde R, Mohapatra S, Baksh SKY, Padhy B, Mukherjee M, Roy S, Chattopadhyay K, Anandan A, Swain P, Sahoo KK, Singh ON, Behera L, Dash SK (2020). Identification of QTLs for high grain yield and component traits in New Plant Types of rice. PLOS One 15(7): e0227785.

Kajal P, Sah RP, Totan A, Pandi Govindharaj GP, Azharuddin TPM, Anilkumar C, Mohapatra SD, Basana Gowda G, Patil Naveenkumar B (2024). Cg SSR marker based trait associations for *Sitotrogacerealella* (Olivier) resistance in stored paddy rice. JournalofStoredProductsResearch107:102340

Khan M, Raghu S, Prasad Sah RP, Azharudheen TPM, Moharana D, Behera S, Mohanty PM, Jeevan, Behera L, Marndi BC, Samantaray S, Anilkumar C(2024). Identification of novel QTL for bakanae disease resistance. Cereal Research Communications. pp. 1-10, https://doi.org/10.1007/s42976-024-00565-9.

Lima JM, Dass A, Sahu SC, Behera L, Chauahan (2007). A RAPD marker identified a susceptible specific locus for gall midge resistance gene in rice cultivar ARC5984. Crop Protection 26: 1431-1435.

Meher C, Pandi Govindharaj GP, Babu SB, Parameswaran C, Samal T, Sah RP, Anilkumar C, Basana Gowda G, Rath PC, Sabarinathan S (2024). Genomic dissection of brown planthopper, *Nilaparvatalugens* (Hemiptera: Delphacidae) resistance in Indica rice genotypes. Annals of Applied Biology 2024: 1-18.

Mohanty SK, Panda RS, Mohapatra SL, Nanda A, Behera L, Jena M, Sahu RK, Sahu SC, Mohapatra T (2017). Identification of novel quantitative trait loci associated with brown planthopper resistance in the rice landrace Salkathi. Euphytica 213: 38.

Mohanty SP, Nayak DK, Sanghamitra P, Barik SR, Pandit E, Behera A, ... , Pradhan SK (2023). Mapping the genomic regions controlling germination rate and early seedling growth parameters in rice. Genes 14(4): 902.

Mohanty SP, Muhammed Azharudheen TP, Anilkumar C, Sasmita Behera S, Pradhan AK, Beena R, Parameswaran C, Devanna BN, Marndi BC, Dash SK, Meher J, Sah RP (2024). Genome-wide association study revealed the genetics of seed vigour traits in rice **(***Oryza sativa* L.). Plant Breeding 0:1-12., https://doi.org/10.1111/pbr.13225.

Nanda A, Mohanty SK, Panda RS, Behera L, Prakash A, Sahu SC (2010). Flanking microsatellite markers for breeding varieties against Asian rice gall midge. Tropical Plant Biology 3(4): 219-226.

Nayak AK, Anilkumar C, Behera S, Sah RP, Lavanya GR, Kumar A, Behera L, Azharudheen TPM (2022a). Genetic dissection of grain size traits through genome-wide association study based on genic markers in rice. Rice Science 29(5): 462−472.

Nayak DK, Sahoo S, Barik SR, Sanghamitra P, Sangeeta S, Pandit E, Pradhan SK (2022b). Association mapping for protein, total soluble sugars, starch, amylose and chlorophyll content in rice. BMC Plant Biology 22(1): 620.

Ngangkham U, Nanda S, Katara JL, Samantaray S (2021). Identification of genomic regions for salinity tolerance at germination stage of rice using doubled haploid mapping population. Indian Journal of Genetics 81(2): 319-321.

Pandit E, Tasleem S, Barik SR, Mohanty DP, Nayak DK, Mohanty SP, Das S, Pradhan SK (2017). Genome-Wide Association Mapping Reveals Multiple QTLs Governing tolerance response for seedling stage chilling stress in *indica* rice. Frontiers in Plant Science 8: 552.

Parameswaran C, Balasubramaniasai C, Behura N, Purty M, Samantaray S, Subudhi HN, Ngangkham U, Devanna BN, Katara JL, Kumar A, Behera L (2021). Effects of high temperature on spikelet sterility in rice (*Oryza sativa* L.): association between molecular markers and allelic phenotypic effect in field condition. Genetic Resources and Crop Evolution 68:1923-1935.

Parameswaran C, Sahu S, Selvaraj S, Reshmi Raj KR, Balasubramaniasai C, Samantaray S, Muduli BC, Annamalai A, Meher J, Chatterjee D, Mohanty S, Swain P, Behera L (2024). Identification of novel marker-trait associations and candidate genes for combined low phosphorus and nitrogen-deficient conditions in rice at seedling stage. Tropical Plant Biology 17: 249-268.

Pawar S, Pandit E, Mohanty IC, Saha D, Pradhan SK (2021). Population genetic structure and association mapping for iron toxicity tolerance in rice. PLoS One 16(3): e0246232.

Pradhan SK, Barik SR, Sahoo A, Mohapatra S, Nayak DK, Mahender A, Meher J, Anandan A, Pandit E (2016). Population structure, genetic diversity and molecular marker-trait association analysis for high temperature stress tolerance in rice. PloS One 11(8): e0160027.

Pradhan SK, Pandit E, Pawar S, Bharati B, Chatopadhyay K, Singh S, Dash P, Reddy JN (2019). Association mapping reveals multiple QTLs for grain protein content in rice useful for biofortification. Molecular Genetics and Genomics 294: 963-983.

Pradhan SK, Pandit E, Pawar S, Naveenkumar R, Barik SR, Mohanty SP, ……, Patnaik SS C (2020). Linkage disequilibrium mapping for grain Fe and Zn enhancing QTLs useful for nutrient dense rice breeding. BMC Plant Biology 20: 1-24.

Sah RP, Nayak AK, Anilkumar C, Behera S, Azharudheen TPM, G Roopa Lavanyab GR (2023). cgSSR marker-based genome-wide association study identified genomic regions for panicle characters and yield in rice (*Oryza sativa* L.). Journal of the Science of Food and Agriculture 103(2): 720-728.

Sahoo S, Sanghamitra P, Nanda N, Pawar S, Pandit E, Bastia R, Mudul KC, Pradhan SK (2020). Association of molecular markers with physio-biochemical traits related to seed vigour in rice. Physiology and Molecular Biology of Plants 26: 1989-2003.

Sahu N, Gowda GB, Rath LK, Anilkumar C, Sah RP, Mandal L, Pandi Govindharaj GP, Patil NB, Adak T, Mahendiran A, Rath PC (2023). Marker-trait association analysis for gall midge (*Orseolia oryzae*) resistance in a diverse rice population. Annals of Applied Biology 182: 361–370.

Sanghamitra P, Nanda N, Barik SR, Sahoo S, Pandit E, Bastia R, Bagchi TB, Pradhan SK (2021). Genetic structure and molecular markers-trait association for physiological traits related to seed vigour in rice. Plant Gene 28: 100338.

Sanghamitra P, Barik SR, Bastia R, Mohanty SP, Pandit E, Behera A, ... , Pradhan SK (2022). Detection of genomic regions controlling the antioxidant enzymes, phenolic content, and antioxidant activities in Rice grain through association mapping. Plants 11(11): 1463.

Sar P, Gupta S, Behera M, Chakraborty K, Ngangkham U, Verma BC, Banerjee A, Hanjagi PS, Bhaduri D, Shil S, Kumar J, Mandal NP, Kole PC, Michael D. Purugganan MD, Roy S (2024). Exploring Genetic Diversity within *aus* Rice Germplasm: Insights into the Variations in Agro-morphological Traits. Rice 17: 20.

Sekhar S, J Kumar J, Mohanty S, Mohanty N, Panda RS, S Das S, Shaw SP, Behera L (2021). Identification of novel QTLs for grain fertility and associated traits to decipher poor grain filling of basal spikelets in dense panicle rice. Scientific Reports 11: 13617.

Shoba D, Raveendran M, Manonmani S, Utharasu S, Dhivyapriya D, Subhasini G, Ramchandar S, Valarmathi R, Grover N, Gopala Krishnan S, Singh AK, Jayaswal P, Kale P, Ramkumar MK, Amitha Mithra SV, Mohapatra T, Singh K, Singh NK, Sarla N, Sheshshayee MS, Kar MK, Robin S, and Sharma RP (2017). Development and Genetic Characterization of A Novel Herbicide (Imazethapyr) Tolerant Mutant in Rice (*Oryza sativa* L.). Rice 10:10.

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**Table 1a. List of QTLs, molecular markers, and prospective candidate genes identified for abiotic stress tolerance in rice using bi-parental mapping populations.**

| Sl No. | Trait | Parentage, donor, mapping population type and size | QTLs | Chrom # | Flanking/ linked markers | Position (cM/ Mb) | LOD | PVE (%) | Additive effect | Contribu-ting parent | Reference |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Salinity tolerance at seedling stage (Chlorophyll fluorescence) | Pokkali (AC41585) / IR64, Pokkali, BIL(BC3F4), 180 | *qFv/Fm1.1* | 1 | RM8085- RM488 | 59 | 6.012 | 16.039 | –0.141 | Pokkali | Chattopadhyay et al. (2020a) |
| | Fv/Fm | | *qFv/Fm2.1* | 2 | RM12548- RM1211 | 3 | 3.731 | 3.874 | –0.151 | Pokkali | |
| | Fv/Fm | | *qFv/Fm2.2* | 2 | RM13263- HvSSr02-50 | 89 | 6.122 | 14.392 | –0.146 | Pokkali | |
| | Fv/Fm | | *qFv/Fm3.1* | 3 | RM1426- RM7 | 56 | 4.447 | 14.909 | –0.144 | Pokkali | |
| | Fv/Fm | | *qFv/Fm4.1* | 4 | RM3317- RM16667 | 106 | 4.901 | 2.9 | –0.214 | Pokkali | |
| | Fv/Fm | | *qFv/Fm4.2* | 4 | RM127- RM241 | 127 | 5.556 | 14.965 | –0.143 | Pokkali | |
| | Fv/Fm | | *qFv/Fm5.1* | 5 | RM289- RM169 | 78 | 3.508 | 2.66 | –0.168 | Pokkali | |
| | Fv/Fm | | *qFv/Fm7.1* | 7 | RM180- RM5436 | 40 | 5.431 | 3.55 | –0.215 | Pokkali | |
| | Fv/Fm | | *qFv/Fm9.1* | 9 | HvSSR09-24- RM23887 | 20 | 6.325 | 13.264 | –0.147 | Pokkali | |
| | Fv/Fm | | *qFv/Fm9.2* | 9 | RM23887- RM24723 | 37 | 7.176 | 15.289 | –0.145 | Pokkali | |
| | Fv/Fm | | *qFv/Fm11.1* | 11 | RM26550- RM206 | 51 | 5.737 | 14.036 | –0.149 | Pokkali | |
| | Fv/Fm | | *qFv/Fm12.1* | 12 | RM27840- HvSSR12-26 | 79 | 7.326 | 10.83 | –0.149 | Pokkali | |
| | Fv/Fm | | *qFv/Fm12.2* | 12 | HvSSR12-26- RM19 | 93 | 4.427 | 2.8 | –0.182 | Pokkali | |
| | ΨEo | | *qΨE01.1* | 1 | RM8085- RM488 | 61 | 4.702 | 17.047 | –0.122 | Pokkali | |
| | ΨEo | | *qΨE02.1* | 2 | RM12548- RM1211 | 4 | 3.878 | 18.92 | –0.121 | Pokkali | |
| | ΨEo | | *qΨE04.1* | 4 | RM127- RM241 | 128 | 5.337 | 14.49 | –0.124 | Pokkali | |
| | ΨEo | | *qΨE09.1* | 9 | RM23887- RM24723 | 41 | 7.626 | 15.761 | –0.121 | Pokkali | |
| | ΨEo | | *qΨE010.1* | 10 | RM24869- RM24891 | 42 | 5.326 | 17.15 | –0.119 | Pokkali | |
| | ΦRo | | *qΦR09.1* | 9 | RM23887- RM24723 | 39 | 2.542 | 17.02 | –0.133 | Pokkali | |
| | ΦEo | | *qΦE01.1* | 1 | RM8085- RM488 | 61 | 5.065 | 17.06 | –0.133 | Pokkali | |
| | ΦEo | | *qΦE02.1* | 2 | RM12548- RM1211 | 4 | 5.131 | 16.26 | –0.133 | Pokkali | |
| | ΦEo | | *qΦE03.1* | 3 | RM1426- RM7 | 57 | 3.379 | 14.52 | –0.136 | Pokkali | |
| | ΦEo | | *qΦE04.1* | 4 | RM127- RM241 | 129 | 4.862 | 9.89 | –0.134 | Pokkali | |
| | ΦEo | | *qΦE09.1* | 9 | HvSSR09-24- RM23887 | 17 | 3.822 | 6.02 | –0.134 | Pokkali | |
| | ΦEo | | *qΦE09.2* | 9 | RM23887- RM24723 | 41 | 6.928 | 10.07 | –0.133 | Pokkali | |
| | ΦEo | | *qΦE010.1* | 10 | RM24869- RM24891 | 42 | 5.721 | 10.75 | –0.133 | Pokkali | |
| | ΦEo | | *qΦE012.1* | 12 | RM27840- HvSSR12-26 | 77 | 4.625 | 15.94 | –0.136 | Pokkali | |
| | PIABS | | *qPIABS9.1* | 9 | RM23887-RM24723 | 42 | 2.979 | 21.53 | –2.207 | Pokkali | |
| | SSI-Na-K | | *qSSI-Na-K9.1* | 9 | HvSSR09-24- RM23887 | 29 | 5.755 | 20.76 | 0.855 | Pokkali | |
| | SSI-Na-K | | *qSSI-Na-K1.1* | 1 | RM8085- RM488 | 58 | 4.8 | 20.8 | 2.34 | Pokkali | |

**Table 1a Contd….**

| Sl No. | Trait | Parentage, donor, mapping population type and size | QTLs | Chrom # | Flanking/ linked markers | Position (cM/ Mb) | LOD | PVE (%) | Additive effect | Contribu-ting parent | Prospective candidate genes | Reference |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 2 | Salinity tolerance at reproductive stage | Pokkali (AC41585), IR64, Pokkali, BIL(BC3F5), 180 | *qDEG-S-2-2* | 2 | RM263- RM13709 | 6.8 | | 34.44 | 6.93 | IR 64 | LOC_Os01g389 80.1 | Chattopadhyay et al. (2021a) |
| | Chlorophyll fluorescence | | *qDEG-S-4-3* | 4 | RM3317- RM16667 | 4.19 | | 17.43 | 7.32 | IR 64 | LOC_Os02g319 10.1 | |
| | | | *qK-S-1-1* | 1 | Os01g32120- RM9 | 5.09 | | 37.78 | 7.74 | AC 41585 | LOC_Os04g329 20.2 | |
| | | | *qSSI-STE-2-1* | 2 | HvSSR02-50-RM13263- RM6942 | 7.02 | | 38.79 | 5.97 | AC 41585 | LOC_Os01g389 80.1 | |
| | | | *qSSI-STE-2-2* | 2 | RM13263- RM7389 | 9.86 | | 42.52 | 6.55 | AC 41585 | LOC_Os01g389 80 | |
| | | | *qSSI-STE-3-1* | 3 | RM16153- RM7389 | 8.27 | | 38.53 | 6.55 | AC 41585 | LOC_Os06g459 40.1 | |
| | | | *qSSI-STE-4-1* | 4 | RM16913- RM349 | 3.36 | | 38.85 | 4.84 | AC 41585 | | |
| | | | *qSSI-STE-11-1* | 11 | RM332- RM224 | 9.31 | | 34.75 | 6.49 | AC 41585 | | |
| | | | *qSSI-Grain-2-1* | 2 | RM263- RM13709 | 6.35 | | 38.47 | -1.82 | AC 41585 | | |
| 3 | Salinity tolerance at germination stage | Pokkali/ Saviiri, Pokkali, DH, BSA, 117 | RM247 | 12 | RM247 | 3.18 Mb | | | | | LOC_Os12g065 60, LOC_Os 12g065 70 | Ngangkham et al. (2021) |
| | | | RM324 | 2 | RM324 | 11.38 Mb | | | | | LOC_Os01g009 550/SNAC3 | |
| | | | RM283 | 1 | RM283 | 4.88 Mb | | | | | LOC_Os01g095 60 | |
| 4 | Stagnant flooding tolerance | Swarna/ Rashpanjor, Rashpanjor, RIL, 180 | | | | | | | | | | Chattopadhyay et al. (2021b) |
| | PH | | *qPH-NS.3.1* | 3 | SNP112 | 3.775291 | 2.45 | 33.5353 | -7.2845 | | Os03g0170900 | |
| | PH | | *qPH-S.5.1* | 5 | SNP190 | 1.859866 | 2.24 | 6.8337 | 4.9925 | | Os05g0132300 | |
| | PH | | *qSSI-PH-6.1* | 6 | SNP232 | 18.9041 | 2.23 | 6.5761 | -0.2453 | | Intergenic region | |
| | EL | | *qEL-NS-1.1* | 1 | SNP23 | 24.82973 | 2.72 | 9.8351 | 4.5552 | | Os01g0592900 | |
| | EL | | *qEL-NS-3.1* | 3 | SNP130 | 29.62379 | 2.44 | 22.9294 | -6.8637 | | Os03g0713400 | |
| | EL | | *qEL-S-11.1* | 11 | SNP450 | 25.76171 | 2.2916 | 9.537 | -4.6522 | | Os11g0615200 | |
| | EL | | *qSTI-EL- 1.1* | 1 | SNP47 | 42.18993 | 2.2929 | 8.57 | -0.217 | | Os01g0923600 | |
| | EL | | *qSTI-EL- 3.1* | 3 | SNP112 | 3.775291 | 2.3647 | 23.3951 | -0.318 | | Os03g0170900 | |

**Table 1a Contd….**

| Sl No. | Trait | Parentage, donor, mapping population type and size | QTLs | Chrom # | Flanking/ linked markers | Position (cM/ Mb) | LOD | PVE (%) | Additive effect | Prospective candidate genes | Reference |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | EL | | *qSTl-EL- 11.1* | 11 | SNP450 | 25.76171 | 2.2771 | 7.9747 | -0.2057 | Os11g0615200 | |
| | EL | | *qSTl-EL- 12.1* | 12 | SNP498 | 20.3287 | 2.0515 | 15.4926 | -0.2605 | Intergenic region | |
| | PN | | *qPN-NS- 4.1* | 4 | SNP186 | 33.80545 | 2.12 | 6.5317 | 10.3181 | Os04g0655000 | |
| | PN | | *qSSl-PN- 12.1* | 12 | SNP501 | 26.37656 | 2.1711 | 6.8919 | 0.1661 | Os12g0616400 | |
| | GW | | *qGW-NS- 10.1* | 10 | SNP389 | 9.647341 | 2.5197 | 54.6806 | 87.2539 | Intergenic region | |
| | GW | | *qSSl-GW-1.1* | 1 | SNP49 | 42.89045 | 2.2332 | 12.9923 | -0.1581 | Os01g0936100 | |
| | GW | | *qSTl-GW- 10.1* | 10 | SNP389 | 9.647341 | 2.1459 | 57.8947 | 0.4844 | Intergenic region | |
| | PW | | *qSSl-PW- 1.1* | 1 | SNP49 | 42.89045 | 2.104 | 6.5974 | -0.049 | Os01g0936100 | |
| | PGW (grain weight/panicle) | | *qSSl-PGW- 1.1* | 1 | SNP49 | 42.89045 | 2.1161 | 6.634 | -0.2747 | Os01g0936100 | |
| 5 | Combined tolerance(salinity and flooding) | Swarna/ Rashpanjor, Rashpanjor, RIL, 1150 | | | | | | | | | Chattopadhyay et al. (2021b) |
| | *qFv/Fm* | | *qFv/Fm-S-1-1* | 1 | SNP15-SNP2 | 16 | 3.2946 | 16.260 | -0.025 | | |
| | *qFv/Fm* | | *qFv/Fm-S-11-1* | 11 | SNP426- SNP409 | 54 | 2.9098 | 11.315 | 0.018 | | |
| | *Y-NO* | | *qY-NO-S-1-1* | 1 | SNP15-SNP2 | 16 | 4.5429 | 33.301 | 0.042 | | |
| | *Y-NO* | | *qY-NO-S-10-1* | 10 | SNP405-SNP389 | 177 | 6.7489 | 32.856 | 0.045 | | |
| | *Y-NO* | | *qY-NO-S-10-2* | 10 | SNP389- SNP407 | 203 | 8.4214 | 34.489 | 0.044 | | |
| | *Y-NO* | | *qY-NO-S-11-1* | 11 | SNP426-SNP409 | 56 | 3.3855 | 17.248 | -0.026 | | |
| | *qL-NS* | | *qqL-NS-5-1* | 5 | SNP200-SNP193 | 78 | 3.0056 | 29.929 | 0.043 | | |
| 6 | Reproductive stage drought stress (DFF) | CR143-2-2,/Krishnahamsa, CR143-2-2, RIL, BSA, 190 | *qDFF1.1* | 1 | RM3825 | 143.7cM | 3.839 | 8.78 | -1.97 | | Barik et al. (2018a) |
| | DFF | | *qDFF6.1* | 6 | RM527 | 61.2cM | 2.04 | 4.77 | -1.33 | | |
| 7 | Relative water content at reproductive stage drought stress | CR143-2-2,/Krishnahamsa, CR143-2-2, RIL, BSA, 190 | *qRWC9.1* | 9 | RM316-RM257 | 21.88cM | 4.27 | 60.87 | 14.56 | | Barik et al. (2018b) |

**Table 1a Contd….**

| Sl No. | Trait | Parentage, donor, mapping population type and size | QTLs | Chrom # | Flanking/ linked markers | Position (cM/ Mb) | LOD | PVE (%) | Additive effect | Reference |
|---|---|---|---|---|---|---|---|---|---|---|
| 8 | Morpho-physiological traits under reproductive stage drought stress | CR143-2-2,/Krishnahamsa, CR143-2-2, RIL, BSA, 190 | | | | | | | | Barik et al. (2019) |
| | Leaf Rolling | | *qLR8.1* | 8 | | 27.1 cM | 2.78 | 60.74 | -1.68 | |
| | Leaf Rolling | | *qLR9.1* | 9 | | 8.21 cM | 7.2 | 67.46 | -1.9 | |
| | Leaf drying | | *qLD9.1 9* | 9 | | 14.8 cM | 27.85 | 80.18 | -1.81 | |
| | Leaf drying | | *qLD12.1* | 12 | | 45 cM | 11.35 | 71.72 | 1.82 | |
| | Harvest Index | | *HI9.1* | 9 | | 11.8 cM | 5.21 | 56.45 | 0.01 | |
| | Spikelet fertility | | *qSF9.1* | 9 | | 23.8 cM | 3.58 | 54.8 | 8.35 | |
| | Relative water content | | qRWC9.1 | 9 | | 21.8 cM | 4.27 | 60.87 | 14.56 | |
| 9 | Physiological traits under reproductive stage drought stress | CR143-2-2,/Krishnahamsa, CR143-2-2, RIL, BSA, 190 | | | | | | | | Barik et al. (2020) |
| | Proline content | | *qPRO3.1* | 3 | RM22-RM557 | 21.2 cM | 13.93 | 78.19 | −61.5 | |
| | Relative chlorophyll content | | *qCHLa1.1* | 1 | RM495-RM6703 | 81.8 cM | 4.13 | 64.5 | −0.65 | |
| | Chlorophyll a | | *qRCC1.1* | 1 | RM6703-RM3825 | 142.8 cM | 4.76 | 12.47 | −2.35 | |

**Table 1b: List of QTLs, molecular markers, and prospective candidate genes identified for abiotic stress tolerance in rice using association-mapping populations.**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/gene | Chrom# | Position (cM/Mb) | P- value/ FDR | PVE (R2) | References |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **High temperature stress tolerance (DAF)** | 59/240 | 2 Indels, 18 lined markers, 20 | INDEL3 | | 9 | 1.5cM | 0.03931 | 7.536 | Pradhan et al. (2016) |
| | Panicle length | | | RM242 | | 9 | 73.3cM | 0.03253 | 8.751 | |
| | Panicle length | | | INDEL3 | | 9 | 1.5cM | 0.0161 | 11.208 | |
| | Flag leaf length | | | RM205 | | 9 | 112.3–112.3 cM | 0.02346 | 9.18 | |
| | Flag leaf length | | | RM547 | | 8 | 58.1cM | 0.03388 | 8.003 | |
| | Flag leaf width | | | RM247 | | 12 | 14.9–44.1 cM | 0.01924 | 9.828 | |
| | Panicle emergence (normal) | | | RM228 | | 10 | 22.8cM | 0.01015 | 11.97 | |
| | Panicle emergence(stress) | | | RM228 | | 10 | 22.8cM | 0.04084 | 7.417 | |
| | Spikelet fertility (stress) | | | RM547 | | 8 | 58.1cM | 0.02597 | 8.852 | |
| | Spikelet sterility (stress) | | | RM547 | | 8 | 58.1cM | 0.02597 | 8.852 | |
| 2 | **High temperature on Spikelet fertility** | 67/198 | 9-heat stress linked markers, 9 | RM205 | | 9 | 18.64-22.41 Mb | 0.022 | 7.75 | Parameswaran et al. (2021) |
| | **Spikelet fertility** | | | RM242 | | 9 | | 0.044 | 6.08 | |
| 3 | **Cold tolerance at seedling stage** | 66/304 | SSR, 60 (58 linked and 2 direct) | RM 328 | *qCTS9* | 9 | 82.4 cM | | 8.2 | Pandit et al. (2017) |
| | | | | RM 341 | *qCTS-2* | 2 | 82.7 cM | | 27.42 | |
| | | | | RM 253 | *qCTS6.1* | 6 | 3.8 Mb | | 15.3 | |
| | | | | RM2634 | *qSCT2* | 2 | 15.6 cM | | 6.5 | |
| | | | | RM4112 | *qSCT11* | 11 | 23.1 cM | | 16.5 | |
| | | | | RM5310 | *qSCT1a* | 1 | 11.3 cM | | 10.6 | |
| | | | | RM7179 | *qCTS-3.1* | 3 | 35.3 Mb | | 15.7 | |
| | | | | RM3701 | *qCTS11.1* | 11 | 63 Mb | | 9 | |
| | | | | RM104 | *qCTS12.1* | 1 | 186.6 cM | | 3.37 | |
| | | | | RM9 | *qCTS-1b* | 1 | 92.4 cM | | 11.31 | |
| | | | | RM6547 | *qCTB2* | 4 | 18.98 cM | | 18.98 | |

**Table 1b Contd….**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/gene | Chrom# | Position (cM/Mb) | P-value/ FDR | PVE (R2) | Prospective candidate genes | References |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 4 | **Low Phosphorpus tolerance** | 120/155 | low-P QTL-linked markers, 78 | | | | | | | | Anandan et al. (2022) |
| | NL | | | RM283 | *qNL1.1* | 1 | 4.89 | 0.0042 | 8.64 | Os01t0178500-02 | |
| | RDW | | | RM297 | *qRDW1.1* | 1 | 32.09 | 0.0002 | 14.97 | Os01t0746400-01 | |
| | SDW | | | RM297 | *qSDW1.1* | 1 | 32.09 | 0.0011 | 11.28 | Os01t0746400-01 | |
| | TDW | | | RM297 | *qTDW1.1* | 1 | 32.09 | 0.0007 | 12.25 | Os01t0746400-01 | |
| | C% | | | RM521 | *qMC2.1* | 2 | 10.81 | 0.0019 | 10.33 | | |
| | NT | | | RM2334 | *qNT3.1* | 3 | 26.55 | 0.0023 | 9.94 | Os03t0672900-01 | |
| | RL | | | RM200 | *qRL3.1* | 3 | 13.4 | 0.0041 | 8.72 | | |
| | TRL | | | RM200 | *qTRL3.1* | 3 | 13.4 | 0.0036 | 8.96 | | |
| | C% | | | RM1272 | *qMC4.1* | 4 | 35.33 | 0.0051 | 8.31 | Os04t0688300-01 | |
| | LW | | | RM574 | *qLW5.1* | 5 | 3.39 | 0.0043 | 8.47 | | |
| | RL | | | RM30 | *qRL6.1* | 6 | 27.25 | 0.0022 | 9.95 | Os03t0672900-01 | |
| | TRL | | | RM3343 | *qTRL6.1* | 6 | 29.1 | 0.0045 | 8.52 | | |
| | ARD | | | RM6966 | *qARD8.1* | 8 | 27.32 | 0.0045 | 8.44 | *Os08g0564000* | |
| | LL | | | RM6966 | *qLL8.1* | 8 | 27.32 | 0.0015 | 10.75 | *Os08g0564000* | |
| | SL | | | RM6966 | *qSL8.1* | 8 | 27.32 | 0.0068 | 7.71 | Os08g0564000 | |
| | TRPA | | | RM6966 | *qTRP8.1* | 8 | 27.32 | 0.006 | 7.99 | Os08g0564000 | |
| | TSA | | | RM6966 | *qTSA8.1* | 8 | 27.32 | 0.006 | 7.98 | Os04t0688300-01 | |
| | LL | | | RM242 | *qLL9.1* | 9 | 18.64 | 0.0046 | 8.5 | Os04t0688300-01 | |
| | NT | | | RM242 | *qNT9.1* | 9 | 18.64 | 0.0022 | 9.97 | Os09t0491740-01 | |
| | NT | | | PAP1 | *qNT11.1* | 11 | 2.43 | 0.007 | 7.67 | Os11t0149100-01 | |
| | RDW | | | RM5926 | *qRDW11.3* | 11 | 28.33 | 0.0066 | 7.76 | | |
| | RV | | | RM5926 | *qRV11.3* | 11 | 28.33 | 0.0007 | 12.46 | | |
| | SDW | | | RM5926 | *qSDW11.2* | 11 | 28.33 | 0.0009 | 11.67 | | |
| | TDW | | | RM5926 | *qTDW11.2* | 11 | 28.33 | 0.0013 | 11.09 | | |
| | RDW | | | K29-3 | *qRDW12.2* | 12 | 15.42 | 0.0072 | 7.6 | | |
| | RL | | | K41 | *qRL12.1* | 12 | 0.26 | 0.0071 | 7.64 | | |
| | SG | | | K20-2 | *qSG12.2* | 12 | 15.41 | 0.001 | 11.56 | | |
| | SG | | | K41 | *qSG12.1* | 12 | 0.26 | 0.0034 | 9.08 | | |
| | TPA | | | K20-2 | *qTPA12.2* | 12 | 15.41 | 0.0019 | 10.51 | | |

**Table 1b Contd….**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/gene | Chrom# | Position (cM/Mb) | P- value/ FDR | PVE (R2) | Prospective candidate genes | References |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 5 | **Low P and N tolerance** | 142 | SNP(GBS), 22214 | 5 | | | | | | | Parameswaran et al. (2024) |
| | RA | | | S3_6252886 | | 3 | | 1.23E-13 | 24.617 - 79.289 | Os03g0213700 | |
| | RA | | | S4_31775073 | | 4 | | 6.50E-09 | 11.849 | Os04g0620000 | |
| | RA | | | S9_21620747 | | 9 | | 1.42E-06 | 11.936 | Os09g0555300 | |
| | RDW | | | S4_34376663 | | 4 | | 2.87E-06 | 41.161 - 47.842 | Os04g0674800 | |
| | RDW | | | S3_6252886 | | 3 | | 3.64E-07 | 46.115 | Os03g0213700 | |
| | RL | | | S2_4834794 | | | | 1.28E-06 | 15.679 | Os02g0180200 | |
| | RL | | | S3_21544808 | | 3 | | 1.05E-06 | 10.225 | Os03g0576700 | |
| | SDW | | | S2_29956617 | | 2 | | 0.000056 | 12.055 | Os02g0722400 | |
| | SDW | | | S4_31775073 | | 4 | | 0.0059 | 10.754 | Os04g0624000 | |
| | NL | | | S3_6992519 | | 3 | | 0.000079 | 12.424 | Os03g0235900 | |
| | NL | | | S6_1377569 | | 6 | | 0.00024 | 10.234 | Os06g0129400 | |
| | SL | | | S12_13141020 | | 12 | | 0.0154 | 14.643 | | |
| | SL | | | S6_4807875 | | 6 | | 0.047 | 10.888 | Os06g0193400 | |
| | SL | | | S1_41400271 | | 1 | | 0.0378 | 10.66 | Os01g0945200 | |
| | SA | | | S11_4084490 | | 11 | | 7.07E-05 | 12.206 | Os11g0178800, Os11g0179700, Os11g0180000 | |
| | SA | | | S11_4154802 | | 11 | | 0.00031 | 12.608 | Os11g0178800, Os11g0179700, Os11g0180000 | |
| | RA | | | S1_6393185 | | 1 | | 8.93E-14 | 13.166 - 69.967 | Os01g0208700 | |
| | RA | | | S3_8446144 | | 3 | | 2.34E-06 | 12.419 | Os03g0263400 | |
| | RA | | | S4_223308 | | 4 | | 2.34E-06 | 17.733 | Os04g0101800 | |
| | RA | | | S9_16231177 | | 9 | | 1.48E-07 | 26.72 | Os09g0439800 | |
| | SL | | | S7_14115790 | | 7 | | 2.85E-06 | 59.41 | Os07g0434700 | |

**Table 1b Contd….**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/gene | Chrom# | Position (cM/Mb) | P- value/ FDR | PVE (R2) | Prospective candidate genes | References |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 6 | **Iron toxicity tolerance** | 119/352 | SSR, gene specific 51 (47 SSR and 4 gene specific markers) | | | | | | | *qFeTox4.3 (Novel)* | Pawar et. al. (2021) |
| | GN | | | RM590 | | | | 0.03905 | 3.765 | *qFeTox6.1 (Novel)* | |
| | GN | | | RM574 | | | | 0.02938 | 4.205 | *qFeTox10.1 (Novel)* | |
| | GN | | | RM3412 | | | | 0.00382 | 7.537 | *qFeTox1.1* | |
| | Yield | | | RM168 | | | | 0.00231 | 8.414 | | |
| | Yield | | | RM5638 | | | | 0.04541 | 3.542 | | |
| | Yield | | | RM7 | | | | 0.01824 | 4.965 | | |
| | Yield | | | Loc_Os01g49 710 | | | | 0.04179 | 3.668 | | |
| | Yield | | | RM7003 | | | | 0.01113 | 5.765 | | |
| | PN | | | RM202 | | | | 0.02907 | 4.029 | | |
| | PN | | | RM269 | | | | 0.00877 | 5.865 | | |
| | PN | | | RM3412 | | | | 0.02493 | 4.258 | | |
| | LBI_Hydroponics | | | RM471 | *qFeTox4.3 (Novel)* | | | 0.00143 | 8.958 | | |
| | LBI_Hydroponics | | | RM3 | *qFeTox6.1 (Novel)* | | | 0.02652 | 4.235 | | |
| | LBI_Hydroponics | | | RM590 | | | | 0.01237 | 5.416 | | |
| | LBI_Hydroponics | | | RM243 | *qFeTox1.1* | | | 0.00899 | 5.923 | | |
| | Fe_Content | | | RM590 | *qFeTox10.1 (Novel)* | | | 0.0406 | 3.82 | | |
| | Fe_Content | | | RM1278 | | | | 0.03209 | 4.193 | | |
| | Fe_Content | | | RM488 | | | | 0.01397 | 5.552 | | |
| | Fe_Content | | | RM17 | | | | 0.01839 | 5.096 | | |
| | Fe_Content | | | RM517 | | | | 0.01236 | 5.756 | | |
| | TW | | | RM31 | | | | 0.03423 | 3.142 | | |
| | TW | | | RM202 | | | | 0.02604 | 3.479 | | |
| | TW | | | OsIRT1 | | | | 0.00212 | 6.771 | | |
| | TW | | | RM245 | | | | 0.02747 | 3.413 | | |

**Table 2a. List of QTLs, molecular markers, and prospective candidate genes identified for biotic stress resistance using bi-parental mapping populations.**

| Sl No. | Trait | Parentage, donor, mapping population type and size | QTLs | Chrom# | Flanking/ Linked markers | Position (cM/Mb/bp) | LOD | PVE (R2) | Additive | Dominance | Prospective candidate genes | Reference |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Sheath blight resistance | Swarna-sub1/ CR 1014, CR 1014, F2, 216 | *qShB-1.1* | 1 | RM11935-RM11943 | 37784288bp-37851779bp | 10.23 | 25.23 | -9.32 | -1.99 | | Bal et al. (2020) |
| | | Swarna-sub1/ CR 1014, CR 1014, F2, 216 | *qShB-1.2* | 1 | RM11069-RM11312 | 19370286bp-24013610bp | 2.51 | 12.59 | -5.09 | -4.85 | LOC_Os01g36930, LOC_Os01g37760, LOC_Os01g39790, LOC_Os01g39800, LOC_Os01g40840, LOC_Os01g41630 | |
| | | Swarna-sub1/ CR 1014, CR 1014, F2:3, 216 | *qShB-1.3* | 1 | RM10037-RM10047 | 562780bp-744440bp | 2.72 | 9.31 | 0.97 | -5.78 | | |
| | | Swarna-sub1/ CR 1014, F2:3, 216 | *qShB-1.1* | 1 | RM11935-RM11968 | 37784288bp-38293480bp | 5.11 | 13.95 | -5.77 | -3.3387 | | |
| | | Tapaswini / CR 1014 (Validation of QTL), CR 1014, F4, 192 | *qShB-1.1* | 1 | RM11935-RM11968 | 37784288bp-38293480bp | 20.56 | 26.9 | -5.67 | 0 | LOC_Os01g65450, LOC_Os01g65900 | |
| | | Swarna-sub1 / CR 1014 (Validation of QTL), CR 1014, F5, 630 | *qShB-1.1* | 1 | RM11935-RM11968 | 37784288bp-38293480bp | 13.51 | 31.54 | -6.89 | -2.089 | LOC_Os01g65450, LOC_Os01g65900 | |
| 2 | Bakanae disease | Thavalakannan / Pooja, Thavalakanan, RIL, 149 | *qBK5.1* | 5 | RM229-RM289 | 63.29 cM | 3.14 | 8.97 | -6.94 | | Os05g0518800, Os05g0228400, Os05g0178100, Os05g0540800 | Khan et al. (2024) |
| 3 | Gall midge resistance(Biotypes 1, 2 and 5) | TN1/ARC5984, ARC5984, RILs, 120 | - | | $OPQ05_{1150}$ | | | 100.0 | | | | Lima et al (2007) |
| 4 | Gall midge resistance (Biotypes 1, 2, 3 and 4) | TN1/PTB10, PTB10, RIL, 112 | *Gm4* | 8 | RM22550-RM547 | 5.591-5.602Mb | | 100.0 | | | | Nanda et al (2010) |
| 5 | BPH resistance | TN1/Salkathi, Salkathi, RILs, 300 | *qBph4.3* | 4 | RM551 -RM335 | 0.177-0.688 Mb | 34.2 | 37.0 | -1.75 | | | Mohanty et al (2017) |
| | | | *qBph4.4* | 4 | RM335 -RM5633 | 0.688 -13.07 Mb | 4.61 | 7.10 | -0.77 | | | |
| | | TN1/Salkathi, Salkathi, RIL, 190 | *qBph4.3* | 4 | TBGI179448-TBGI182095 | 0.62-1.39 | 6.3 | 11.13 | -10.88 | | LOC_Os04g02510, LOC_Os04g02860 LOC_Os04g02920 | |
| | | | *qBph4.4* | 4 | TBGI198748 - TBGI205343 | 18.63 to 23.85 | 8.0 | 14.15 | --12.32 | | LOC_Os04g3425 | |
| 6 | Hebicide tolerance | HTM-N22/Pusa 1656, HTM-N22, F2:3, 254, BSA | AHAS (AcetoHydroxy Acid Synthase) | 2 | RM6844 | 18169413 | | - | - | | LOC_Os02g30630 | Shoba et al. (2017) |

**Table 2b. List of QTLs, molecular markers, and prospective candidate genes identified for biotic stress resistance using association-mapping populations.**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/ gene | Chrom# | Position | P- value/ FDR | Prospective candidate genes | References |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **Gall midge resistance** | 200 | Gene linked markers, 13 | RM17480 | *gm3* | 4 | | 0.04 | Loc_os04g02640, Loc_os04g30760, Loc_os04g40570, Loc_os04g34600, Loc_os04g04230 | Sahu et al. (2023). |
| 2 | **BPH Resistance** | 104 | SSR, 87 | RM222 | *Bph30* | 10 | | 1.E- 06** | | Anant et al. (2021). |
| | Percent Damage (PD) | | | RM6997 | *bph6* | 4 | | 0.002** | | |
| | PD | | | RM17006 | *Bph33* | 4 | | 0.002** | | |
| | PD | | | RM6308 | *bph19* | 3 | | 0.041* | | |
| | PD | | | RM463 | *bph2* | 12 | | 0.406 | | |
| | PD | | | RM28561 | *Bph21* | 12 | | 0.011 | | |
| | PD | | | RM586 | *bph4* | 6 | | 0.131 | | |
| | PD | | | RM309 | *Bph26* | 12 | | 0.39 | | |
| | PD | | | RM5479 | *Bph25* | 12 | | 0.279 | | |
| | Nymphal Survival (NS) | | | RM222 | *Bph30* | 10 | | 1.E- 08** | | |
| | NS | | | RM6997 | *bph6* | 4 | | 0.002** | | |
| | NS | | | RM17006 | *Bph33* | 4 | | 0.003** | | |
| | NS | | | RM6308 | *bph19* | 3 | | 0.01 | | |
| | NS | | | RM463 | *bph2* | 12 | | 0.009 | | |
| | NS | | | RM28561 | *Bph21* | 12 | | 0.011 | | |
| | NS | | | RM586 | *bph4* | 6 | | 0.15 | | |
| | NS | | | RM309 | *Bph26* | 12 | | 0.372 | | |
| | NS | | | RM5479 | *Bph25* | 12 | | 0.255 | | |
| | Feeding Mark (FM) | | | RM222 | *Bph30* | 10 | | 5.E- 09** | | |
| | FM | | | RM6997 | *bph6* | 4 | | 0.001** | | |
| | FM | | | RM17006 | *Bph33* | 4 | | 0.092 | | |
| | FM | | | RM6308 | *bph19* | 3 | | 0.011* | | |
| | FM | | | RM463 | *bph2* | 12 | | 0.005** | | |
| | FM | | | RM28561 | *Bph21* | 12 | | 0.007** | | |
| | FM | | | RM586 | *bph4* | 6 | | 0.021* | | |
| | FM | | | RM309 | *Bph26* | 12 | | 6.E- 07** | | |
| | FM | | | RM5479 | *Bph25* | 12 | | 0.147 | | |
| | Area fed ($cm^2$)(AF) | | | RM222 | *Bph30* | 10 | | 3.E- 05** | | |
| | AF | | | RM6997 | *bph6* | 4 | | 0.013* | | |
| | AF | | | RM17006 | *Bph33* | 4 | | 0.002** | | |
| | AF | | | RM6308 | *bph19* | 3 | | 0.004** | | |
| | AF | | | RM463 | *bph2* | 12 | | 0.012 | | |
| | AF | | | RM28561 | *Bph21* | 12 | | 0.012 | | |
| | AF | | | RM586 | *bph4* | 6 | | 0.176 | | |
| | AF | | | RM309 | *Bph26* | 12 | | 0.461 | | |
| | AF | | | RM5479 | *Bph25* | 12 | | 0.147* | | |

**Table 2b Contd….**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/ gene | Chrom# | Position | P- value/ FDR | PVE (R2) | References |
|---|---|---|---|---|---|---|---|---|---|---|
| 3 | **BPH Resistance** | 268 | SSR, 93 | RM19291 | *Bph30* | 6 | | 1E-05** | 13.8 | Babu et al. (2022). |
| | Percent Damage (PD) | | | RM28472 | *Bph18* | 12 | | 0.002* | 11.4 | |
| | PD | | | RM28449 | *Bph17* | 12 | | 0.211 | 7 | |
| | PD | | | RM7 | *Qbph4.3* | 3 | | 2E-11** | 7.1 | |
| | PD | | | RM5633 | *Qbph4.4* | 4 | | 0.008 | 3.5 | |
| | Nymphal Survival (NS) | | | RM19291 | *Bph30* | 6 | | 1E-05** | 13.4 | |
| | NS | | | RM28472 | *Bph18* | 12 | | 0.005* | 11.7 | |
| | NS | | | RM28449 | *Bph17* | 12 | | 0.2 | 7.6 | |
| | NS | | | RM7 | *Qbph4.3* | 3 | | 0.001 | 6.3 | |
| | NS | | | RM5633 | *Qbph4.4* | 4 | | 0.442 | 6.1 | |
| | Feeding Mark | | | RM19291 | *Bph30* | 6 | | 0.002* | 7.4 | |
| | FM | | | RM28472 | *Bph18* | 12 | | 0.003* | 11.3 | |
| | FM | | | RM28449 | *Bph17* | 12 | | 0.154 | 9.6 | |
| | FM | | | RM7 | *Qbph4.3* | 3 | | 5E-07** | 5.5 | |
| | FM | | | RM5633 | *Qbph4.4* | 4 | | 0.001 | 4.7 | |
| | Area fed ($cm^2$)(AF) | | | RM19291 | *Bph30* | 6 | | 2E-05** | 13.5 | |
| | AF | | | RM28472 | *Bph18* | 12 | | 0.001* | 12.3 | |
| | AF | | | RM28449 | *Bph17* | 12 | | 0.255 | 4.4 | |
| | AF | | | RM7 | *Qbph4.3* | 3 | | 5E-10** | 6.8 | |
| | AF | | | RM5633 | *Qbph4.4* | 4 | | 0.021 | 3.2 | |

**Table 2b Contd….**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/ gene | Chrom# | Position | P- value/ FDR | PVE (R2) | References |
|---|---|---|---|---|---|---|---|---|---|---|
| 4 | **BPH resistance** | 191 | Linked SSR markers to 23 BPH resistance genes, 81 | RM314 | *Bph6* | 6 | | 2E-04** | 7.8 | Meher et al. (2024) |
| | Average %of PD | | | RM6732 | *Bph15* | 12 | 2,19,49,619 | 0.056 | 1.9 | |
| | | | | RM16999 | *Bph6* | 4 | 2,12,42,848 | 6E-04** | 72 | |
| | Average %of PD | | | RM7 | *QBph3* | 3 | | 0.081 | 1.6 | |
| | Average %of PD | | | RM7102 | *Bph1* | 12 | 1,32,11,325 | 0.035* | 2.3 | |
| | Average %of PD | | | RM401 | *bph4* | 4 | 1,31,54,172 | 0.162 | 1 | |
| | % NS | | | RM314 | *Bph6* | 6 | | 4E-05** | 9.5 | |
| | % NS | | | RM6732 | *Bph15* | 12 | 2,19,49,619 | 0.069 | 1.7 | |
| | % NS | | | RM16999 | *Bph6* | 4 | 2,12,42,848 | 2E-05** | 9.9 | |
| | % NS | | | RM7 | *QBph3* | 3 | | 0.092 | 1.5 | |
| | % NS | | | RM7102 | *Bph1* | 12 | 1,32,11,325 | 0.041* | 2.1 | |
| | % NS | | | RM314 | *Bph6* | 4 | 1,31,54,172 | 0.212 | 0.8 | |
| | FM (♀/plant) | | | RM314 | *Bph6* | 6 | | 0.005* | 4 | |
| | FM (♀/plant) | | | RM6732 | *Bph15* | 12 | 2,19,49,619 | 0.045* | 1.9 | |
| | FM (♀/plant) | | | RM16999 | *Bph6* | 4 | 2,12,42,848 | 0.027* | 2.5 | |
| | FM (♀/plant) | | | RM7 | *QBph3* | 3 | | 0.550* | 9.4 | |
| | FM (♀/plant) | | | RM7102 | *Bph1* | 12 | 1,32,11,325 | 0.012* | 3.1 | |
| | FM (♀/plant) | | | RM401 | *bph4* | 4 | 1,31,54,172 | 0.185 | 0.8 | |
| | Area fed (cm2) | | | RM314 | *Bph6* | 6 | | 0.06 | 1.9 | |
| | Area fed (cm2 | | | RM6732 | *Bph15* | 12 | 2,19,49,619 | 0.138 | 1.1 | |
| | Area fed (cm2 | | | RM16999 | *Bph6* | 4 | 2,12,42,848 | 0.573 | 0.2 | |
| | Area fed (cm2 | | | RM7 | *QBph3* | 3 | | 5E-05** | 5.6 | |
| | Area fed (cm2 | | | RM7102 | *Bph1* | 12 | 1,32,11,325 | 0.038* | 2.3 | |
| | Area fed (cm2 | | | RM401 | *bph4* | 4 | 1,31,54,172 | 0.205 | 0.8 | |
| 5 | ***Sitotroga cerealella*** | 80 | cgSSR, 39 | | | | | | | Kajal et al. (2024) |
| | Grain size | | | M8 | *SDG725* | 2 | 20899808 | 0.01 | 18 | |
| | Amylose content and grain size | | | M16 | *FLO2* | 4 | 32835169 | 0.04 | 13 | |

**Table 3. List of QTLs, molecular markers, and prospective candidate genes for seed and seedling vigour traits in rice using association-mapping populations.**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/ gene, | Chrom# | Position | PVE (R2) | P- value/ FDR | Reference |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | **Early seedling vigor (ESV)** | 96/629 | SSR, 39/52 | | | | | | | Anandan et al. (2016) |
| | Leaf length (14) | | | RM13 | | 1 | | 7.00 | 0.01 | |
| | Leaf length (28) | | | RM223 | | 8 | | 8.00 | 0.0 | |
| | Leaf width (14) | | | RM230 | | 8 | | 5.00 | 0.03 | |
| | Leaf width (14) | | | RM125 | | 7 | | 4.00 | 0.05 | |
| | Root length (14) | | | RM3839 | | 4 | | 5.00 | 0.03 | |
| | Root length (14) | | | RM230 | | 8 | | 5.00 | 0.03 | |
| | Root length (28) | | | RM249 | | 5 | | 5.00 | 0.03 | |
| | Root length (28) | | | RM249 | | 5 | | 5.00 | 0.03 | |
| | Root weight (28) | | | RM250 | | 2 | | 4.00 | 0.05 | |
| | Shoot length (14) | | | RM13 | | 1 | | 5.00 | 0.03 | |
| | Shoot length (14) | | | RM16 | | 3 | | 6.00 | 0.02 | |
| | Shoot weight (28) | | | RM341 | | 2 | | 5.00 | 0.02 | |
| | Shoot weight (28) | | | RM224 | | 11 | | 4.00 | 0.04 | |
| | Vigor index (14) | | | RM341 | | 2 | | 5.00 | 0.03 | |
| | Vigor index (28) | | | RM341 | | 2 | | 5.00 | 0.03 | |

**Table 3 Contd….**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/ gene, | Chrom# | Position | PVE (R2) | P- value/ FDR | Reference |
|---|---|---|---|---|---|---|---|---|---|---|
| 2 | Physio-biochemical traits related to seed vigour | 120 | SSR, 50 | | | | | | | Sahoo et. al. (2020) |
| | Chlorophyll a | | | RM235 | | 12 | | 20.63 | 0.00306 | |
| | Chlorophyll b | | | RM7571 | | 7 | | 15.86 | 0.00963 | |
| | Chlorophyll b | | | RM3735 | | 4 | | 17.576 | 0.00665 | |
| | Chlorophyll b | | | RM5793 | | 7 | | 18.204 | 0.00582 | |
| | Chlorophyll b | | | RM6100 | | 10 | | 17.637 | 0.00657 | |
| | Chlorophyll b | | | RM7003 | | 12 | | 17.653 | 0.00655 | |
| | Total Chlorophyll | | | RM3735 | | 4 | | 15.497 | 0.00983 | |
| | Total Chlorophyll | | | RM5793 | | 7 | | 16.718 | 0.00751 | |
| | Total Chlorophyll | | | RM235 | | 12 | | 18.314 | 0.00532 | |
| | Carotenoids | | | RM582 | | 1 | | 19.269 | 0.00358 | |
| | Carotenoids | | | RM223 | | 8 | | 15.215 | 0.0089 | |
| | Carotenoids | | | RM547 | | 8 | | 18.819 | 0.00395 | |
| | Starch | | | RM582 | | 1 | | 21.372 | 0.00339 | |
| | Starch | | | RM223 | | 8 | | 19.085 | 0.00537 | |
| | Amylose | | | RM440 | | 5 | | 32.59 | 5.18E-04 | |
| | Total anthocyanin | | | RM6275 | | 2 | | 26.187 | 6.67E-04 | |
| | Total anthocyanin | | | RM486 | | 1 | | 19.598 | 0.00276 | |
| | Total anthocyanin | | | RM547 | | 8 | | 14.715 | 0.00859 | |
| | Gamma oryzanols | | | RM286 | | 11 | | 17.167 | 0.00487 | |
| | Gamma oryzanols | | | RM222 | | 10 | | 25.573 | 7.72E-04 | |
| | gamma oryzanols | | | RM547 | | 8 | | 15.233 | 0.00768 | |
| | Total phenolic compounds | | | RM286 | | 11 | | 16.74 | 0.00579 | |
| | Total phenolic compounds | | | RM222 | | 10 | | 16.112 | 0.00669 | |

**Table 3 Contd….**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/ gene, | Chrom# | Position | PVE (R2) | P- value/ FDR | Reference |
|---|---|---|---|---|---|---|---|---|---|---|
| 3 | **Physio-Morphological traits related to seed vigour** | 48/120 | SSR, 165 | | | | | | | Sanghamitra et al. (2021) |
| | Seedling dry weight(g) | | | RM486 | | | | 13.749 | 0.00802 | |
| | Seedling dry weight(g) | | | RM440 | | | | 13.043 | 0.00967 | |
| | Seedling dry weight(g) | | | RM223 | | | | 7.056 | 0.00345 | |
| | Seed Vigour index I | | | RM167 | | | | 17.959 | 0.00559 | |
| | seed Vigour index II | | | RM 7364 | | | | 10..3 | 0.0096 | |
| | seed Vigour index II | | | RM235 | | | | 10.637 | 0.00857 | |
| | Rate of root growth (cm/day) | | | RM256 | | | | 20.851 | 0.00422 | |
| | Seedling dry weight(g) | | | RM486 | | | | 13.749 | 0.00802 | |
| | Rate of root growth (cm/day) | | | RM6547 | | | | 24.52 | 0.00209 | |
| | Rate of root growth (cm/day) | | | RM25181 | | | | 28.289 | 0.00104 | |
| | Rate of root growth (cm/day) | | | RM328 | | | | 28.289 | 0.00104 | |
| | Rate of root growth (cm/day) | | | RM201 | | | | 25.25 | 0.00182 | |
| | Rate of shoot growth (cm/day) | | | RM20A | | | | 23.295 | 0.00251 | |
| | Rate of shoot growth (cm/day) | | | RM13335 | | | | 27.109 | 0.00122 | |
| | Rate of shoot growth (cm/day) | | | RM216 | | | | 20.124 | 0.00466 | |
| | Relative growth rate (cm/day) | | | RM405 | | | | 16.994 | 0.00584 | |
| | Absolute growth rate (cm/day) | | | RM20A | | | | .152.59 | 0.00979 | |
| | Absolute growth rate (cm/day) | | | RM201 | | | | 18.332 | 0.00496 | |
| | Mean germination time (cm/day) | | | RM235 | | | | 19.631 | 0.00306 | |
| | Mean germination time (cm/day) | | | RM286 | | | | 0.15554 | 0.00771 | |

**Table 3 Contd….**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/ gene, | Chrom# | Position | PVE (R2) | P- value/ FDR | Reference |
|---|---|---|---|---|---|---|---|---|---|---|
| 4 | **Seed vgour index, root parameter, germination %** | 120/274 | SSR, 136 | | | | | | | Barik et. al. (2022) |
| | Seed vigour index I | | | RM3701 | *qSVI11.1* | 11 | 46 cM | 5.653 | 0.00545 | |
| | Seed vigour index I | | | RM502 | *qSVI8.1* | 8 | 178 cM | 5.085 | 0.00829 | |
| | Seed vigour index II (SVII) | | | RM13335 | *qSVII2.1* | 2 | 8 cM | 5.385 | 0.00917 | |
| | Seed vigour index II (SVII) | | | RM103 | *qSVII6.1* | 6 | 90cM | 8.726 | 0.00101 | |
| | Seed vigour index II (SVII) | | | RM3 | *qSVII6.2* | 6 | 190 cM | 8.545 | 0.00113 | |
| | Seed vigour index II (SVII) | | | RM441 | *qSVII11.1* | 11 | 348 cM | 5.549 | 0.0082 | |
| | Rate of root growth (RRG) | | | RM222 | *qRRG10.1* | 10 | 18 cM | 6.625 | 0.00313 | |
| | Rate of root growth (RRG) | | | RM337 | *qRRG8.1* | 8 | 27cM | 6.092 | 0.00455 | |
| | Rate of root growth (RRG) | | | RM223 | *qRRG8.2* | 8 | 60 cM | 14.029 | 2.51E-05 | |
| | Rate of root growth (RRG) | | | RM494 | *qRRG6.1* | 6 | 222 cM | 8.176 | 0.00108 | |
| | Rate of root growth (RRG) | | | RM16686 | *qRRG4.1* | 4 | 297 cM | 7.898 | 0.00131 | |
| | Root-shoot ratio (RSR) | | | RM3701 | *RSR11.1* | 11 | 46 cM | 6.994 | 0.00478 | |
| | Root-shoot ratio (RSR) | | | RM405 | *qRSR5.1* | 5 | 109 cM | 9.854 | 8.81E-04 | |
| | Root-shoot ratio (RSR) | | | RM6641 | *qRSR2.1* | 2 | 187 cM | 7.421 | 0.00369 | |
| | Root-shoot ratio (RSR) | | | RM168 | *qRSR3.1* | 3 | 199 cM | 6.578 | 0.00617 | |
| | Germination %(GP) | | | RM225 | *qGP6.2* | 6 | 93 cM | 6.994 | 0.00365 | |
| | Germination %(GP) | | | RM7179 | *qGP6.3* | 6 | 159 cM | 7.805 | 0.00218 | |
| | Germination %(GP) | | | RM502 | *qGP8.1* | 8 | 178 cM | 5.61 | 0.00898 | |

**Table 3 Contd….**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/ gene, | Chrom# | Position | PVE (R2) | P- value/ FDR | Prospective candidate genes | Reference |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 5 | **Germination Rate and Early Seedling Growth Parameters** | 124/278 | SSR, 143 | | | | | | | | Mohanty et al. (2023) |
| | Absolute growth rate (AGR) | | | RM337 | *qAGR8.1(Novel)* | 8 | 27 | 7.805 | 0.00246 | | |
| | Absolute growth rate (AGR) | | | RM7179 | *qAGR86.1(Novel)* | 6 | 159 | 8.381 | 0.00173 | | |
| | Absolute growth rate (AGR) | | | RM494 | *qAGR6.2(Novel)* | 6 | 221 | 8.129 | 0.00202 | | |
| | Absolute growth rate (AGR) | | | RM16686 | *qAGR4.1(Novel)* | 4 | 300 | 9.531 | 8.62E−04 | | |
| | Relative shoot growth (RSG) | | | RM337 | *qRSG8.1* (Novel) | 8 | 27 | 11.592 | 8.55E−05 | | |
| | Relative shoot growth (RSG) | | | RM22034 | *qRSG7.1(Novel)* | 7 | 56 | 5.41 | 0.00634 | | |
| | Relative shoot growth (RSG) | | | RM494 | *qRSG6.1(Novel)* | 6 | 221 | 10.454 | 1.83E−04 | | |
| | Relative shoot growth (RSG) | | | RM1812 | *qRGR11.1* (Novel) | 11 | 44 | 7.091 | 0.00295 | | |
| | Mean Germination rate rate (MGR) | | | RM3735 | *qGR4.1(Validated)* | 4 | 80 | 10.52 | 1.75E−04 | | |
| 6 | **Seed vigour** | 163 | SSR, 295 | | | | | | | | Mohanty et al. (2024) |
| | SVI | | | RM11943 | — | 1 | 37851779 | 13.22 | 0.002 | | |
| | SVI | | | M123 | *OsTDC3* | 8 | 2270568 | 11.67 | 0.006 | | |
| | GI | | | RM3643 | — | 4 | 19948112 | 21.65 | 0.0 | | |
| | GI | | | M200 | *OsPAP10C* | 1 | 38120760 | 20.41 | 0.001 | | |
| | GI | | | M57 | *THIS1* | 1 | 31527177 | 18.73 | 0.004 | | |
| | GI | | | M169 | *OsMIK* | 3 | 30247380 | 18.16 | 0.006 | | |
| | SL | | | RM11943 | — | 1 | 37851779 | 9.93 | 0.001 | | |
| | RL | | | M134 | *GS3* | 3 | 16753200 | 9.58 | 0.004 | | |
| | RL | | | RM431 | — | 1 | 38893890 | 9.45 | 0.004 | | |
| | RL | | | RM249 | — | 5 | 10776565 | 8.21 | 0.01 | | |
| | SDW | | | SPIKE-03SNP | — | 3 | 12001288 | 6.7 | 0.006 | | |
| | SDW | | | SCM2 | — | 6 | 27480082 | 6.64 | 0.006 | | |
| | SFW | | | M80 | *RSR1* | 5 | 1160267 | 5.72 | 0.004 | LOC_Os05g03040 | |
| | SDW | | | M66 | *GW2* | 2 | 8114961 | 4.44 | 0.01 | | |
| | RDW | | | SPIKE-indel3 | *NAL1* | 4 | 31204979 | 9.31 | 0.002 | | |
| | SDW | | | Gn1a-indel3 | — | 1 | 5270103 | 8.15 | 0.005 | LOC_Os04g52479.1 | |
| | SDW | | | RM593 | — | 5 | 2818823 | 7.49 | 0.009 | | |
| | SDW | | | M18 | *OsBAK1* | 8 | 4344171 | 7.43 | 0.009 | | |
| | RFW | | | M80 | *RSR1* | 5 | 1160267 | 6.02 | 0.004 | LOC_Os05g03040 | |
| | RFW | | | Rf3_DRRM-Rf30 | — | 1 | 4985143 | 5.06 | 0.008 | | |

**Table 3 Contd….**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/ gene. | Chrom# | Position | PVE (R2) | P- value/ FDR | Prospective candidate genes | Reference |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 7 | **Early seedling vigour** | 181 aus | SNP, 918, 863 | | *qVg2..1* | 2 | 32823442 | 3.25-5.09 | 1.07E-16 | | Basha et al. (2024) |
| | Vegetative vigour (Vg) | | | 76094365 | *qVg8.1* | 8 | 27264307 | 50.70-71.75 | 1.86E-10 | *OsPDR1, OsERF028* | |
| | Vg | | | 269293835 | *qVg8.2* | 8 | 17112201 | 15.28 | 9.19E-13 | | |
| | Vg | | | 259141729 | *qVg10.1* | 10 | 2343321 | 1.17-2.77 | 2.59E-16 | | |
| | Vg | | | 295828591 | *qVg11.1* | 11 | 10659827 | 1.12-63.59 | 5.03E-20 | | |
| | Vg | | | 327352384 | *qVg12.1* | 12 | 21860018 | 0.40 | 1.92E-08 | | |
| | Vg | | | 367573681 | *qAGR3.1* | 3 | 29922827 | 7.98 | 1.13E-08 | *OSH1* | |
| | Average growth rate (AGR) | | | 109131000 | *qAGR7.1* | 7 | 20186986 | 5.45-48.20 | 1.98E-16 | *OsGLR3.4, OsRPL44* | |
| | AGR | | | 232518893 | *qAGR8.1* | 8 | 20019565 | 3.72 | 2.13E-08 | | |
| | AGR | | | 262049093 | *qAGR9.1* | 9 | 11725818 | 15.1 | 8.57E-14 | | |
| | AGR | | | 282198368 | *qDW2.1* | 2 | 18359158 | 56.05-74.98 | 8.54E-16 | *OsSAUR10, OsGRX8* | |
| | Seedling biomass 28 DAS (DW) | | | 61630081 | *qDW7.2* | 7 | 24086549 | 0.84 | 2.24E-09 | | |
| | DW | | | 236418456 | *qDW7.3* | 7 | 28654350 | 7.24 | 5.20E-10 | | |
| | DW | | | 240986257 | *qDW9.2* | 9 | 12427777 | 4.87 | 2.36E-13 | | |
| | | | | | | | | | | | |
| | | | | | | | | | | | |

**Table 4a. List of List of QTLs, molecular markers, and prospective candidate genes identified for agro-morphological and yield traits in rice using bi-parental mapping populations.**

| Sl No. | Trait | Parentage, donor, mapping population type and size | QTLs | Chrom# | Flanking/ linked markers | Position (cM/ MB/Bp) | LOD | PVE (%) | Additive effect | Contributing parent | Season | Prospective candidate genes | Reference |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Grain Fertility and associated traits | PDK Shriram/ Heera, RIL, 188PDK Shriram | | | | | | | | | | | Sekhar et al. (2021) |
| | Spikelet fertility | | *qSFP1.1* | 1 | RM10552- HVSSR1-31 | | 7.037 | 10.64 | -23.86 | PDK Shriram | Kharif 2017 | | |
| | Spikelet fertility | | *qSFP3.1* | 3 | RM14906- RM16 | | 4.752 | 10.23 | -23.83 | PDK Shriram | Kharif 2017 | | |
| | Spikelet fertility | | *qSFP6.1* | 6 | RM20500 | 26,795,543-26,795,937 | 6.107 | 10.00 | 16.23 | Heera | Kharif 2017 | XP_015642751.1, XP_025881923.1, XP_015641892.1, XP_015644414.1, XP_015642592.1 | |
| | Spikelet fertility | | *qSFP8.1* | 8 | RM23513- RM20506 | | 3.045 | 7.57 | -3.00 | PDK Shriram | Kharif 2017 | | |
| | Panicle compactness | | *qIGS3.2* | 3 | RM14906- RM264 | | 10.87 | 11.46 | -0.25 | PDK Shriram | Kharif 2017 | | |
| | Panicle compactness | | *qIGS4.1* | 4 | RM16952- RM16 | | 3.66 | 11.44 | -0.05 | PDK Shriram | Kharif 2017 | | |
| | Panicle compactness | | *qIGS6.1* | 6 | RM588- RM19480 | 16,049,580-16,049,767 | 6.19 | 12.65 | 0.15 | Heera | Kharif 2017 | XP_015641250.1 XP_015644486.1 XP_015644371.1 XP_015641573.1 XP_015641668.1 XP_015642210.2 XP_015641200.1 XP_015641438.2 XP_015642939.1 XP_015643752.1 | |
| | Panicle compactness | | *qIGS6.2* | 6 | RM19480- RM19496 | | 7.98 | 11.83 | 0.15 | Heera | Kharif 2017 | | |
| | Panicle compactness | | *qIGS6.3* | 6 | RM20500- RM20506 | 26,596,664-26,597,121 | 16.85 | 9.09 | 0.25 | Heera | Kharif 2017 | XP_015642751.1, XP_025881923.1, XP_015641892.1, XP_015644414.1, XP_015642592.1 | |
| | Phytohormone ethylene | | *qETH1.1* | 1 | HVSSR1-31- HVSSR1-44 | | 18.53 | 5.71 | -0.05 | PDK Shriram | Kharif 2017 | | |

**Table 4a Contd….**

| Sl No. | Trait | Parentage, donor, mapping population type and size | QTLs | Chrom# | Flanking/ linked markers | Position (cM/ MB/Bp) | LOD | PVE (%) | Additive effect | Contributing parent | Season | Prospective candidate genes | Reference |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Phytohormone ethylene | | ***qETH1.2*** | 1 | Affx93259116- RM12224 | 33213458-42248647 | 19.56 | 6.00 | -0.05 | PDK Shriram | Kharif 2017 | Os01g0797600, Os01g0813300, Os01g0868000, Os01g0868000, Os01g0885900, Os01g0899800, Os01g0952500 | Sekhar et al. (2021) |
| | Phytohormone ethylene | | *qETH3.1* | 3 | RM14272- RM14292 | | 7.46 | 6.47 | 0.04 | Heera | Kharif 2017 | | |
| | Phytohormone ethylene | | *qETH4.1* | 4 | RM16519- RM16569 | | 10.79 | 5.42 | 0.05 | Heera | Kharif 2017 | | |
| | Phytohormone ethylene | | ***qETH6.1*** | 6 | RM19496- RM20045 | 1,611,398-1,611,524 | 8.35 | 6.45 | 0.04 | Heera | Kharif 2017 | XP_015641250.1 XP_015644486.1 XP_015644371.1 XP_015641573.1 XP_015641668.1 XP_015642210.2 XP_015641200.1 XP_015641438.2 XP_015642939.1 XP_015643752.1 | |
| | Spikelet fertility | | *qSFP1.1* | 1 | RM10552- HVSSR1-31 | | 12.38 | 9.79 | -24.96 | PDK Shriram | Kharif 2018 | | |
| | Spikelet fertility | | *qSFP3.1* | 3 | RM14906- RM16 | | 7.81 | 9.53 | -24.96 | PDK Shriram | Kharif 2018 | | |
| | Spikelet fertility | | *qSFP6.1* | 6 | RM20500- RM20506 | | 10.76 | 10.35 | 28.00 | Heera | Kharif 2018 | | |
| | Panicle compactness | | *qIGS1.1* | 1 | RM10552- HVSSR1-31 | | 4.34 | 9.56 | -0.16 | PDK Shriram | Kharif 2018 | | |
| | Panicle compactness | | *qIGS3.1* | 3 | RM14825- RM14906 | | 5.10 | 10.49 | -0.13 | PDK Shriram | Kharif 2018 | | |
| | Panicle compactness | | *qIGS3.2* | 3 | RM14906-RM16 | | 4.09 | 11.00 | -0.14 | PDK Shriram | Kharif 2018 | | |
| | Panicle compactness | | *qIGS4.1* | 4 | RM16952- RM17063 | | 5.20 | 11.47 | -0.08 | PDK Shriram | Kharif 2018 | | |
| | Panicle compactness | | *qIGS4.2* | 4 | RM17063- RM252 | | 4.45 | 9.04 | -0.08 | PDK Shriram | Kharif 2018 | | |
| | Panicle compactness | | *qIGS6.1* | 6 | RM588- RM19480 | | 4.46 | 5.99 | 0.13 | Heera | Kharif 2018 | | |
| | Panicle compactness | | *qIGS6.2* | 6 | RM19480- RM19496 | | 4.18 | 6.35 | 0.13 | Heera | Kharif 2018 | | |
| | Phytohormone ethylene | | *qETH1.2* | 1 | Affx93259116- RM12224 | | 25.46 | 5.47 | -0.05 | PDK Shriram | Kharif 2018 | | |
| | Phytohormone ethylene | | *qETH3.1* | 3 | RM14272- RM14292 | | 14.53 | 6.87 | 0.05 | Heera | Kharif 2018 | | |
| | Phytohormone ethylene | | *qETH4.1* | 4 | RM16519- RM16569 | | 21.00 | 5.45 | 0.05 | Heera | Kharif 2018 | | |
| | Phytohormone ethylene | | *qETH4.2* | 4 | RM16569- RM16770 | | 9.42 | 6.56 | 0.05 | Heera | Kharif 2018 | | |
| | Phytohormone ethylene | | *qETH6.2* | 6 | RM19480- RM19496 | | 14.11 | 6.85 | 0.05 | Heera | Kharif 2018 | | |

**Table 4b. List of QTLs, molecular markers, and prospective candidate genes identified for agro-morphological and yield traits in rice using association-mapping populations.**

| Sl No. | Trait | Mapping population size | Type and no. of markers used | Associated Marker | Associated QTL/ gene, | Chrom# | Position | PVE (R2) | P- value/ FDR | Prospective candidate genes | References |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Plant type characters and yield | 88 | cGSSR, 142 | | | | | | | | Azharudheen et al. (2022a) |
| | Plant height (in cm) | | | M18 | *OsMADS18* | 7 | 2,47,88,476 | 15 | 0.01 | | |
| | Plant height (in cm) | | | M63 | *PIL16* | 5 | 22,46,835 | 15 | 0.01 | | |
| | Plant height (in cm) | | | M60 | *OsGID1* | 5 | 1,98,68,419 | 14 | 0.02 | | |
| | Plant height (in cm) | | | M24 | *RePRP2.1* | 7 | 1,33,66,416 | 13 | 0.03 | | |
| | Plant height (in cm) | | | M16 | *OS-PYDK* | 7 | 2,64,85,308 | 13 | 0.03 | | |
| | Plant height (in cm) | | | M78 | *OsSUT1* | 3 | 38,04,132 | 12 | 0.04 | | |
| | Effective bearing Tillers | | | M55 | *SHO1* | 4 | 2,54,89,003 | 18 | 0.004 | | |
| | Effective bearing Tillers | | | M71 | *OsFBK12* | 3 | 38,33,954 | 14 | 0.03 | | |
| | Effective bearing Tillers | | | M18 | *OsMADS18* | 7 | 2,47,88,476 | 13 | 0.04 | | |
| | Number of leaves | | | M87 | *EP3* | 2 | 90,42,076 | 23 | 0.001 | | |
| | Number of leaves | | | M24 | *RePRP2.1* | 7 | 1,33,66,416 | 18 | 0.01 | | |
| | Number of leaves | | | Sdi9 | *OsBAK1* | 8 | 43,44,171 | 18 | 0.01 | | |
| | Number of leaves | | | M74 | *OsBBS1* | 3 | 1,42,06,981 | 17 | 0.01 | | |
| | Number of leaves | | | M91 | *OsbHLH107* | 2 | 3,43,56,787 | 16 | 0.03 | | |
| | Number of leaves | | | M81 | *YGL98* | 3 | 3,39,55,198 | 16 | 0.03 | | |
| | Grain Yield per hectar (tons) | | | Sd17 | *IDEF1* | 8 | 67,639 | 11 | 0.04 | | |
| | Grain Yield per hectar (tons) | | | M60 | *OsGID1* | 5 | 1,98,68,419 | 11 | 0.04 | | |
| 2. | Yield and plant architectural traits | 181 aus | SNP, 453K | | | | | | | | Sar et al. (2024). |
| | PC1 (DtF, Ht, PnL, PnW, SpkN) | | | 4521776 | *qPC1-1.1* | 1 | 4521776 | 5.06 | 9.3 (-log10(P) | *OsGI* | |
| | PC1 (DtF, Ht, PnL, PnW, SpkN) | | | 29651634 | *qPC1-1.2* | 1 | 29651634 | 1.47 | 8.38 (-log10(P) | *OsLFL* | |
| | PC1 (DtF, Ht, PnL, PnW, SpkN) | | | 24835927 | *qPC1-2.1* | 2 | 24835927 | 2.05 | 7.18 (-log10(P) | *qPH2, YLD2.1* | |
| | PC1 (DtF, Ht, PnL, PnW, SpkN) | | | 27801414 | *qPC1-4.1* | 4 | 27801414 | 2.05 | 8.59 (-log10(P) | *OsGPX1* | |
| | PC1 (DtF, Ht, PnL, PnW, SpkN) | | | 19616683 | *qPC1-5.1* | 5 | 19616683 | 5.8 | 7.32(-log10(P) | *qSW5* | |
| | PC1 (DtF, Ht, PnL, PnW, SpkN) | | | 888054 | *qPC1-7.1* | 7 | 888054 | 7.97 | 15.81(-log10(P) | *OsSAC1* | |
| | PC1 (DtF, Ht, PnL, PnW, SpkN) | | | 18001305 | *qPC-8.1* | 8 | 18001305 | 5.13 | 7.63(-log10(P) | *WFP* | |
| | PC2 (PnW, Yld, HI) | | | 21316516 | *qPC1-8.2* | 8 | 21316516 | 1.11 | 9.3 (-log10(P) | *IPA1* | |
| | PC2 (PnW, Yld, HI) | | | 28087887 | *qPC2-1.1* | 1 | 28087887 | 10.53 | 9.85 (-log10(P) | *OsGLT1, PUP4* | |
| | PC2 (PnW, Yld, HI) | | | 21700005 | *qPC2-7.1* | 7 | 21700005 | 2.58 | 7.61 (-log10(P) | *dth7.1, Ph7a* | |
| | PC2 (PnW, Yld, HI) | | | 26611742 | *qPC2-7.2* | 7 | 26611742 | 1.23 | 7.62 (-log10(P) | *dep2, srs1, fzp* | |
| | PC2 (PnW, Yld, HI) | | | 3412660 | *qPC2-11.1* | 11 | 3412660 | 3.98 | 10.3(-log10(P) | *Os11g235200* | |
| | PC2 (PnW, Yld, HI) | | | 4552359 | *qPC2-11.2* | 11 | 4552359 | 1.6 | 7.99 (-log10(P) | | |
| | PC3 (Tn, GW, Yld) | | | 4789451 | *qPC3-1.1* | 1 | 4789451 | 6.2 | 7.69 (-log10(P) | *OsDOS* | |
| | PC3 (Tn, GW, Yld) | | | 41821709 | *qPC3-1.2* | 1 | 41821709 | 6.51 | 7.45 (-log10(P) | *se3* | |
| | PC3 (Tn, GW, Yld) | | | 18218891 | *qPC3-3.1* | 3 | 18218891 | 2.07 | 7.18 (-log10(P) | *GS3* | |
| | PC3 (Tn, GW, Yld) | | | 14156143 | *qPC3-5.1* | 5 | 14156143 | 5.86 | 10.16 (-log10(P) | | |
| | PC3 (Tn, GW, Yld) | | | 27904519 | *qPC3-5.2* | 5 | 27904519 | 0.37 | 7.04 (-log10(P) | *OsIPT7* | |

**Table 4b Contd….**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/ gene, | Chrom# | Position | PVE (R2) | P- value/ FDR | References |
|---|---|---|---|---|---|---|---|---|---|---|
| 3 | High grain yield and component traits | 60 | SSR, 85 | | | | | | | Donde et al. (2020) |
| | DFF | | | RM_212** | *qFD-1.1* | 1 | 180.2 | 18.49 | 2.95E-03 | |
| | DFF | | | RM_20285 | *qFD-6.1* | 6 | 121.6 | 13.51 | 3.86E-03 | |
| | DFF | | | RM_25 | *qFD-8.1* | 8 | 52.2 | 20.46 | 1.65E-03 | |
| | DFF | | | *RM_5709* @**** | *qFD-4.1* | 4 | 109.9 | 26.16-33.69 | 7.43-7.67E-04 | |
| | DFF | | | RM_219*** | *qFD-9.1* | 9 | 11.7 | 14.37 | 3.06E-03 | |
| | PH | | | *RM_3827* @ | *qPHT-6.1* | 6 | 80.4 | 15.15-15.66 | 1.92-4.42E-03 | |
| | PH | | | *RM_285* @@** | *qPHT-9.1* | 9 | 1.8 | 23.29-26.777 | 1.62-2.63E03 | |
| | PH | | | *RM_5709* @@@@***** | *qPHT4-a* | 4 | 109.9 | 32.62-32.965 | 5.96-9.37E-04 | |
| | TL | | | RM_26499 | *qTL-11.1* | 11 | 0 | 14.21 | 2.99E-03 | |
| | TL | | | RM_3276 | *qTL-4.1* | 4 | 102.4 | 13.71 | 3.89E-03 | |
| | TL | | | RM_3827 | *qTL-6.1* | 6 | 70.4 | 13.77 | 3.81E-03 | |
| | TL | | | RM_287 @ | *qTL-11.1/gpl 11.1* | 11 | 68.6 | 17.31 | 2.46E-03 | |
| | PL | | | RM_168 | *qPL-3.1* | 3 | 171.2 | 30.13 | 3.66E-05 | |
| | PL | | | RM_171 | *qPL-10.1* | 10 | 92.8 | 13.89 | 3.36E-03 | |
| | PL | | | RM_297**** | *qPL-1.1* | 1 | 161.3 | 24.73 | 6.15E-05 | |
| | PL | | | RM_154** | *qPL-2.1* | 2 | 4.8 | 21.86 | 3.36E-03 | |
| | PL | | | RM_551** | *qPL-4.1* | 4 | 15 | 15.86 | 1.79E-03 | |
| | PL | | | *RM_5709* @@**** | *qPL-4.1, qSPP-4.1* | 4 | 109.9 | 26.63-45.846 | 1.96-3.23E-03 | |
| | PL | | | RM_5575**** | *qPL-5.1* | 5 | 0 | 29.70 | 8.08E-06 | |
| | PL | | | RM_204** | *qPL-6.1* | 6 | 25.1 | 28.38 | 3.43E-04 | |
| | PL | | | RM_5711** | *qPL-7.1* | 7 | 24.2 | 19.38 | 2.40E-03 | |
| | PL | | | RM_234**** | *qPL-7.2* | 7 | 88.2 | 21.54 | 2.14E-04 | |
| | PL | | | RM_22899** | *qPL-8.1* | 8 | 0 | 14.25 | 3.20E-03 | |
| | PL | | | RM_447 | *qPL-8* | 8 | 124.6 | 15.00 | 2.44E-03 | |
| | PL | | | RM_17** | *qPL-12b* | 12 | 109.1 | 18.60 | 6.48E-04 | |
| | FLL | | | RM_447 | *qFLL-8.1* | 8 | 124.6 | 16.84 | 1.25E-03 | |
| | FLL | | | RM_297*** | *qFLL-1.1* | 1 | 161.3 | 17.96 | 8.23E-04 | |
| | FLL | | | RM_5709** | *qFLL-4.1a* | 4 | 109.9 | 25.43 | 9.92E-04 | |
| | FLL | | | RM_285 @@ | *qFLL-9.1* | 9 | 1.8 | 22.19 | 3.05E-03 | |
| | FLW | | | RM_204 | *qFLW-6.1* | 6 | 25.1 | 30.37 | 1.37E-04 | |
| | FLW | | | RM_20285 | *qFLW-6.2* | 6 | 121.6 | 13.86 | 3.39E-03 | |
| | FLW | | | RM_206 | *qFLW-11.1* | 11 | 102.9 | 17.54 | 4.51E-03 | |
| | FLW | | | RM_19 | *qFLW-12.1* | 12 | 20.9 | 13.41 | 4.33E-03 | |
| | FLW | | | RM_297**** | *qFLW-1.1* | 1 | 161.3 | 29.80 | 7.77E-06 | |
| | FLW | | | RM_154** | *qFLW-2.1* | 2 | 4.8 | 22.42 | 2.79E-03 | |
| | FLW | | | RM_168** | *qFLW-3.1* | 3 | 171.2 | 19.40 | 2.38E-03 | |
| | FLW | | | RM_470 @** | *qFLW-4.1a* | 4 | 115.5 | 18.523-21.71 | 6.68-7.78E-04 | |
| | FLW | | | RM_5709 @*** | *qFLW4.1* | 4 | 109.9 | 25.44-30.72 | 1.43-4.22E-03 | |
| | FLW | | | RM_5575*** | *qFLW-5.1* | 5 | 0 | 21.47 | 2.19E-04 | |
| | FLW | | | RM_1132 | *HFLW-7* | 7 | 83.3 | 22.65 | 2.59E-03 | |

**Table 4b Contd….**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/ gene, | Chrom# | Position | PVE (R2) | P- value/ FDR | References |
|---|---|---|---|---|---|---|---|---|---|---|
| | FLW | | | RM_22899**** | *qFLW-8.1* | 8 | 0 | 18.71 | 6.24E-04 | |
| | FLW | | | RM_5711 @ | *qFG-7.1* | 7 | 24.2 | 21.64 | 3.46E-03 | |
| | FLW | | | RM_447 | *qFLW-8.1a* | 8 | 124.6 | 7.30 | 1.30E-03 | |
| | FG | | | RM_1132 | *qFG-7.1* | 7 | 83.3 | 24.65 | 1.30E-03 | |
| | FG | | | RM_5709 | *qFGP-4.1* | 4 | 109.9 | 26.19 | 7.60E-04 | |
| | FG | | | RM_324 @ | *qFG-7.1* | 7 | 68.9 | 14.74 | 4.59E-03 | |
| | TG | | | RM_1132 | *qFG-a7.1* | 7 | 83.3 | 21.09 | 4.34E-03 | |
| | TG | | | ***RM_324 @*** | *qTG-2.1* | 2 | 68.9 | 13.583-15.788 | 3.43-4.08E-03 | |
| | TG | | | RM_5709** | *qTG-2.2* | 4 | 109.9 | 24.30 | 1.47E-03 | |
| | TGW | | | RM_297 @** | *qTGW-a1.1* | 1 | 161.3 | 15.02-23.383 | 4.24-9.08E-03 | |
| | TGW | | | RM_201** | *qTGW-a9.1* | 9 | 81.2 | 14.93 | 2.29E-03 | |
| | TGW | | | RM_219 | *qTGW-a9.2* | 9 | 11.7 | 14.56 | 2.87E-03 | |
| | TGW | | | RM_171 | *qTGW-a10.1* | 10 | 92.8 | 13.20 | 4.68E-03 | |
| | TGW | | | RM263 @**** | *qTGW-2.1, qGn2.1, qYLD-2.1* | 2 | 127.5 | 18.98-35.74 | 1.58-5.75E03 | |
| | TGW | | | RM_5575*** | *qTGW-5.1* | 5 | 0 | 15.38 | 2.12E-03 | |
| | TGW | | | RM_22899** | *qTGW-8.1* | 8 | 0 | 15.56 | 1.99E-03 | |
| | SLBR | | | RM_204 | *qSlb-a6.1* | 6 | 25.1 | 25.11 | 9.68E-04 | |
| | SLBR | | | RM_1256***** | *qSlb-3.1* | 3 | 48.2 | 19.92 | 3.95E-04 | |
| | SLBR | | | RM_5709 @@@@***** | *qSlb-4.1* | 4 | 109.9 | 24.31-26.79 | 1.47-3.18E-03 | |
| | SLBR | | | RM_287**** | *qSlb-11.1* | 11 | 68.6 | 13.57 | 4.09E-03 | |
| | YLD | | | RM_6100 @ | *qYLD-10.1* | 10 | 53.9 | 16.15 | 3.10E-03 | |
| | YLD | | | RM_1132** | *qYLD-a7.1* | 7 | 83.3 | 21.45 | 3.86E-03 | |
| | YLD | | | RM_222 | *qYLD-a10.1* | 10 | 11.3 | 15.12 | 2.33E-03 | |
| | YLD | | | RM_297** | *qYLD-1.1* | 1 | 161.3 | 14.66 | 2.76E-03 | |
| | YLD | | | RM_154**** | *qYLD-2.1, qts1* | 2 | 4.8 | 27.71 | 4.40E-04 | |
| | YLD | | | RM_168*** | *qYLD-3.1* | 3 | 171.2 | 17.37 | 4.79E-03 | |
| | YLD | | | RM_551*** | *qYLD-4, qPL-4.1* | 4 | 15 | 14.20 | 3.27E-03 | |
| | YLD | | | RM_5709***** | *qYLD-4.1* | 4 | 109.9 | 37.85 | 7.93E-06 | |
| | YLD | | | RM_5575***** | *qYLD-5.1* | 5 | 0 | 30.25 | 6.43E-06 | |
| | YLD | | | RM_20285***** | *Qyld-6.1* | 6 | 121.6 | 18.86 | 5.89E-04 | |
| | YLD | | | RM_5711*** | *qYLD-7.1* | 7 | 24.2 | 19.22 | 2.54E-03 | |
| | YLD | | | RM_234***** | *Ppl7.1* | 7 | 88.2 | 16.47 | 1.43E-03 | |
| | YLD | | | RM_26499 | *qYLD-11.1* | 11 | 0 | 13.14 | 4.78E-03 | |
| | YLD | | | RM_19**** | *qYLD-12.1, qSpn-12.1* | 12 | 20.9 | 17.18 | 1.10E-03 | |
| | YLD | | | RM_204** | *qYLD-6.1* | | 6 | 28.64 | 2.70E-04 | |

**Table 4b Contd….**

| Sl No. | Trait | Mapping population size | Type and of markers used | Associated Marker | Associated QTL/ gene, | Chrom# | Position | PVE (R2) | P- value/ FDR | References |
|---|---|---|---|---|---|---|---|---|---|---|
| 4 | Grain size | 88 | cGSSR, 142 | | | | | | | |
| | 1000-grain weight | | | M69 | *OSBC1L4* | 5 | 18 724 905 | 11.01 | 0.01 | Nayak et al. (2022a) |
| | 1000-grain weight | | | Sd14 | *OsC1* | 6 | 5 315 178 | 10.23 | 0.02 | |
| | 1000-grain weight | | | M55 | *SHO1* | 4 | 25 489 003 | 10 | 0.02 | |
| | 1000-grain weight | | | Sdi21 | *RSR1* | 5 | 1 160 267 | 9.54 | 0.04 | |
| | Grain length; | | | M55 | *SHO1* | 4 | 25 489 003 | 6.34 | 0.04 | |
| | Grain width | | | M35 | *NPP1* | 8 | 26 439 584 | 13.25 | 0.01 | |
| | Grain width | | | Sdi1 | *OsD2* | 1 | 5 236 623 | 13.07 | 0.01 | |
| | Grain width | | | M99 | *Rd* | 1 | 25 382 698 | 11 | 0.02 | |
| | Grain width | | | M69 | *OSBC1L4* | 5 | 18 724 905 | 10.56 | 0.02 | |
| | Length-width ratio | | | Sdi1 | *OsD2* | 1 | 5 236 623 | 8 | 0.02 | |
| 5 | Panicle characters and yield | 88 | cgSSR, 114 | | | | | | | Sah et al. (2022) |
| | Panicle length (cm) | | | M17 | *EP2* | 7 | 25 381 698 | 7 | 0.02 | |
| | Panicle length (cm) | | | M81 | *YGL98* | 3 | 33 955 198 | 6 | 0.03 | |
| | Number of primary branches per panicle | | | M91 | *OsbHLH107* | 2 | 34 356 787 | 13 | 0.004 | |
| | Number of primary branches per panicle | | | M78 | *OsSUT1* | 3 | 3 804 132 | 9 | 0.03 | |
| | Number of primary branches per panicle | | | M88 | *BLS1* | 2 | 34 689 723 | 8 | 0.03 | |
| | Number of primary branches per panicle | | | Sdi21 | *RSR1* | 5 | 1 160 267 | 8 | 0.04 | |
| | Number of grains per panicle | | | M82 | *Osgl1-2* | 2 | 4 362 388 | 6 | 0.02 | |
| | Number of grains per panicle | | | M34 | *OsAHP1* | 8 | 27 904 573 | 4 | 0.04 | |
| | Number of grains per panicle | | | M36 | *COE1* | 8 | 21 583 634 | 4 | 0.04 | |
| | Panicle weight (g) | | | M92 | *GH2* | 2 | 4 874 082 | 8 | 0.02 | |
| | Panicle weight (g) | | | M34 | *OsAHP1* | 8 | 27 904 573 | 8 | 0.03 | |
| | Panicle weight (g) | | | M82 | *Osgl1-2* | 2 | 4 362 388 | 8 | 0.03 | |
| | Panicle weight (g) | | | M91 | *OsbHLH107* | 2 | 34 356 787 | 8 | 0.03 | |
| | Panicle weight (g) | | | M57 | *D11* | 4 | 23 471 594 | 7 | 0.03 | |
| | Panicle weight (g) | | | M36 | *COE1* | 8 | 21 583 634 | 7 | 0.03 | |
| | Gain yield per hill (g) | | | Sd17 | *IDEF1* | 8 | 67 639 | 11 | 0.04 | |
| | Gain yield per hill (g) | | | M60 | *OsGID1* | 5 | 19 868 419 | 11 | 0.04 | |

**Table 5a. List of QTLs, molecular markers, and prospective candidate genes identified for grain quality traits in rice using bi-parental mapping populations.**

| Sl No. | Trait | Parentage, donor, mapping population type and size | QTLs | Chrom# | Flanking/ linked marker | Position cM/ MB) | LOD | PVE (%) | Additive effect | Prospective candidate genes | Reference |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | High grain protein content | ARC10075, Naveen, BIL(BC3F4), 190 | *qGPC1.1* | 1 | | 0.86104 | 3.832 | 13.855 | −0.426 | *Os01g0111900* | Chattopadhyay et al. (2019) |
| | GPC(Grain protein content) | | *qSGPC1.1* | 1 | Affx- 93237905 | 0.86104 | 2.897 | 10.37 | −0.083 | | |
| | SGPC (Single grain protein content) | | *qSGPC2.1* | 2 | Affx- 93237905 | 5.66506 | 3.316 | 6.703 | 0.059 | | |
| | SGPC | | *qSGPC7.1* | 7 | Affx- 93260438 | 22.2475 | 3.51 | 7.678 | 0.067 | *Os07g0570100, Os07g0570300, Os07g0570500* | |
| | SGPC | | *qSGPC11.1* | 11 | Affx- 93225742 | 3.78772 | 2.873 | 6.424 | 0.076 | *Os11g0184800(OsAsp1)* | |
| | GPC | | *qGPC1.1* | 1 | | 0.86104 | 4.017 | 13.851 | −0.581 | | |
| | GPC | | *qGPC2.1* | 2 | Affx- 93237905 | 9.97632 | 3.186 | 17.353 | 0.923 | *Os02g0268300,Os02g0252400 (RPBF)* | |
| | SGPC | | *qSGPC1.2* | 1 | | 39.0664 | 3.309 | 18.463 | 0.492 | Os01g0878700 (OsAAP6) | |
| | SGPC | | *qSGPC1.3* | 1 | Affx- 93230672 | 8.35788 | 4.07 | 16.401 | 0.481 | Os01g0254000 (Sar1 c) | |
| | SGPC | | *qSGPC2.1* | 2 | | 5.66506 | 3.528 | 14.636 | 0.54 | | |
| | SGPC | | *qSGPC3.1* | 3 | Affx- 93256429 | 36.3227 | 4.115 | 14.653 | 0.542 | Os03g0826500 | |
| | SGPC | | *qSGPC7.1* | 7 | Affx- 93253793 | 22.2475 | 3.328 | 7.813 | 0.091 | | |
| | SGPC | | *qSGPC8.1* | 8 | Affx- 93225742 | 0.95055 | 4.548 | 23.547 | 0.336 | | |
| | SGPC | | *qSGPC12.1* | 12 | | 2.32059 | 2.966 | 14.486 | 0.531 | *Os01g0111900* | |

**Table 5b: List of QTLs, molecular markers, and prospective candidate genes identified for grain quality traits in rice using association-mapping populations.**

| Sl No. | Trait | Mapping population size | Type and no. of markers used | Associated marker | Associated QTL/ gene | Chrom# | Position | PVE (R2) | P- value/ FDR | References |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Mean grain protein content | 105/305 | SSR, 98 | RM243 | *qProt1* | 1 | | 6.508 | 0.01141 | Pradhan et al. (2019) |
| | | | | RM7 | *qPC3.1 (Novel)* | 3 | 9.82 Mb | 4.871 | 0.02798 | |
| | | | | RM6712 | | 3 | | 4.872 | 0.02796 | |
| | | | | RM6209 | *qPC5.1 (Novel)* | 5 | 0.56 Mb | 5.154 | 0.02388 | |
| | | | | RM407 | *qPC8* | 8 | 3-8.6Mb | 13.471 | 3.44E − 04 | |
| | | | | RM204 | *qPC6.1* | 6 | | 5.69 | 0.01777 | |
| | | | | RM296 | | | | 4.158 | 0.04194 | |
| | | | | RM34 | *qPC9.1(Novel)* | 9 | 11.76 Mb | 5.784 | 0.01688 | |
| | | | | RM339 | | | | 4.258 | 0.0396 | |
| | | | | OSNAC | | 3 | | 8.605 | 0.0038 | |
| 2 | Grain Iron and Zinc content | 102/485 | SSR, 100 | | | | | | | Pradhan et al. (2020) |
| | Fe content | | | RM243 | | | | 5.798 | 0.01733 | |
| | Fe content | | | RM122 | | | | 7.044 | 0.00892 | |
| | Fe content | | | RM234 | | | | 7.975 | 0.0055 | |
| | Fe content | | | RM7 | | | | 4.01 | 0.04684 | |
| | Fe content | | | RM168 | | | | 4.883 | 0.02862 | |
| | Fe content | | | RM80 | | | | 7.534 | 0.00691 | |
| | Fe content | | | RM339 | | | | 5.195 | 0.02408 | |
| | Fe content | | | RM1132 | | | | 5.557 | 0.01975 | |
| | Fe content | | | OSZIP8 | | | | 5.203 | 0.02398 | |
| | Fe content | | | OSZIP6A | | | | 7.304 | 0.00779 | |
| | Zn content | | | RM260 | | | | 4.563 | 0.03423 | |
| | Zn content | | | RM80 | | | | 5.237 | 0.02354 | |
| | Zn content | | | RM300 | | | | 7.666 | 0.00645 | |
| | | | | RM339 | | | | 4.147 | 0.04332 | |
| | Zn content | | | RM340 | | | | 4.733 | 0.03111 | |
| | Zn content | | | RM1132 | | | | 6.301 | 0.01322 | |
| | Zn content | | | GRMM9–1 | | | | 12.291 | 6.44E-04 | |

**Table 5b Contd….**

| Sl No. | Trait | Mapping population size | Type and no. of markers used | Associated marker | Associated QTL/gene | Chrom# | Position | PVE (R2) | P- value/ FDR | References |
|---|---|---|---|---|---|---|---|---|---|---|
| 3 | Antioxidant enzymes, phenolic content | 117/270 | SSR, 131 | | | | | | | Sanghamitra et al. (2022) |
| | Catalase | | | RM3231 | *qCAT8.1* | 8 | 32.7 cM | 7.179 | 0.006 | |
| | Catalase | | | RM1341 | *qCAT11.1* | 11 | 80.2 cM | 7.457 | 0.00514 | |
| | DPPH | | | RM247 | *qACD12.2* | 12 | 31.85 Mb | 9.162 | 0.00196 | |
| | DPPH | | | RM3701 | *qACD11.1* | 11 | 45.3cM | 10.093 | 0.00118 | |
| | DPPH | | | RM13600 | *qACD2.2* | 2 | 242.46cM | 6.264 | 0.00994 | |
| | FRAP | | | RM247 | *qFRAP12.1* | 12 | 31.85 cM | 6.551 | 0.00868 | |
| | FRAP | | | RM3701 | *qFRAP11.1* | 11 | 81.001 cM | 8.236 | 0.00338 | |
| | FRAP | | | RM309 | *qFRAP12.2* | 12 | 214.54 cM | 6.745 | 0.00777 | |
| | CUPRAC | | | RM3701 | *qCUPRAC11.1* | 11 | 81.001 cM | 8.678 | 0.00241 | |
| | CUPRAC | | | RM235 | *qCUPRAC12.1* | 1 | 45.3 cM | 9.024 | 0.00199 | |
| | CUPRAC | | | RM148 | *qCUPRAC3.1* | 3 | 358.35 cM | 6.324 | 0.0092 | |
| | | | | | | | | | | |
| 4 | Antioxidants | 120/270 | SSR, 136 | | | | | | | |
| | Superoxide dismutase (SOD) | | | RM582 | *qSOD1.1* | 1 | 66.4–66.4 cM | 9.191 | 0.00169 | Bastia et al. (2022) |
| | Superoxide dismutase (SOD) | | | RM405 | *qSOD5.1* | 5 | 28.6–28.6 cM | 10.661 | $7.52 \times 10^{-4}$ | |
| | Superoxide dismutase (SOD) | | | RM467 | *qSOD10.1* | 10 | 46.8–46.8 cM | 8.612 | 0.00234 | |
| | Total anthocyanin content | | | RM440 | | | 92.7–92.7 cM | 8.013 | 0.00323 | |
| | Total anthocyanin content | | | RM5638 | *qANC3* | 1 | 86–86 cM | 9.768 | 0.0012 | |
| | Total anthocyanin content | | | RM253 | | | 37–37 cM | 9.297 | 0.00157 | |
| | Total anthocyanin content | | | RM5626 | | | 99–99 cM | 8.276 | 0.00278 | |
| | γ-oryzanol (OZ) | | | RM3701 | | | 45.3–45.3 cM | 8.155 | 0.00282 | |
| | γ-oryzanol (OZ) | | | RM502 | | | 121.8–121.8 cM | 7.3 | 0.00463 | |
| | Total flavonoids content (TFC) | | | RM3701 | *qTFC11.1* | 11 | 45.3–45.3 cM | 7.279 | 0.00341 | |
| | Total flavonoids content (TFC) | | | RM235 | *qTFC12.1* | 12 | 101.8–103.8 cM | 7.484 | 0.003 | |
| | Total flavonoids content (TFC) | | | RM494 | *qTFC6.1* | 6 | 124.4–124.4 cM | 7.839 | 0.00241 | |
| | ABTS activity | | | RM3701 | *qAC11.1* | 11 | 45.3–45.3 cM | 9.699 | 0.00125 | |
| | ABTS activity | | | RM235 | *qAC12* | 12 | 101.8–103.8 cM | 6.243 | 0.00902 | |

**Table 5b Contd….**

| Sl No. | Trait | Mapping population size | Type and no. of markers used | Associated marker | Associated QTL/ gene, | Chrom# | Position | PVE (R2) | P- value/ FDR | References |
|---|---|---|---|---|---|---|---|---|---|---|
| 5 | Total soluble sugars, starch, amylose and chlorophyll content | 120/274 | SSR, 136 | | | | | | | Nayak et. al. (2022b) |
| | Chl. a | | | RM1347 | *qChla2.1* | 2 | 82 | 7.251 | 0.00356 | |
| | Chl. a | | | RM405 | *qChla5.1* | 5 | 109 | 6.111 | 0.00729 | |
| | Chl. a | | | RM3231 | *qChla8.1* | 8 | 363 | 9.82 | 7.50E-04 | |
| | Chl. b | | | RM440 | *qChlb5.1* | 5 | 67 | 6.28 | 0.00623 | |
| | Chl. b | | | RM5436 | *qChlb7.1* | 7 | 136 | 5.549 | 0.00999 | |
| | Chl. b | | | RM3231 | *qChlb8.1* | 8 | 363 | 7.5 | 0.00288 | |
| | Starch | | | RM3701 | *qSC11.1* | 11 | 48 | 6.645 | 0.00613 | |
| | Starch | | | RM20377 | *qSC6.1* | 6 | 212 | 7.099 | 0.00466 | |
| | Starch | | | RM6374 | *qSC2.1* | 2 | 249 | 5.994 | 0.00913 | |
| | Amylose | | | RM3701 | *qAC11.1* | 11 | 48 | 11.376 | 3.95E-04 | |
| | Amylose | | | RM315 | *qAC1.2* | 1 | 92 | 7.193 | 0.00444 | |
| | Amylose | | | RM167 | *qAC11.2* | 11 | 123 | 7.918 | 0.00288 | |
| | Amylose | | | RM6091 | *qAC11.3* | 11 | 304 | 10.99 | 4.91E-04 | |
| | Total protein content | | | RM566 | *qPC8.2* | 8 | 234 | 5.832 | 0.00878 | |
| | Total protein content | | | RM220 | *qPC1.1* | 1 | 240 | 5.812 | 0.00889 | |
| | Total protein content | | | RM5638 | *qPC1.2* | 1 | 282 | 7.168 | 0.00378 | |
| | Total protein content | | | RM253 | *qTSS6.1* | 6 | 355 | 6.559 | 0.00554 | |
| | Total soluble sugar | | | RM247 | *qTSS12.1* | 12 | 23 | 6.081 | 0.00871 | |
| | Total soluble sugar | | | RM337 | *qTSS8.1* | 8 | 27 | 6.916 | 0.00524 | |
| | Total soluble sugar | | | RM248 | *qTSS7.1* | 7 | 157 | 12.074 | 2.67E-04 | |
| | Total soluble sugar | | | RM566 | *qTSS8.2* | 8 | 236 | 6.644 | 0.00617 | |
| 6 | Grain phytic content | 96 | Gene based markers (cgSSR), 14 | M13 | *SPDT/ OsSultr3;4* | 6 | | 0.16-7.84 | | Azharudheen et al. (2022b) |
| | | | | M14 | *OsPT8* | 10 | | 0.81-18.49 | | |

**Table 5b Contd….**

| Sl No. | Trait | Mapping population size | Type and no. of markers used | Associated marker | Associated QTL/ gene | Chrom# | Position | PVE (R2) | P- value/ FDR | Allelic effect | Co-localized QTL | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 7 | Grain physicochemical and nutritional traits | 96/300 | SSR, 122/250 | | | | | | | | | Chattopadhyay et al. (2023). |
| | AC | | | RM1075 | *qAC2.1* | 2 | 3833177 | 26.0 | 0.024 | 1.15 | *qFe2.1* | |
| | AC | | | RM324 | *qAC2.2* | 2 | 11389704 | 26.0 | 0.017 | 1.94 | *qKB2.1* | |
| | AC | | | RM17600 | *qAC4.1* | 4 | 33596398 | 25.0 | 0.037 | 4.43 | *qGPC4.1* | |
| | AC | | | RM1272 | *qAC4.2* | 4 | 35110870 | 25.0 | 0.037 | 4.43 | *qGPC4.2* | |
| | AC | | | RM18136 | *qAC5.1* | 5 | 7764190 | 25.0 | 0.034 | 2.3 | *qKB3.1* | |
| | AC | | | RM 87 | *qAC5.2* | 5 | 129200000 | 27.0 | 0.012 | 2.01 | | |
| | AC | | | RM 21521 | *qAC7.1* | 7 | 15985258 | 25.0 | 0.048 | -1.15 | *qKL7.1* | |
| | AC | | | RM25022 | *qAC10.1* | 10 | 3589942 | 25.0 | 0.046 | -1.55 | *qGC10.1* | |
| | ASV | | | RM181 | *qASV2.1* | 2 | 201993 | 18.0 | 0.033 | -0.33 | | |
| | ASV | | | RM14761 | *qASV3.1* | 3 | 9782360 | 20.0 | 0.009 | -0.41 | *qKL3.1* | |
| | ASV | | | RM135 | *qASV3.2* | 3 | 27411671 | 18.0 | 0.022 | 0.4 | | |
| | ASV | | | RM197 | *qASV6.1* | 6 | 3085639 | 18.0 | 0.029 | 0.3 | *qGORY6.1* | |
| | ASV | | | RM276 | *qASV6.2* | 6 | 6230045 | 18.0 | 0.035 | 0.3 | | |
| | ASV | | | RM162 | *qASV6.3* | 6 | 24035491 | 18.0 | 0.04 | 0.47 | *qZn6.2* | |
| | ASV | | | RM210 | *qASV8.1* | 8 | 22471837 | 18.0 | 0.035 | -0.55 | | |
| | ASV | | | RM149 | *qASV8.2* | 8 | 24721365 | 18.0 | 0.03 | -0.43 | | |
| | GC | | | RM13928 | *qGC2.1* | 2 | 30409991 | 24.0 | 0.029 | -2.99 | | |
| | GC | | | RM32 | *qGC5.1* | 5 | 4200000 | 24.0 | 0.021 | 3.72 | | |
| | GC | | | RM25022 | *qGC10.1* | 10 | 3589942 | 24.0 | 0.027 | 4.02 | *qAC10.1* | |
| | HD | | | RM13604 | *qHD2.1* | 2 | 24549546 | 6.0 | 0.017 | 1376.6 | *qVER2.1* | |
| | HD | | | RM175 | *qHD3.1* | 3 | 3865706 | 4.0 | 0.036 | -998.4 | | |
| | HD | | | RM281 | *qHD8.1* | 8 | 27895505 | 9.0 | 0.004 | 2702.8 | *qZn8.1* | |
| | HD | | | RM28828 | *qHD12.1* | 12 | 27478976 | 6.0 | 0.017 | -1764.2 | *qGPC12.1* | |
| | KB | | | RM324 | *qKB2.1* | 2 | 11389704 | 13.0 | 0.01 | 0.16 | *qLB2.1* | |

**Table 5b Contd….**

| Sl No. | Trait | Mapping population size | Type and no. of markers used | Associated marker | Associated QTL/ gene | Chrom# | Position | PVE (R2) | P- value/ FDR | Allelic effect | Co-localized QTL | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | KB | | | RM16138 | *qKB3.1* | 3 | 34611863 | 11.0 | 0.036 | -0.11 | *qVER3.1* | |
| | KB | | | RM142 | *qKB4.1* | 4 | 20518899 | 11.0 | 0.037 | -0.16 | | |
| | KB | | | RM3663 | *qKB5.1* | 5 | 21363398 | 11.0 | 0.037 | -0.09 | *qLB5.1* | |
| | KB | | | RM182 | *qKB7.1* | 7 | 77700000 | 10.0 | 0.048 | 0.15 | | |
| | KB | | | RM257 | *qKB9.1* | 9 | 17719660 | 10.0 | 0.046 | 0.07 | | |
| | KB | | | RM285 | *qKB9.2* | 9 | 66000000 | 13.0 | 0.009 | 0.2 | *qLB9.1* | |
| | KL | | | RM12678 | *qKL2.1* | 2 | 5764761 | 10.0 | 0.039 | 0.19 | | |
| | KL | | | RM71 | *qKL2.2* | 2 | 8760433 | 10.0 | 0.045 | 0.17 | *qFe2.2* | |
| | KL | | | RM14761 | *qKL3.1* | 3 | 9782360 | 12.0 | 0.02 | 0.26 | *qASV3.1* | |
| | KL | | | RM142 | *qKL4.1* | 4 | 20518899 | 13.0 | 0.009 | -0.45 | | |
| | KL | | | RM 21521 | *qKL7.1* | 7 | 15985258 | 14.0 | 0.004 | 0.31 | *qZn7.1* | |
| | KL | | | RM286 | *qKL11.1* | 11 | 383711 | 11.0 | 0.021 | 0.23 | | |
| | KL | | | RM4862 | *qKL11.2* | 11 | 9980302 | 10.0 | 0.038 | 0.4 | *qTPC11.1* | |
| | LB | | | RM8050 | *qLB1.1* | 1 | 42072506 | 6.0 | 0.027 | 0.19 | *qFe1.3* | |
| | LB | | | RM324 | *qLB2.1* | 2 | 11389704 | 6.0 | 0.027 | -0.21 | *qKB2.1* | |
| | LB | | | RM3663 | *qLB5.1* | 5 | 21363398 | 7.0 | 0.015 | 0.16 | | |
| | LB | | | RM285 | *qLB9.1* | 9 | 66000000 | 9.0 | 0.006 | -0.32 | *qANTH9.1* | |
| | KLAC | | | RM25754 | *qKLAC10.1* | 10 | 20198093 | 7.0 | 0.026 | -0.65 | | |
| | KLAC | | | RM27177 | *qKLAC11.1* | 11 | 25297111 | 7.0 | 0.021 | 0.56 | *qDPPH11.1* | |
| | VER | | | RM13604 | *qVER2.1* | 2 | 24549546 | 11.0 | 0.015 | 0.06 | *qHD2.1* | |
| | VER | | | RM16138 | *qVER3.1* | 3 | 34611863 | 10.0 | 0.023 | -0.06 | *qKB3.1* | |
| | TFC | | | RM17115 | *qTFC4.1* | 4 | 23207668 | 15.0 | 0.022 | 26.18 | *qDPPH4.1* | |
| | TFC | | | RM24616 | *qTFC9.1* | 9 | 19580580 | 14.0 | 0.037 | -19.22 | *qTPC9.1* | |
| | TPC | | | RM24616 | *qTPC9.1* | 9 | 19580580 | 17.0 | 0.022 | -44.81 | *qTFC9.1* | |
| | TPC | | | RM4862 | *qTPC11.1* | 11 | 9980302 | 16.0 | 0.03 | 73.08 | *qKL11.2* | |
| | ANTH | | | RM18136 | *qANTH5.1* | 5 | 7764190 | 13.0 | 0.037 | -7.64 | *qAC5.1* | |
| | ANTH | | | RM285 | *qANTH9.1* | 9 | 66000000 | 16.0 | 0.006 | -9.12 | *qDPPH9.1* | |
| | | | | RM28828 | *qANTH12.1* | 12 | 27478976 | 13.0 | 0.027 | 5.47 | *qGPC12.1* | |
| | DPPH | | | RM17115 | *qDPPH4.1* | 4 | 23207668 | 8.0 | 0.022 | 12.94 | *qTFC4.1* | |
| | | | | RM502 | *qDPPH8.1* | 8 | 26492117 | 7.0 | 0.038 | 43.64 | | |

**Table 5b Contd….**

| Sl No. | Trait | Mapping population size | Type and no. of markers used | Associated marker | Associated QTL/ gene | Chrom# | Position | PVE (R2) | P- value/ FDR | Allelic effect | Co-localized QTL | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | DPPH | | | RM285 | *qDPPH9.1* | 9 | 66000000 | 7.0 | 0.042 | 14.65 | *qANTH9.1* | |
| | DPPH | | | RM27177 | *qDPPH11.1* | 11 | 25297111 | 7.0 | 0.031 | -10.04 | *qKLAC11.1* | |
| | GOTY | | | RM12678 | *qGORY2.1* | 2 | 5764761 | 8.0 | 0.044 | -3.53 | | |
| | GOTY | | | RM14761 | *qGORY3.1* | 3 | 9782360 | 14.0 | 0.002 | -6.63 | | |
| | GOTY | | | RM197 | *qGORY6.1* | 6 | 3085639 | 8.0 | 0.038 | 3.86 | *qASV6.1* | |
| | GPC | | | RM24217 | *qGORY9.1* | 9 | 13094087 | 8.0 | 0.043 | 6.05 | | |
| | GPC | | | RM17600 | *qGPC4.1* | 4 | 33596398 | 9.0 | 0.017 | -2.31 | *qAC4.1* | |
| | GPC | | | RM1272 | *qGPC4.2* | 4 | 35110870 | 9.0 | 0.017 | -2.31 | *qAC4.2* | |
| | GPC | | | RM105 | *qGPC9.1* | 9 | 55000000 | 7.0 | 0.037 | -0.91 | | |
| | GPC | | | RM4455 | *qGPC10.1* | 10 | 11665805 | 9.0 | 0.016 | -0.63 | | |
| | GPC | | | RM467 | *qGPC10.2* | 10 | 13488471 | 7.0 | 0.042 | -0.51 | | |
| | GPC | | | RM28828 | *qGPC12.1* | 12 | 27478976 | 7.0 | 0.033 | 0.72 | *qANTH12.1, qHD12.1* | |
| | Fe | | | RM10725 | *qFe1.1* | 1 | 11456035 | 16.0 | 0.049 | -3.19 | | |
| | Fe | | | RM11292 | *qFe1.2* | 1 | 23439423 | 16.0 | 0.047 | -3.45 | | |
| | Fe | | | RM8050 | *qFe1.3* | 1 | 42072506 | 17.0 | 0.028 | -4.1 | *qLB1.1* | |
| | Fe | | | RM1075 | *qFe2.1* | 2 | 3833177 | 18.0 | 0.012 | -3.42 | *qAC2.1* | |
| | Fe | | | RM71 | *qFe2.2* | 2 | 8760433 | 18.0 | 0.01 | 3.06 | *qKL2.2* | |
| | Fe | | | RM489 | *qFe3.1* | 3 | 4333680 | 16.0 | 0.035 | -3.76 | | |
| | Zn | | | RM18600 | *qZn5.1* | 5 | 19018217 | 7.0 | 0.043 | 6.18 | | |
| | Zn | | | RM510 | *qZn6.1* | 6 | 2831443 | 8.0 | 0.031 | -3.8 | | |
| | Zn | | | RM162 | *qZn6.2* | 6 | 24035491 | 7.0 | 0.042 | -5.78 | *qASV6.3* | |
| | Zn | | | RM 21521 | *qZn7.1* | 7 | 15985258 | 7.0 | 0.042 | 3.77 | *qKL7.1* | |
| | Zn | | | RM281 | *qZn8.1* | 8 | 27895505 | 8.0 | 0.029 | -6.47 | *qHD8.1* | |
| | Zn | | | RM24448 | *qZn9.1* | 9 | 16699860 | 8.0 | 0.028 | -3.86 | | |

**Table 6: List of varieties developed/promising lines identified using identified QTLs/genes.**

| Sl No. | Traits | QTLs/Genes (NRRI) | Other QTLs/ Genes | Donor | RP | Status of development | Promising lines selected | Name of variety Released/ Stage in AICRP trials | Year of release | Importance of variety | References |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | BPH resistance | *qBph4.3* and *qBph4.4* | | CR 3006-8-2 | Naveen | Variety released | | CR Dhan 805 (Naveen Shakti) | 2023 | BPH resistant variety released through SVRC for Odisha. Suitable for growing in BPH endemic areas of Odisha. | Kar e al. (2023) |
| 2 | BPH resistance | *qBph4.3* and *qBph4.4* | | CR 3006-8-2 | Naveen | Variety released | | CR Dhan 809 | 2024 | BPH resistant variety released through CVRC for Odisha, Tripura, West Bengal, Bihar, Jharkhand and Assam | Kar et al. (2024) |
| 3 | Herbicide (Imazethapyr) tolerance | *AHAS* | | Robin | Sahbhagidhan | Variety released | | CR Dhan 807 | 2024 | Herbicide (Imazethapyr) tolerant near isogenic line (NIL) of mega variety Sahbhagidhan developed through marker assisted backcross breeding. Suitable for rainfed upland condition. Released through CVRC for Jharkhand, Odisha, Andhra Pradesh, Tamil Nadu, Chhattisgarh and Gujarat | Kar et al. (2024) |
| 4 | Submergence and herbicide tolerance | *AHAS* | *Sub1* | Swarna-*Sub1* and Robin | Swarna | Breeding lines under testing in AICRIP trial | IET 32123 (CR 4430-1-3-2-1) and IET 32124 (CR 4430-13-19-1-1) | AVT-2- RSL | 2024 | | Kar et al. (2024) |
| 5 | Herbicide (Imazethapyr) tolerance | *AHAS* | | Robin | Pooja | Breeding lines under testing in AICRIP trial | IET 32130 (CR 4431-117-3-2-1) and IET 32131 (CR 4431-63-2-1-1) | AVT-2- RSL | 2024 | | Kar et al. (2024) |

**Table 7: Timeline for QTLs, molecular markers, and prospective candidate genes identified for different traits in rice.**

| Year | No of QTLs, markers/MTAs and prospective candidate genes. | Associated Trait | Reference |
|---|---|---|---|
| 2007 | RAPD marker, $OPQ05_{1150}$ | Gall midge resistance/susceptibility in ARC5984 | Lima et al. (2007) |
| 2010 | Flanking markers, RM22550-RM547 | Gall midge resistance in PTB10 | Nanda et al (2010) |
| 2016 | 15 MTAs | Seven early seedling vigor related traits in an association panel of 96 rice genotypes. | Anandan et al. (2016) |
| 2016 | 9 MTAs | Five traits related to high temperature stress tolerance in a panel of 59 rice genotypes. | Pradhan et al. (2016) |
| 2017 | 11 QTLs | Traits related to tolerance response for seedling stage chilling stress a panel of 66 rice genotypes | Pandit et al. (2017) |
| 2017 | *qBph4.3* and *qBph4.4*, and 4 prospective candidate genes | Resistance to BPH in rice landrace Salkathi | Mohanty et al. (2017) |
| 2017 | AHAS (LOC_Os02g30630) | Herbicide (Imazethapyr) tolerance | Shoba et al. (2017 |
| 2018 | *qDFF1.1* and *qDFF6.1* | DFF under reproductive stage drought stress condition in CR143-2-2 | Barik et al. (2018a) |
| 2018 | *qRWC9.1* | Relative water content under reproductive stage drought stress condition in CR143-2-2 | Barik et al. (2018b) |
| 2019 | Seven QTLs | Five morpho-physiological traits under reproductive stage drought stress conditions in CR143-2-2 | Barik et al. (2029) |
| 2019 | 3 QTLs for GPC and 11 QTLs for SGPC and 10 prospective candidate genes | High grain protein content (GPC) and single grain protein content (SPC) in ARC10075. | Chattopadhyay et al. (2019) |
| 2019 | 10 MTAs | Mean Grain protein content in an panel of 105 rice genotypes | Pradhan et al. (2019) |
| 2020 | 29 QTLs | Chlorophyll fluorescence under salinity stress conditions at seedling stage in Pokkali (AC41585) | Chattopadhyay et al. (2020a) |
| 2020 | 7 QTLs | Fv/Fm (maximum quantum yield of primary PS II photochemistry), Y-NO (quantum yield of non-regulated energy dissipation) and qL (coefficient of photochemical quenching) | Chattopadhyay et al. (2020b) |
| 2020 | *qPRO3.1*, *qCHLa1.1* and *qRCC1.1* | Three physiological traits under reproductive stage drought stress conditions in CR143-2-2 | Barik et al. (2020) |
| 2020 | *qShB-1.1*, *qShB-1.2* and *qShB-1.3;* and two prospective candidate genes | Sheath blight resistance in CR 1014 | Bal et al. (2020) |
| 2020 | 23 MTAs | Nine physio-biochemical traits related to seed vigour in a panel of 120 rice genotypes | Sahoo et al. (2020) |
| 2020 | 30 novel QTLs | 11 traits related to yield in an panel of 60 rice genotypes | Donde et al. (2020) |
| 2021 | 10 MTAs for Fe and 7 for Zn content | High grain Fe and Zn contents in an panel of 102 rice genotypes | Pradhan et al. (2020) |
| 2021 | 9 QTLs and six prospective candidate genes | Chlorophyll fluorescence under salinity stress conditions at reproductive stage in Pokkali (AC41585) (7 QTLs) and IR64 (2 QTLs) | Chattopadhya et al. (2021a) |
| 2021 | 17 QTLs | Six traits under stagnant flooding stress conditions in Rashpanjor | Chattopadhya et al. (2021b) |
| 2021 | RM247 and two prospective candidate genes | Salinity tolerance at germination stage in Pokkali (AC41585) | Ngangkham et al.(2021) |
| 2019 | RM205 | Spikelet fertility under high temperature stress condition in a panel of 198 varieties | Parameswaran et al. (2021) |

**Table 7 Contd….**

| Year | No of QTLs, markers/MTAs and prospective candidate genes. | Associated Trait | Reference |
|---|---|---|---|
| 2021 | 24 MTAs | Six traits under Fe-toxicity soil conditions in an panel of 119 genotypes | Pawar et al. (2021) |
| 2021 | 9 MTAs | 4 parameters associated with BPH resistance in an panel of 104 varieties | Anant et al. (2021) |
| 2021 | 20 QTLs and six prospective candidate genes | Spikelet fertility and associated traits like panicle compactness and ethylene production in PDK Shriram and Heera | Sekhar et al. (2021) |
| 2021 | 20 MTAs | Eight physio-morphological traits related to seed vigour in an panel of 48 rice genotypes | Sanghamitra et al. (2021) |
| 2022 | 29 QTLs and 10 prospective candidate genes | Leaf number per plant and 18 related traits under low phosphorous conditions in an panel of 120 rice genotypes | Anandan et al. (2022) |
| 2022 | 5 MTAs | Four parameters associated with BPH resistance in an panel of 96 rice landraces | Babu et al. (2022) |
| 2022 | 17 QTLs and two prospective candidate genes | Four traits related to plant type characters and grain yield in an panel of 88 rice genotypes | Azharudheen et al. (2022a) |
| 2022 | 2 MTAs (genes) | Grain phytic content in an panel of 96 rice genotypes | Azharudheen et al. (2022b) |
| 2022 | 18 QTLs | Seed vgour index, root parameter, and germination % in an panel of 120 rice genotypes | Barik et al. (2022) |
| 2022 | 10 MTAs/QTLs | Grain size (TGW, GL, GW, GLWR) in an panel of 88 rice genotypes | Nayak et al. (2022a) |
| 2022 | 14 MTAs | Five traits superoxide dismutase, flavonoids, anthocyanins, Carotenoids, γ-Oryzanol and antioxidant Activity in an panel of 120 rice genotypes | Bastia et al. (2022) |
| 2022 | 21 QTLs | Total soluble sugars, starch, amylose and chlorophyll content in an panel of 120 rice genotypes | Nayak et al. (2022b) |
| 2022 | 11 QTLs | 4 traits related to antioxidant enzymes, and phenolic contents in an panel of 117 rice genotypes | Sanghamitra et al. (2022) |
| 2023 | RM17480 (*gm3*) and four prospective candidate genes | Gall midge resistance in an panel of 200 rice genotypes | Sahu et al. (2023) |
| 2023 | 9 QTLs | Germination rate and two early seedling growth parameters in an panel of 163 rice genotypes | Mohanty et al. (2023) |
| 2023 | 17 MTAs/ QTLs | Five traits related to panicle characters and yield in an panel of 88 rice genotypes | Sah et al. (2023) |
| 2023 | 78 QTLs | 16 parameters related to grain physicochemical and nutritional traits in an panel of 96 rice genotypes | Chattopadhyay et al. (2023) |
| 2024 | 21 MTAs | Eight traits under low P and N conditions in an panel of 142 rice genotypes | Parameswaran et al. (2024) |
| 2024 | *qBK5.1* and 4 prospective candidate genes | Resistance to bakanae disease in Thavalakannan | Khan et al. (2024) |
| 2024 | 6 MTAs | Four parameters associated with BPH resistance in an panel of 191 rice genotypes | Meher et al. (2024) |
| 2024 | *SDG725* and *FLO2* | Grain size and amylose content against Angoumois grain moth (*Sitotroga cerealella*) infestation in an panel of 80 rice varieties | Kajal et al. (2024) |
| 2024 | 20 MTAs and two prospective candidate genes | Seven traits related to seed vigor in an panel of 163 rice genotypes | Mohanty et al. (2024) |
| 2024 | 18 MTAs and 21 known genes | Seven traits related to yield and plant architecture in an panel of 188 *Aus* rice genotypes | Sar et al. (2024) |
| 2024 | 13 QTLs and 7 prospective candidate genes | Three early seedling vigour traits (Vg, AGR, and DW) | Basha et al. (2024) |

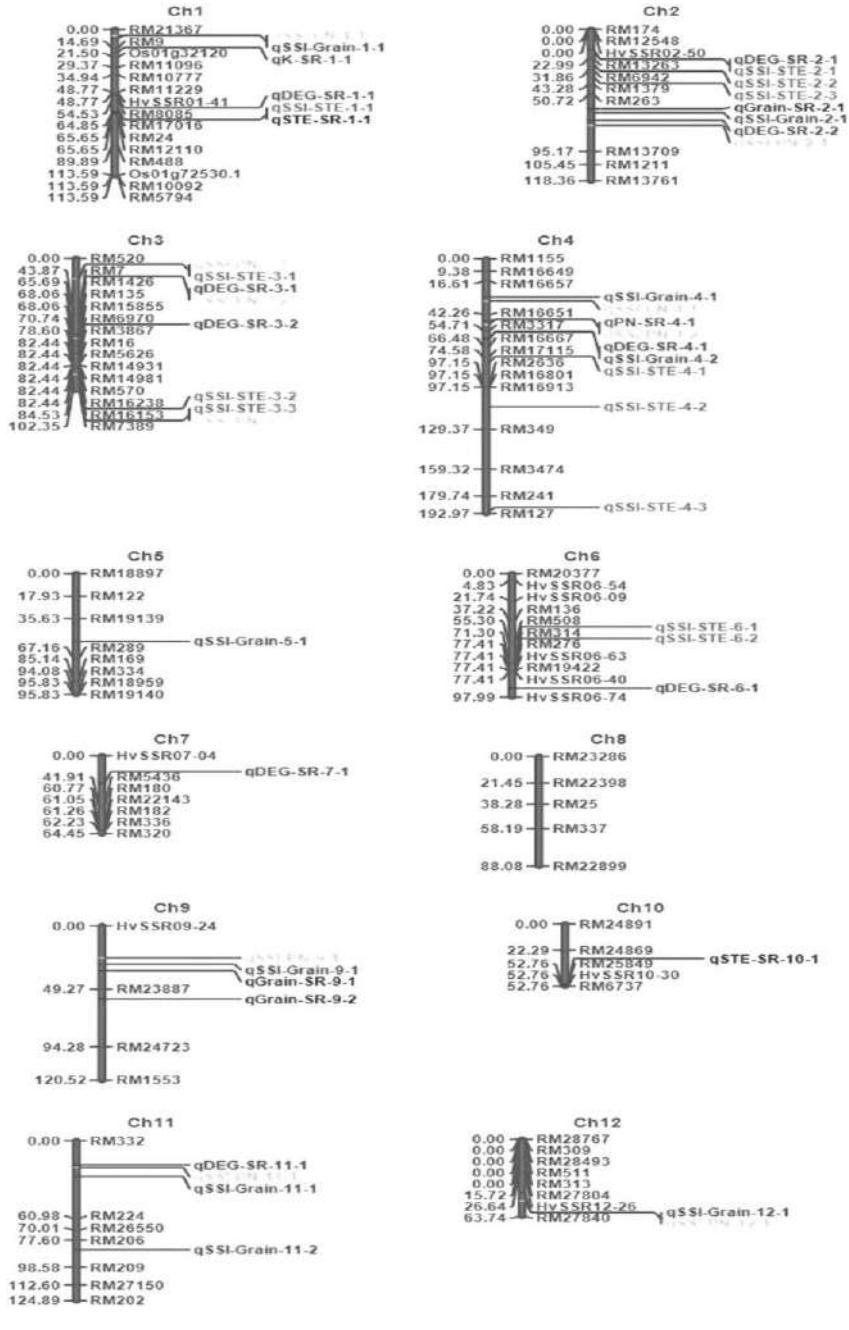


Fig. 1: Distribution of QTLs on 12 rice chromosomes for component traits and their stress susceptibility index for salinity tolerance at the reproductive stage detected in the wet season of 2015 through analysis of a backcross-derived mapping population from IR 64/Pokkali (AC41585). *Source: Chattopadhyay et al. (2021a).*

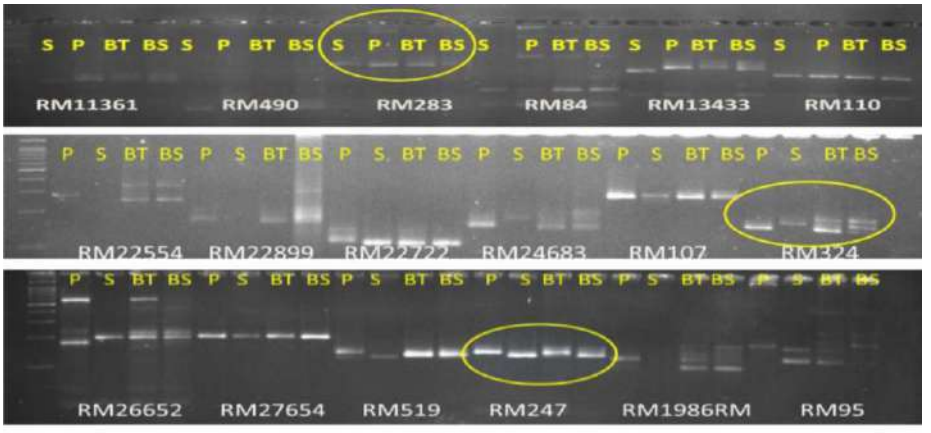


**Fig. 1. Gel electrophoresis of BSA. P, S, BT and BS denoted genomic DNA of Pokkali, Savitri, tolerant bulk and susceptible bulk. Circle indicates the genetic association of markers with the traits of interest**

Fig. 2: Banding pattern of Savitri (S), Pokkali (P), tolerant bulk (BT), and susceptible bulk (BS) amplified by microsatellite markers. The circles indicate markers associated with salt tolerance at the germination stage.

*Source: Ngangkham et al. (2021).*

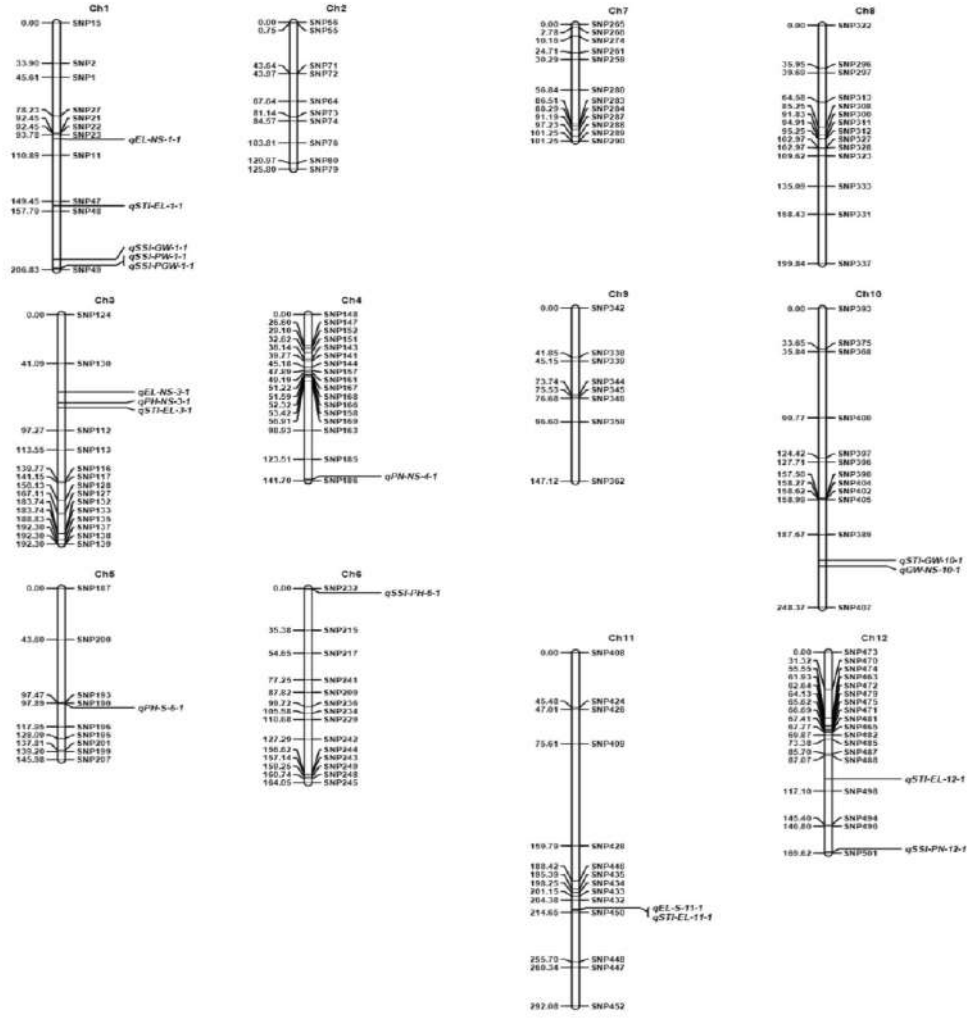


Fig. 3: Linkage map showing 17 QTLs using SNP associated with agro-morphological and yield-related traits under stagnant flooding conditions in the RIL population derived from the Swarna and Rashpanjor cross.

*Source: Chattopadhyay et al. (2021b).*

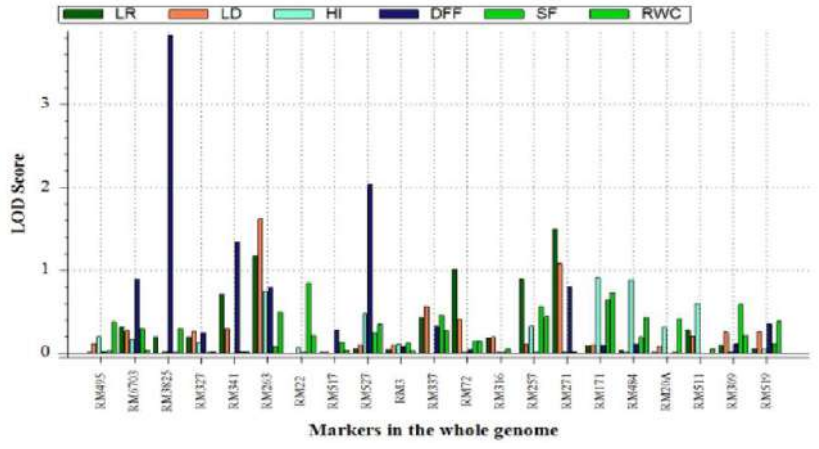


Fig. 4: Markers associated with days to 50% flowering (DFF) under reproductive stress drought stage conditions using SMA.

*Source: Barik et al. (2018a).*

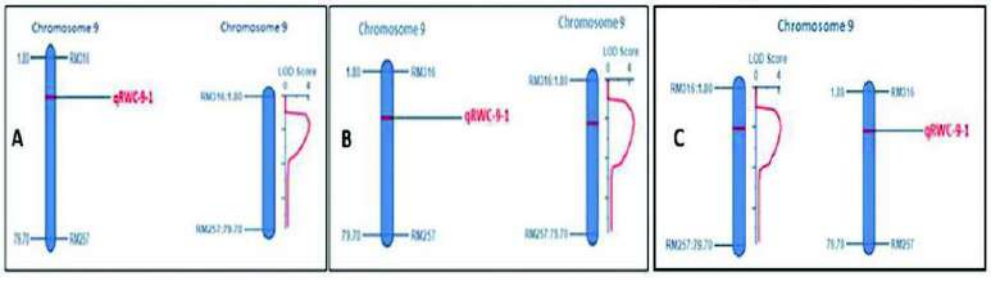


Fig. 5: The main effect QTL, *qRWC9.1*, detected in chromosome 9 associated with relative water content (RWC) under drought stress stage conditions. (A) RWC estimates of 2014, (B) RWC estimates of 2015, and (C) Pooled correct is RWC but not RWC estimates for both years.

*Source: Barik et al. (2018b).*

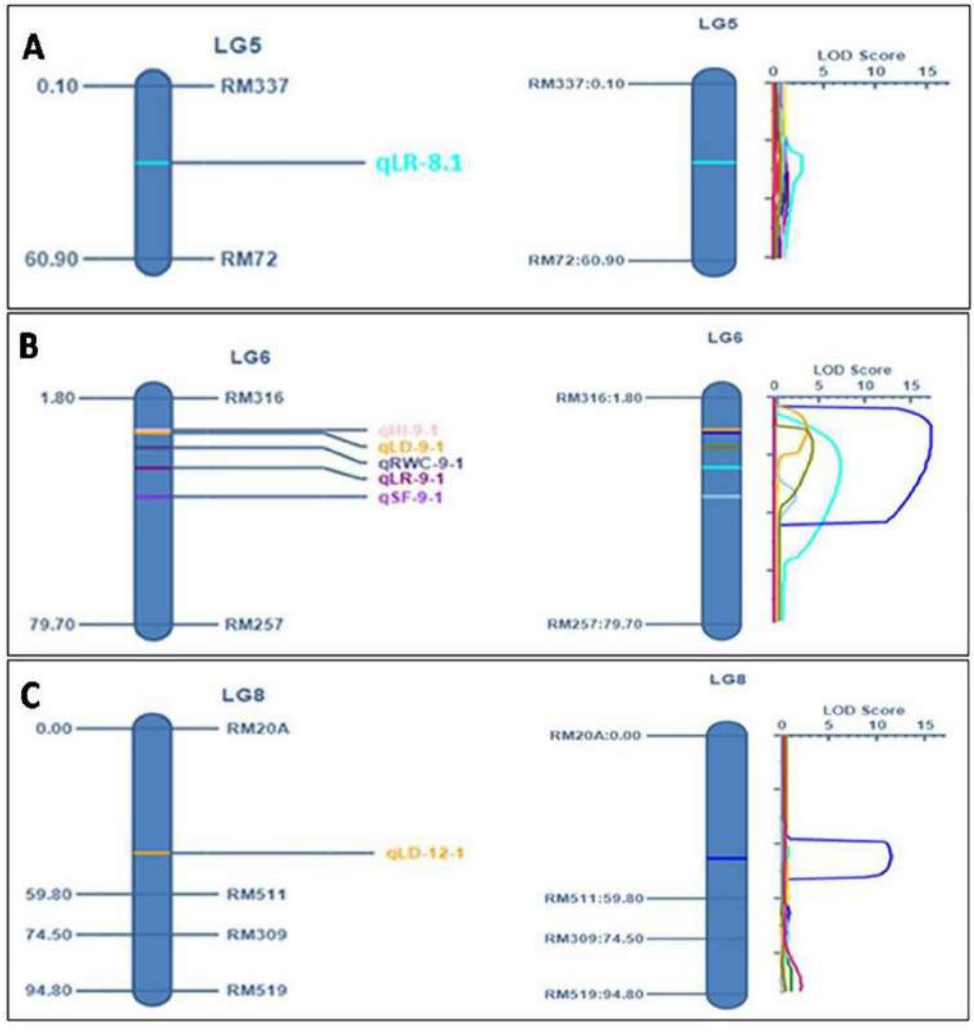


Fig. 6: A) QTL detected on chromosome 8 (LG5) (light green colour) for leaf rolling, B) chromosome 9 (LG6): pink colour represents harvest index, yellow colour represents leaf drying, deep blue represents relative water content, maroon colour represents leaf rolling, and violet colour represents spikelet fertility. C) QTL detected on chromosome 12 (LG8) (yellow colour) for leaf drying under stress drought stage conditions.

*Source: Barik et al. (2019).*

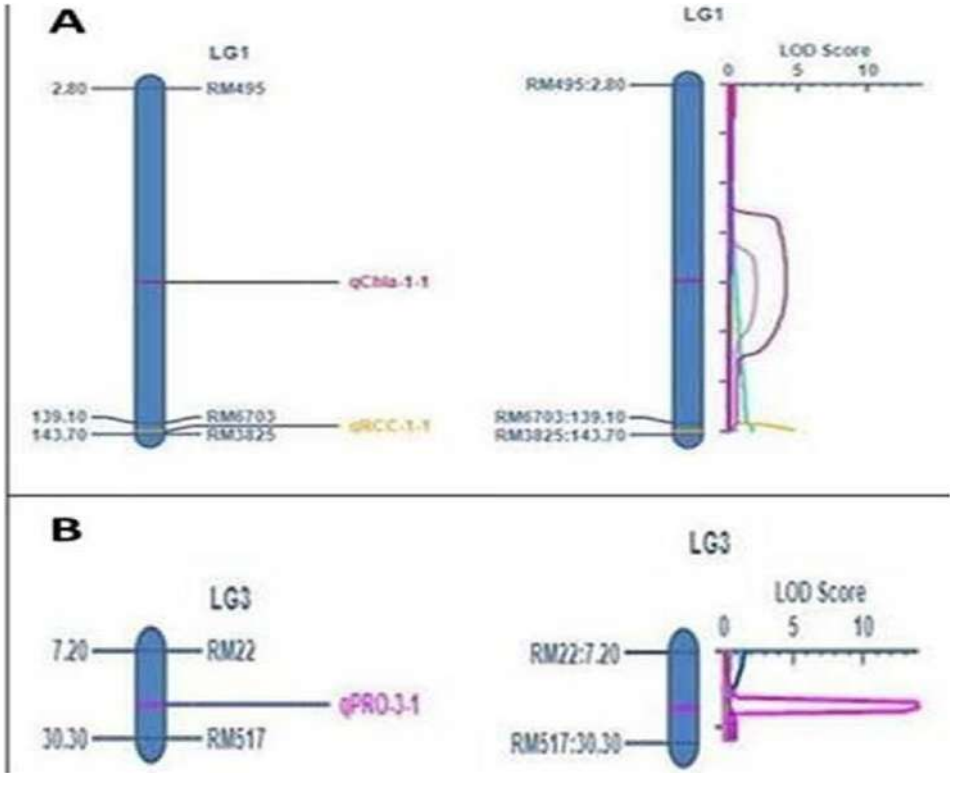


Fig. 7: A) QTL detected on chromosome 1 (violet colour) for chlorophyll a, for relative chlorophyll content (and yellow colour), B) QTL detected on chromosome 3 (pink colour) for proline content.

*Source: Barik et al. (2020).*

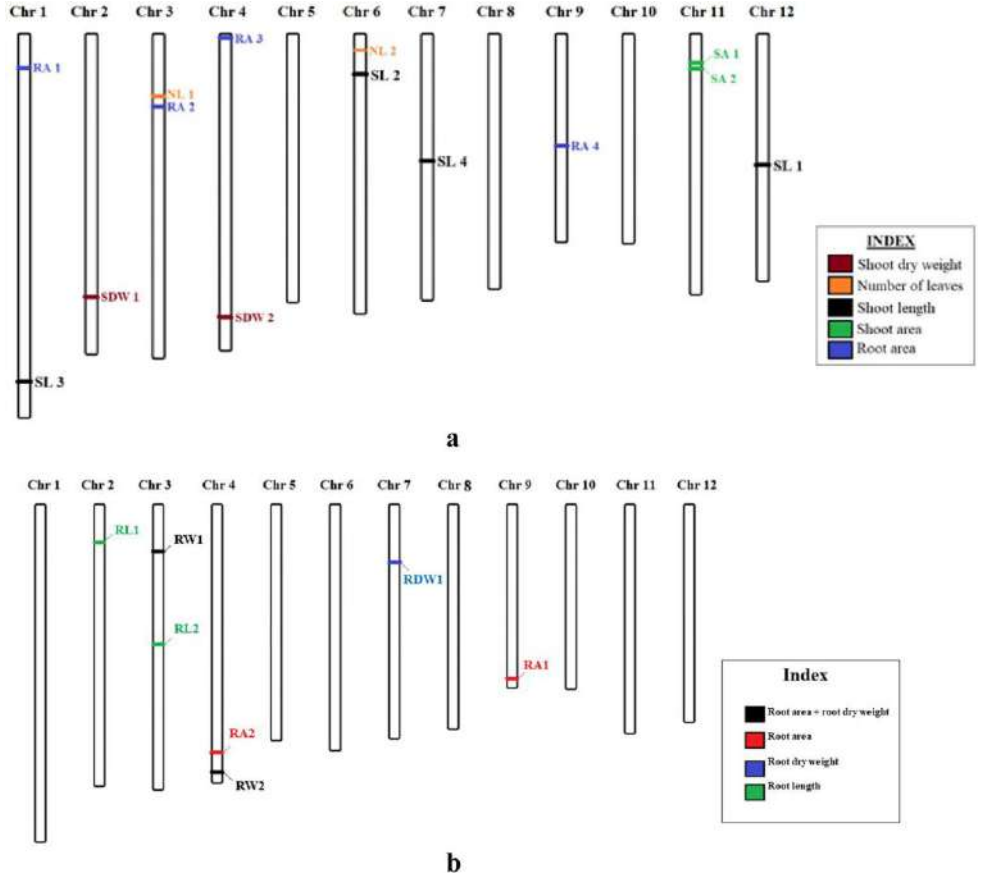


Fig. 8: a) Physical position of significantly associated SNPs under low P-low N conditions for different phenotypic traits, SDW 1, SDW 2, NL 1, NL 2, SL 1, SL 2, SL 3, SL 4, SA 1, SA 2, RA 1, RA 2, RA 3, RA 4; b) Physical position of significantly associated SNPs under control conditions for different phenotypic traits, RW, RW2, RA1, RA2, RDW1, RL1, RL2.

*Source: Parameswaran et al. (2024).*

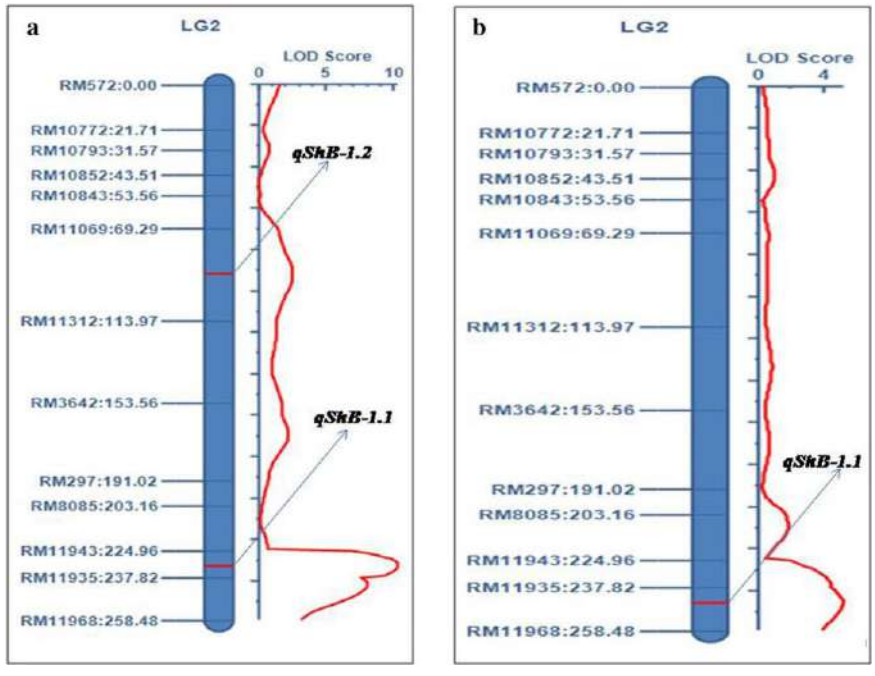


Fig. 9: Graphical representation of QTLs for sheath blight (ShB) resistance mapped on chromosome 1 (LG2) using mapping populations derived from the cross of Swarna-Sub1/CR 1014. a) QTLs *qShB-1.1* and *qShB-1.2 were* mapped in the $F_2$ generation; b) the QTL *qShB-1.1* was again mapped in the $F_{2:3}$ generation. *Source: Bal et al. (2020).*

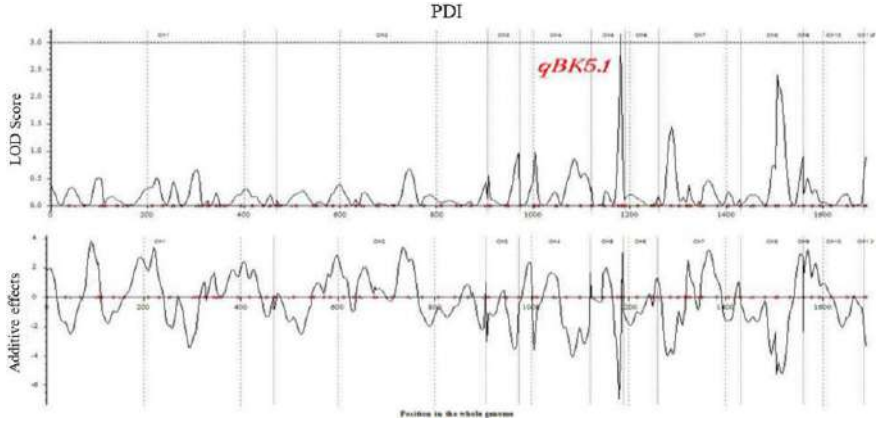


Fig. 10: The main effect of QTL, *qBK5.1,* identified on chromosome 5 for bakanae disease resistance and the additive effect of the identified QTL. The inverted peak in the additive effects represents that the QTL favours a lower disease score, i.e., resistance, in the mapping population. *Source: Khan et al. (2024).*

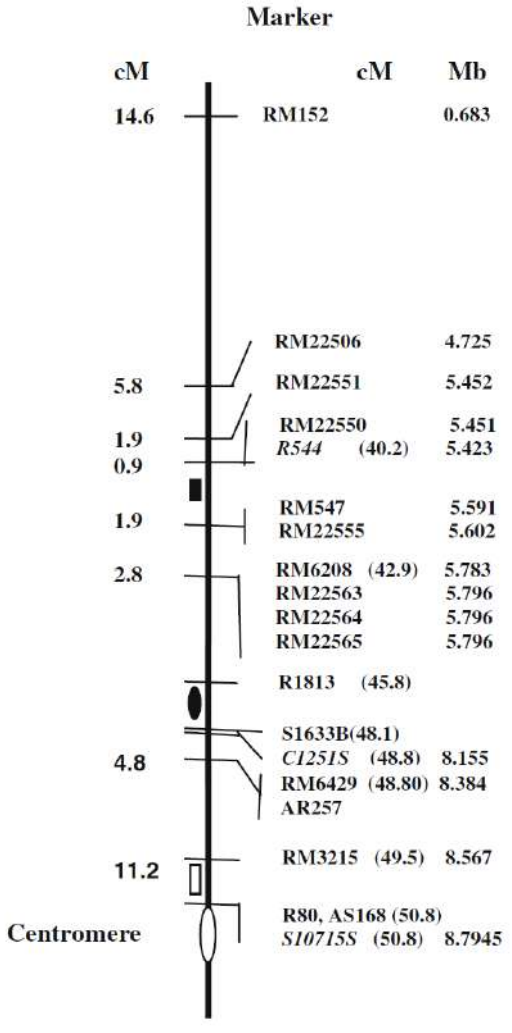


Fig. 11: Linkage map of the short arm of rice chromosome 8 showing positions of molecular markers linked to gall midge resistance genes. Numbers on the left side of the map show genetic distances in centimorgans (cM) of linked markers from the gall midge resistance gene present in PTB10 obtained in the present study, while numbers on the right side of the map show physical distances in Mb and genetic distances in centimorgans (cM) (given in parentheses) on chromosome 8. ■ shows the position of the gall midge resistance gene present in PTB10, identified in the present study. ⬮ shows the position of gall midge resistance gene, *Gm4*, present in Abhaya (Mohan et al. 1997; Nair et al. 1996). ▯ shows the position of the gall midge resistance gene, *Gm8*, present in cv. Jhitipiti (Jain et al. 2004)

*Source: Nanda et al. (2010).*

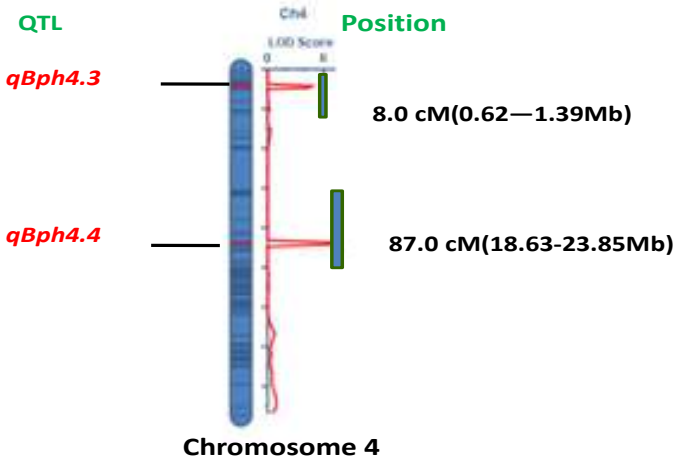


Fig. 12: Positioning of two QTLs, *qBph4.3* and *qBph4.4*, associated with BPH resistance in the rice landrace, Salkathi, using microsatellite markers initially and then by 40K Affymetrix SNP Chip. *Source: Mohanty et al. (2017).*

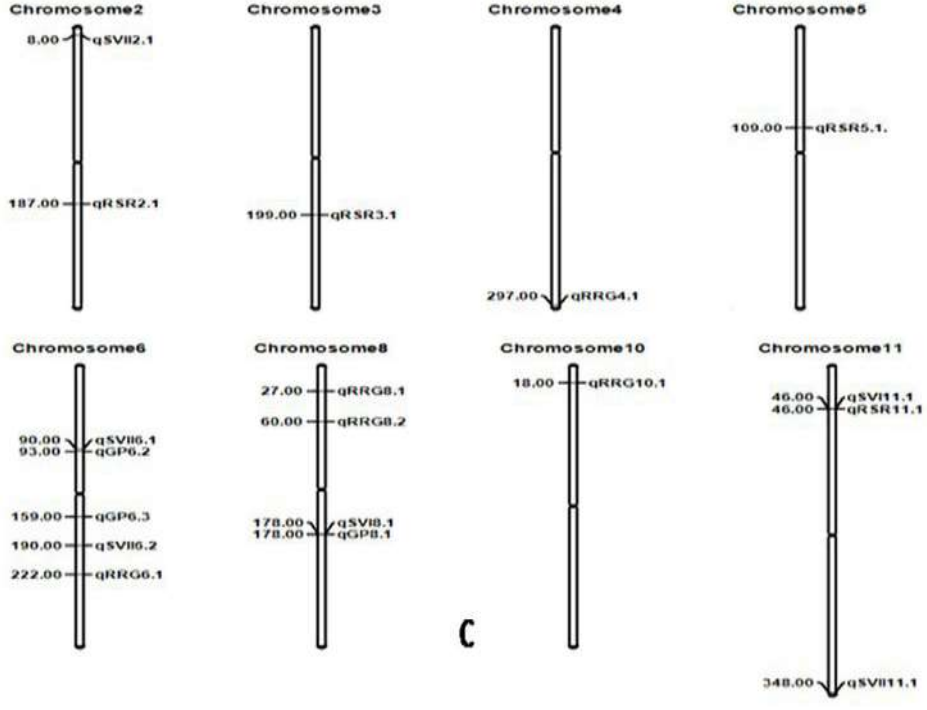


Fig. 13: Positions of the QTLs on the chromosomes for RSG, RGR, AGR, and MGR traits detected by association mapping. *Source: Barik et al. (2022).*

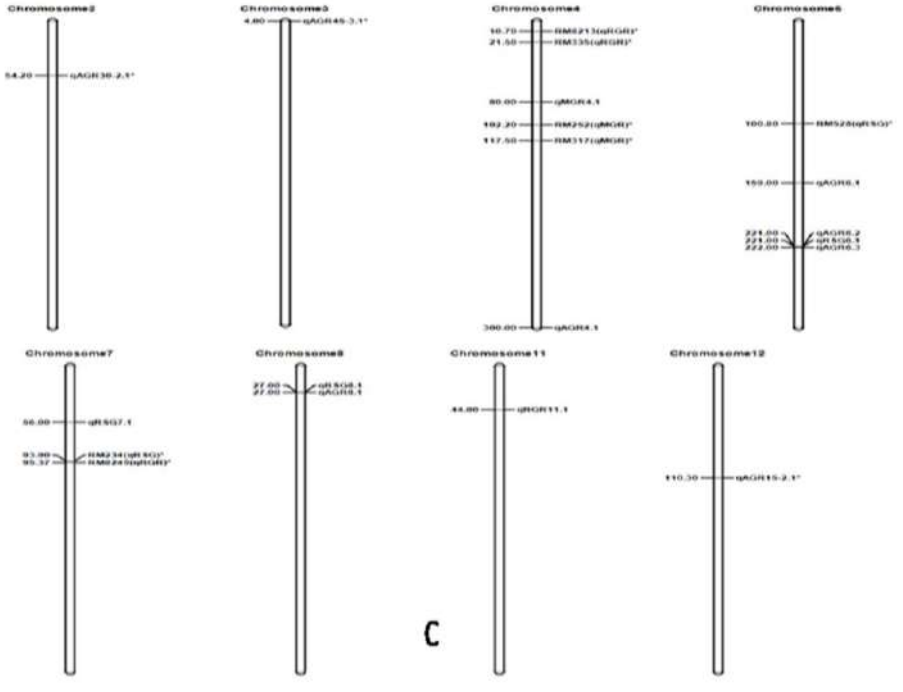


Fig. 14: Positions of the QTLs on the chromosomes for seed vigour-related traits, RSG, RGR, AGR, and MGR, detected by association mapping.

*Source: Mohanty et al. (2024).*

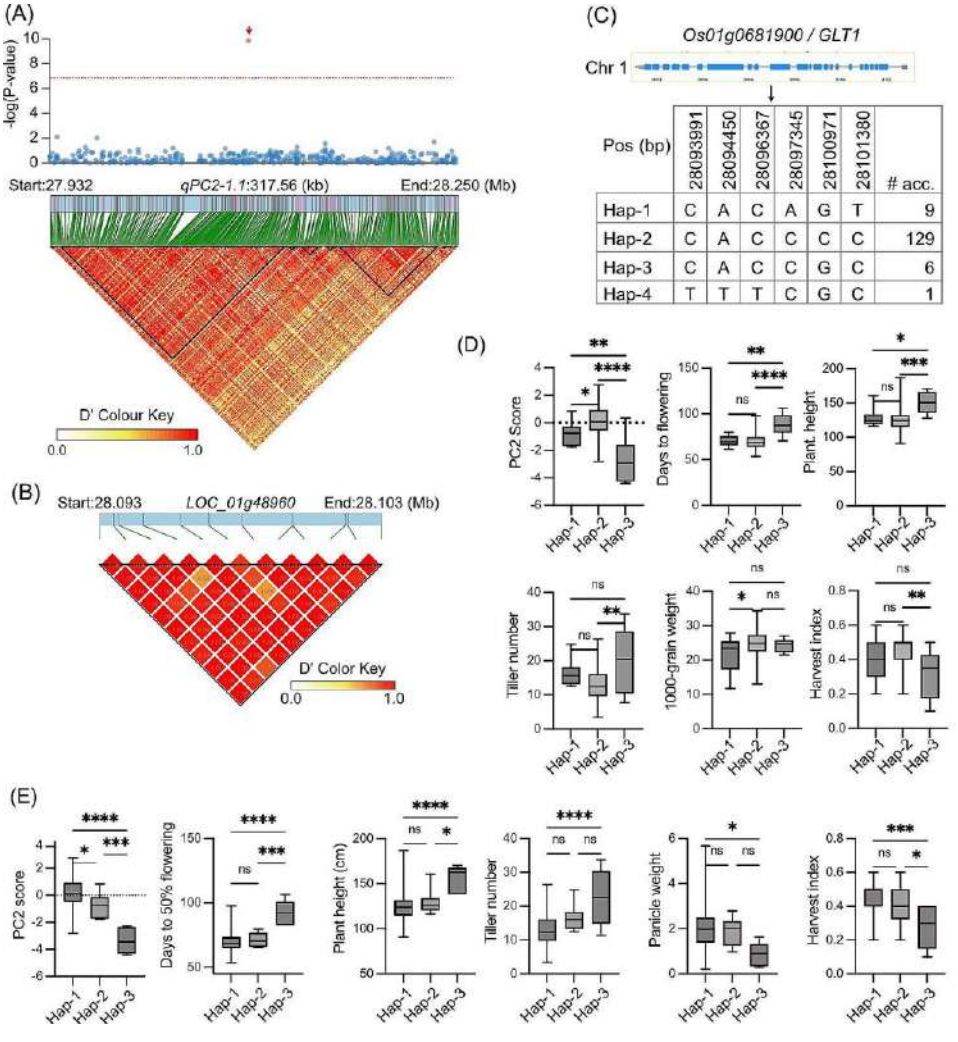


Fig. 15: Haplotype analysis within *qPC2-1.1*. A) Local Manhattan plot and LD heat map for *qPC2-1.1* on chromosome 1. The red arrow (top panel) indicates the position of *OsGLT1*. B) LD heat map of *LOC_Os01g48960*. C) Structure and DNA polymorphism of *OsGLT1*. D) Box plots of PC2 score and agro-morphological traits for three haplotypes, Hap-1 (*n*=9), Hap-2 (n=126), and Hap-3 (n=6), of *OsGLT1*. E) Box plots of PC2 score and agro-morphological traits for three haplotypes, Hap-1 (*n*=116), Hap-2 (n=11), and Hap-3 (n=7), of *OsPUP4*. Box edges represent the 0.25 and 0.75 quantiles, with the median values shown within boxes. Whiskers extend to the extreme point, which is no more than 1.5 times the interquartile range. Differences between the haplotypes were statistically tested using multiple comparisons with Tukey's t-test (ns, not significant, *, ***, and **** represent *P* values <0.05, <0.01, <0.001, and <0.0001, respectively).

*Source: Sar et al. (2024).*

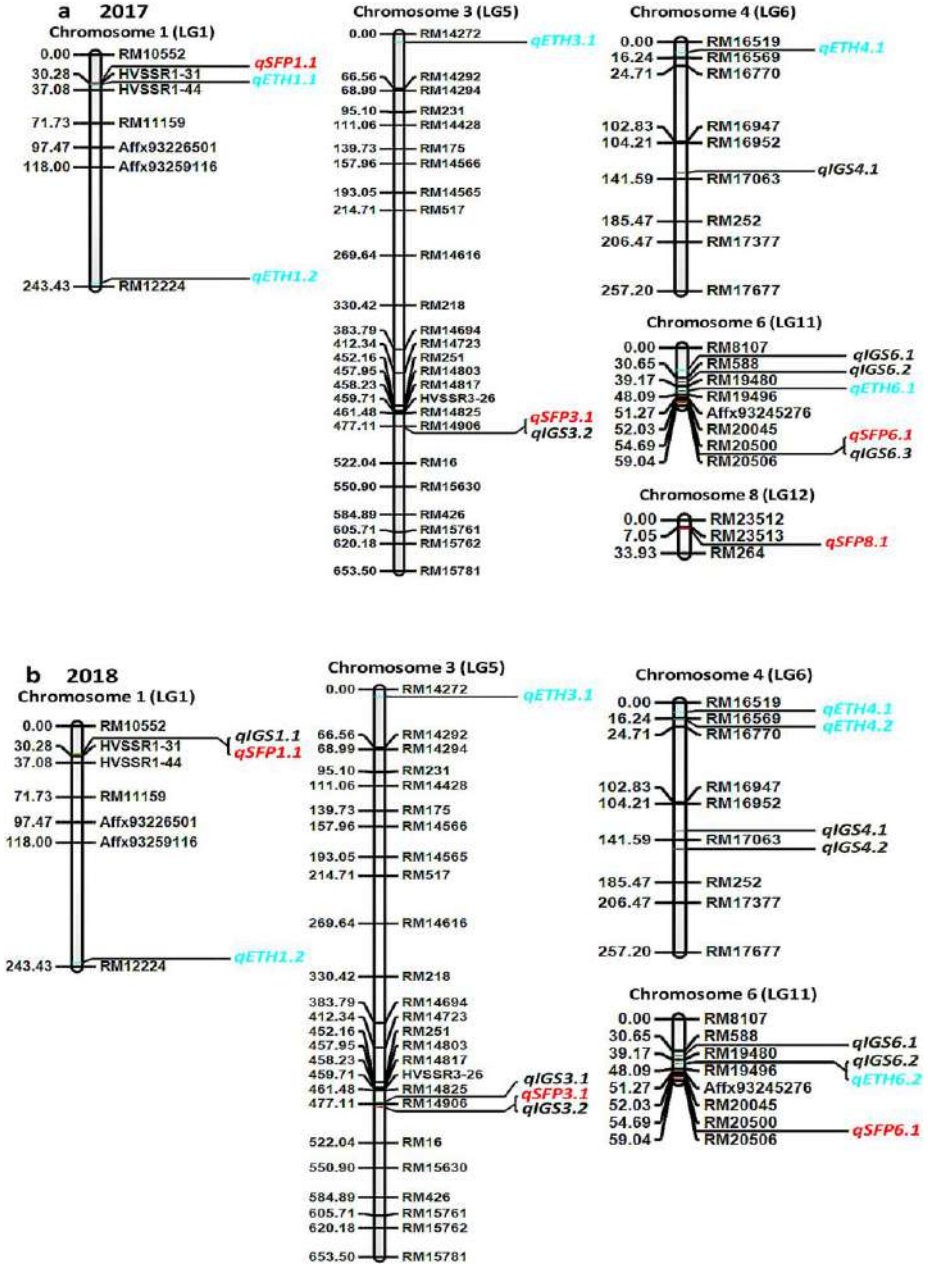


Fig. 16: Linkage map showing QTLs associated with spikelet fertility (SFP), inter-grain space (IGS), and ethylene production (ETH) in (a) *Kharif* 2017 and (b) *Kharif* 2018. Markers and QTLs are represented on the right side of the linkage group, while values on the left side represent the linkage distance in cM in the LG-Linkage group. *Source: Sekhar et al. (2021).*

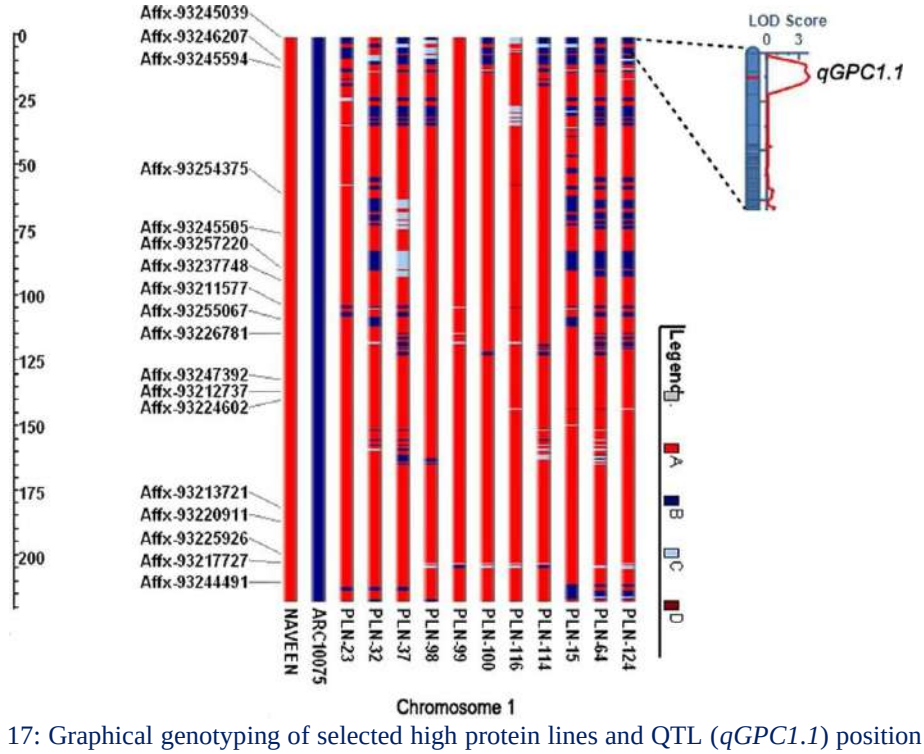


Fig. 17: Graphical genotyping of selected high protein lines and QTL (*qGPC1.1*) position on the telomeric region of the short arm of chromosome 1 (Note: A: Naveen genome, B: ARC10075 genome, C: heterozygote, D: missing/unknown). *Source: Chattopadhyay et al. (2019).*

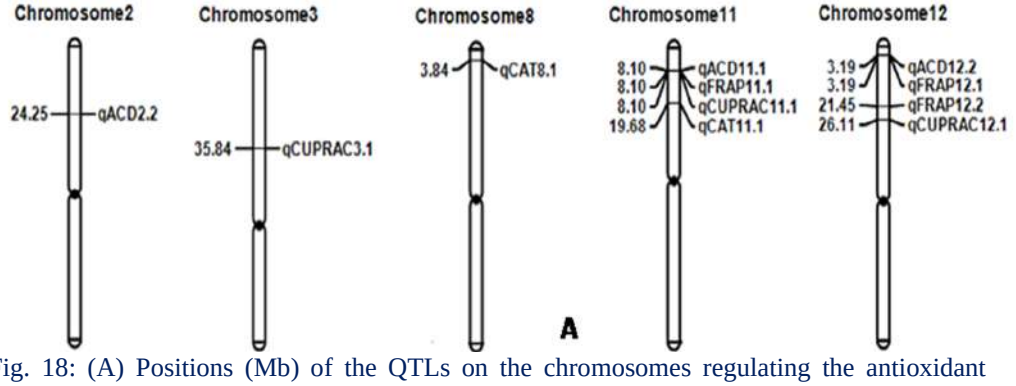


Fig. 18: (A) Positions (Mb) of the QTLs on the chromosomes regulating the antioxidant traits, catalase, peroxidase, DPPH, FRAP, and CUPRAC detected by association mapping.

*Source: Sanghamitra et al. (2022).*

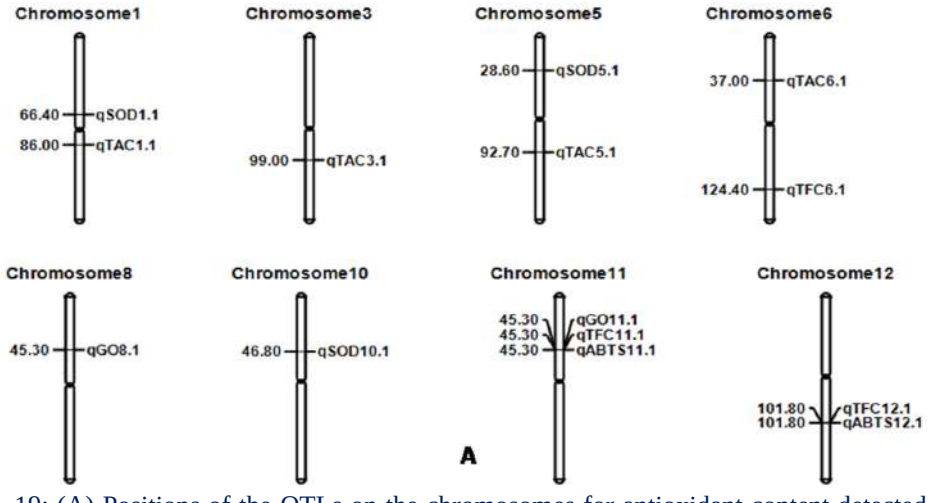


Fig. 19: (A) Positions of the QTLs on the chromosomes for antioxidant content detected by association mapping. *Source: Bastia et al. (2022).*

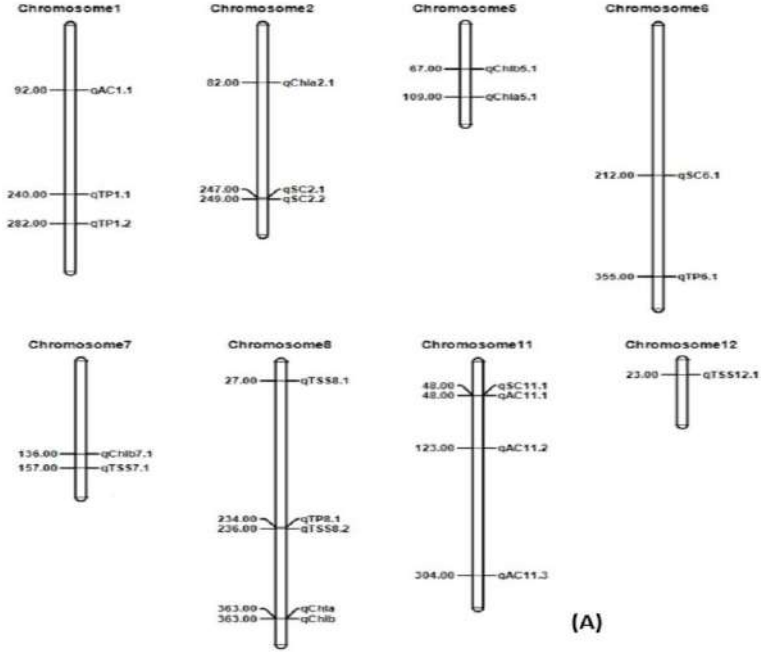


Fig. 20: A) Positions of the QTL on the chromosomes for chlorophyll a, chlorophyll b, starch, amylose, total protein, and total soluble sugars. *Source: Nayak et al. (2022b).*


Fig. 21: Brown planthopper resistant rice variety CR Dhan 805.


Fig. 22: Brown planthopper resistant rice variety CR Dhan 809.


Fig. 23. NILs of Pooja carrying BPH resistance QTLs of Salkathi showing resistance against BPH in artificial screening compared to the susceptible reaction of Pooja.


Fig. 24: Herbicide-tolerant rice variety CR Dhan 807.

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