Extended Summary

1st Indian Rice Congress

Rice Research and Development for Achieving Sustainable Development Goals

December 8-9, 2020
ICAR-NRRI, Cuttack, Odisha

Organized by

Association of Rice Research Workers
Cuttack, India

in collaboration with

1st Indian Rice Congress – 2020

RICE RESEARCH AND DEVELOPMENT FOR ACHIEVING SUSTAINABLE DEVELOPMENT GOALS

December 8-9, 2020

Extended Summaries

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PREFACE

As per the report of 'Consultative Group on International Agricultural Research' (CGIAR), rice (*Oryza sativa* L.) and rice related activities will be able to address 9 of the 17 United Nations Sustainable Development Goals (SDG). It is estimated that 40% of the world's population consume rice as their major source of food, and 1.6 billion people in Asia take rice as their mainstay food. Further, rice production is an important source of livelihood for around 144 million rice-farming households and for millions of people working on rice farms as labourers. Paradoxically, rice farming is assumed to be associated with poverty in several countries. Moreover, ~900 million of the world's poor depend on rice as producers or consumers. Out of these, some 400 million poor and undernourished people are engaged in growing rice. Therefore, SDGs comprising of No Poverty (Goal 1), Zero Hunger (Goal 2) and rice cultivation are highly related and achieving the first two SDGs is dependent on the profitable rice farming. Apart from Goal 1 and 2 of SDGs, rice production is also related with Gender equality (Goal 5), Clean water and sanitation (Goal 6), Decent work and economic growth (Goal 8), Responsible consumption and production (Goal 12), Climate action (Goal 13), Life on Land (Goal 15) and Partnerships (Goal 17).

Above mentioned SDGs related with rice cultivation could only be achieved through integrated rice research, wide dissemination of technologies, empowerment of women, sustainable resource management, etc. The partnerships among the government institutions, public and private organizations, farmers, policy makers, and other stakeholders are essential for attaining the SDGs through rice cultivation. Keeping in mind those facts, the objective of this congress is to provide a platform for all rice stakeholders to interact and exchange ideas about recent advances in rice science and brainstorm key policies to meet the United nations' SDGs as well as to sustain rice cultivation in India. The Congress is divided into four broad thematic areas 1. Enhancing rice productivity and quality, 2. Sustainable rice farming, 3. Biotic-stress management in rice and 4. Rice for livelihood security, equity, and profitability.

We have received overwhelming responses from the rice researchers from the country and abroad. A total of 388 extended summaries were accepted for the Congress. This compilation was not possible without the support from the scientists from different partner institutes and from ICAR-National Rice Research Institute, Cuttack. At the end, we thank all the participants of this Congress without whose handwork and dedication for rice research, it was not possible to document the present trend of rice science. The great enthusiasm shown by honourable delegates from all around the world is praiseworthy.

Chairman and Members
Programme and Publication Committee

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THEME - I

Enhancing rice productivity and quality

ETHYLENE COULD BE THE RETROGRADE SIGNAL FOR THE TRADE OFF BETWEEN SPIKELET NUMBER AND GRAIN FILLING

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Rice plant is unique cereal because of significant variation in phenotype, physiology and genotype inherent in diversity of cultivars used. Unlike other cereals, rice is versatile of being comparatively sturdy and resilient to various physicochemical stresses and feeds more people on earth. Significance of rice to mankind is based on factors like a. Rice cultivation and consumption is associated with human food security, b. Small and marginal farmers numbering 144 million with farm size lesser than one hectare, c. Rice is important source of food, employment and income for rural poor, d. Rich biodiversity ensures diffusion into habitats contrasting for land topology, moisture regime and other cultural conditions, e. Long history of cultivation intricately related to food habit and human culture with important influence on social order, religion and traditional customs.

Origin of cultivated rice

For rice depth of water level of the field dictates the phenology of the crop, short duration ephemeral low yielding cultivars are grown in the absence of accumulated water and long duration tall phenotypes inhabit ponded water habitat. Evolution and speciation of rice has taken place according to land topology and physical properties of soil to retain water. In the long process of evolution, a putative progenitor like perennial Oryza *rufipogon* living in swampy ditches was probably transformed into an annual form *Oryza sativa*, native of seasonal water limited land habitat. The hall mark of domestication was increase of grain number per panicle. Articulation of high numbers of grains in compact orientation had accrued yield benefits. But overcrowding large number of spikelets into crammed space of panicle rachis in the more recently developed cultivars has marginalised this advantage.

Spikelet filling of rice panicle is location specific

Rice plant bears a complex racemose type inflorescence, where pedicellate spikelets are borne on nodes and tips of branches. Each spikelet bears a grain at maturity. Individual grain development is location specific; spikelets of upper primary branches reach anthesis early and develop faster compared to those on basal branches. The apical spikelets produce quality grains for human consumption, whereas poorly filled grains on inferior spikelets become brittle and fragile during hulling. This heterogeneous pattern of development was preferred in traditional rice is an important strategy for plant survival in fickle climatic conditions. Homogeneity of development would have been disastrous for the seed formation in a situation where inclement weather coincides with sensitive stages of development. Because grain yield was low in traditional rice, rice breeders improved panicle spikelet number in new super rice cultivars; in the process the heterogeneous panicle architecture was partially compromised to a relatively homogeneous pattern through reduction of apical dominance. The extra spikelets are accommodated on secondary branches. Increase of spikelet density under-rated grain filling by compromising with activities of key starch synthesising enzymes like sucrose synthase, ADPglucose pyrophosphorylase and starch synthase in inferior spikelets.

Hormonal control of endosperm starch biosynthesis

The spikelet specific discrimination in starch synthesis in rice panicle has not been prejudiced to any discrimination in supply of assimilates. The concept of a poor assimilate supply owing to possible limitations of source activity not supportive of causality in reduced endosperm starch synthesis has extended exploration of hormonal factors regulating grain development in rice. As of today, manipulation of spikelet development with hormones was thought to be an option for improved starch synthesis. Hormone actions are far from simple and involve interactions between positive and negative regulators. Bereft of any significant breakthrough, initial research focussed more attention on the positive regulators in rice. In fact, intrinsic levels of cytokinin, auxin and gibberellic acid were low in the inferior spikelets and their external application improved grain filling significantly, but the explorations were not fruitful for raising yield ceiling of rice.

Ethylene as regulator for grain filling.

The role of ethylene inhibiting grain filling of inferior spikelets was discovered first by Mohapatra et al (2000). The hormone was found affecting starch filling and grain quality of the under-developed spikelets by impeding activities of enzymes of sucrose metabolism. Later it was noted that the inferior spikelets generate more ethylene compared to the superior apical spikelets at anthesis. High ethylene level slackens endosperm cell division and starch synthesis. Additionally, crammed space for spikelet accommodation generates more ethylene. High ethylene production owing to spikelet compaction up-regulates expression of genes encoding ethylene signal transduction that conflicts with expression of starch synthesizing enzymes genes. The pernicious effects of ethylene on expression of genes for starch biosynthesis enzymes could be countered in compact panicle, with ethylene action inhibitor 1-MCP applied at booting stage. Application of the inhibitor not only reduces expression of genes for ethylene synthesis and signal transduction, but also enhanced expression of various starch synthesizing enzyme genes. This research has identified the close linkage of ethylene action with endosperm starch synthesis of rice caryopsis, making it a possible target for manipulation through biotechnological intervention in the forthcoming years.

IRC/TM-1/OP-2

ADVANCES IN DEVELOPING MULTI-GENE ABIOTIC AND BIOTIC-STRESSES TOLERANT RICE VARIETIES

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Increasing incidences of multiple abiotic stresses together with increasing population are the major constraints to attain the global food security. Rice, the major staple food crop is very much prone to various abiotic and biotic stresses which can occur one at a time or two or more together in a single crop growing season and adversely affects the rice production and productivity. The devastating effect of multiple stresses on rice crop is much more erratic and complex leading to higher losses in the crop grain yield. The concurrent occurrence of multiple streeses can destroy rice production in many of the rainfed areas of South and Southeast-Asia. Genomics-assisted breeding strategies have been instrumental in introgression of various major effect QTLs/genes into rice mega varieties and have proven successful in achieving the desired level of tolerance/resistance to various abiotic stresses in diffferent crop species. Keeping the present scenario of changing climate in mind, the paper presents the success in combining tolerance to two or more abiotic stresses in mega rice varieties applying genomics-assisted breeding and development of high-yielding climate resilient rice through stacking of multiple genes/ QTLs, which can withstand in a cascade of multiple stresses occurring regularly under direct seeded cultivation conditions.

MATERIAL AND METHODS

To combine anaerobic germination, blast resistance, brown planthopper resistance, bacterial blight resistance, gall midge resistance, grain yield under direct-seeded cultivation conditions, early vigor, nodal roots and early and uniform emergence in the background of high yielding irrigated rice cultivar IR09N538 (IRRI 132/PR 30138-35-2//IR04N114) with preferable grain type, a genomics-assisted breeding (GAB) program began in the 2014 DS with 12 donors, including donors for biotic and abiotic stress tolerance and DSR-adapted traits. GAB was attempted to introgress and assemble multiple QTL/genes for traits that increase adaptability to direct seeded rice conditions such as root traits [nodal root number ($qNR_{4.1}$, $qNR_{5.1}$) and root hair density ($qRHD_{1.1}$, $qRHD_{5.1}$, $qRHD_{8.1}$)], early vegetative vigor ($qEVV_{9.1}$), early uniform emergence ($qEUE_{1.1}$, $qEUE_{11.1}$), grain yield under DSR conditions ($qGY_{1.1}$, $qGY_{8.1}$, $qGY_{10.1}$) (Sandhu et al. 2015), and lodging resistance ($qLDG_{4.1}$) (Dixit et al. 2015) had been pyramided with abiotic stresses (drought QTLs-$qDTY_{1.1}$, $qDTY_{2.1}$, $qDTY_{3.1}$ and $qDTY_{12.1}$) as well as biotic resistance (gall midge-*Gm4*, blast- *Pi9*, *Pita 2*, bacterial leaf blight- *Xa4* , *Xa21*, *xa5*, *xa13*, and brown plant hoppers-*Bph3* and *Bph17*) using marker-assisted selection approach. The polymorphic SSRs, indel and gene specific markers for the introgressed genomic regions were exploited for the detection of the true F_1s and the progenies. As the introgressed genomic regions/genes are many in number and also were not fine mapped, sequential genotyping approach was used to make genotyping labor and cost effective. The first stage selection was done only on the phenotypically selected plants using the peak markers associated with the introgressed QTLs. The second stage selection was done on the selected plants harbouring the specific donor allele using the flanking and all other markers underlying the genomic regions.

RESULTS

The grain yield performance of conventionally and genomic assisted derived breeding lines was compared, the genomics assisted derived breeding lines showed better results in term of improve yield, adaptability and multiple stress tolerance/resistance over traditional conventional breeding dervied breeding lines. The developed promising breeding lines with superior grain quality and better adaptability carrying 7-11 QTLs/genes for various biotic and abiotic tolerance/resistance have the potential to be released as DSR varieties in different countries of South and South East Asia.

The grain yield advantage in conventionally derived multiparent breeding lines ranged from 2.0 to 6.6 t ha^{-1} while the grain yield advantage in biparental breeding lines ranged from 1.5 to 6.3 t ha^{-1}. Genomic assisted derived multiparent breeding lines yielded significantly higher (3.3 to 6.7 t ha^{-1}) than the multiparent lines developed from the conventional breeding (2.1 to 6.6 t ha^{-1}). Eleven such promising breeding lines developed from the genomic assisted breeding program carrying 7-11 QTLs/genes and 8 breeding lines from the conventional breeding program with grain-yield improvement of 0.7 to 1.6 t ha^{-1} and 0.07 to 0.7 t ha^{-1}, respectively over best check were selected.

DISCUSSION

The increased grain yield of breeding lines developed under conventional breeding program involving multi-parent performed better than the bi-parental breeding lines across generations which may result from the accumulation of alleles for traits increasing rice adaptability to direct seeded cultivation situation. Though, the multi-parent cross requires more time and higher costs for the population development, but the increased genetic variations may open window to improve grain yield and adaptability under direct seeded cultivation situation. The better performance of the breeding lines derived from the genomics assisted breeding program over the breeding lines from the conventional breeding program in term of grain yield improvement under direct seeded cultivation situation could be result of precise marker based selection that help reduce the undesirable linkage drags.

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IRC/TM-1/OP-3

COMBINING HIGH-THROUGHPUT PHENOTYPING AND GENOME-WIDE ASSOCIATION STUDIES FOR GENETIC DISSECTION OF NITROGEN USE EFFICIENCY IN RICE

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Low nitrogen use efficiency and apply high rate of nitrogen fertilizers in rice production strongly affected farmer income and ecosystem damage. Breeding rice with higher nitrogen use efficiency is critical for food security, sustainable development to gain more yield from less fertilizer for more efficiency. In the rice breeding program, screening large number of accession and donor identification play a vital role. Nitrogen use efficiency (NUE) is complex traits, inherent by nitrogen uptake, assimilation and remobilization. It is governed by multiple quantitative traits and strongly affected by environmental conditions such as soil type, rainfall pattern, soil nitrogen soil water availability (Xu et al., 2020). Therefore, uniform environment is critical. Huge germplasms are often initially screened under controlled environmental conditions, with subsets of promising lines selected for subsequence field study. Recent advances in crop phenomics and genomics have provided powerful tools forquantifying traits and discovering associatedwith numerous abiotic stress in plants as well as for N studies.High-throughput phenotyping is non-destructive, time series capture large number of genotypes and plant traits such as growth, architectural, physiological and biomass-related traits with high precision and accuracy.Genome-wide association study (GWAS) of natural genetic variation considered as a potential tool accelerates the discovery of key genes and alleles associated with the NUE traits. (Xu et al., 2020; Yang et al., 2014). Therefore, combining high-throughput phenotyping and genome-wide association studies is novel approach, draw a whole picture of the genetic architecture of NUE in rice. The objective of this study to identify donors for NUE in rice using high-throughput phenomics approach and to map QTLs/ genes governing NUE in rice genotypes.

METHODOLOGY

To select the best performingrice genotypes with high nitrogen use efficiencyideotype to accelerate the cultivar release, rice experiment with 300 diverse genotypes under pot condition. Two factor experiment with recommended nitrogen level (120kg/ha ~ 1.245g/ pot) and without nitrogen supply was conducted at Nanaji Deshmukh Plant Phenomics Centre, ICAR – Indian Agricultural Research Institute in *kharif* season 2019.Plant of rice genotypes grown in plastic pots filled with 15 kg soil.Rice genotypes was sown under field condition on 8th July, 2019. Twenty-three day after sowing, observe frequently until seedlings have 3-4 true leaves, it transplanted in pots, with 1 seedling per 1 pot. Before transplanting, basal application of 120N:60P:80K where applied with three split doses of nitrogen in control treatment. Five weeks after transplanting, two uniformed pots per treatment were load and laid out randomized block design (RBD) in automated plant transport and imaging systems

(LemnaTec Scanalyzer 3D). The growth conditions in the greenhouse were set to 32°C during day time and 28°C at night with day light period lasted about 14 hours starting from 7 am.

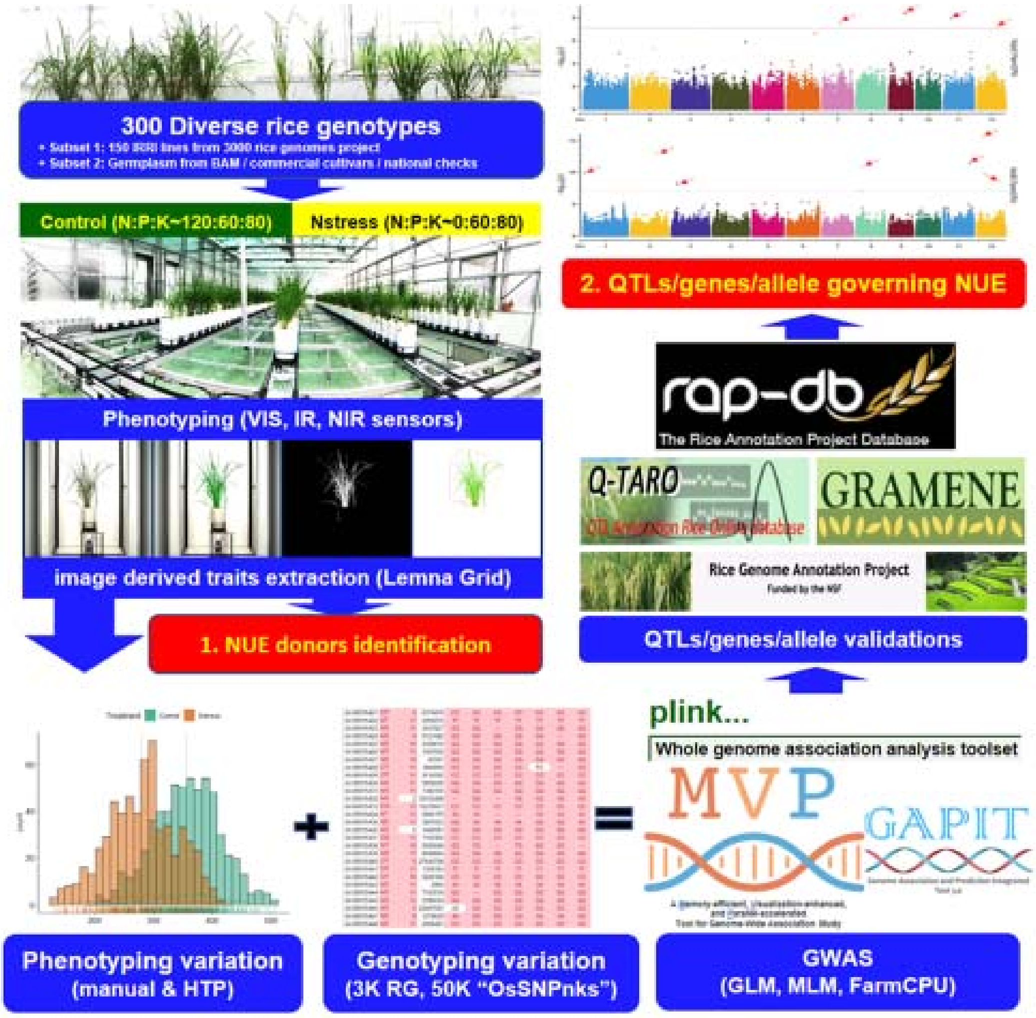
At 68 days after sowing (DAS), 75DAS and 83DAS, rice plants were captured using visible range of the light spectrum (VIS), infrared (IR) and near-infrared (NIR) sensors. The image of the rice was acquiredusing a 3D-scanalyzer (LemnaTec, Germany) and analyzed using LemnaGrid program. Manual measurement traits were collected such as booting time, heading time, maturity time, grain yield, biomass at harvesting stage. Nitrogen content analysis in shoot and dehulled grain at maturity followed Dumas combustion method using Euro EA3000 Elemental Analyzer (Euro Vector, Italy).Selection of rice donors with contract nitrogen use efficiency using multi-trait genotype-ideotype distance index (MGIDI). All statistical tests and graphs were performed using R v.4.0.2.The 150 first rice accessions from this study were delivered from the 3K rice genome project ((3K RGP, 2014; Wang et al., 2018). The second subset included 147 genotypes was derived 50 K rice genic SNP chip 'OsSNPnks'. PLINK program version 1.9was used to obtain a subset of 3,576,323 SNPs in the first subset and 27,835 SNPs in the second subset with a minor allele frequency (MAF) > 5% and a missing data ratio < 0.1 for association analyses. GWAS was performed withGeneral Linear Model (GLM), Mixed Linear Model (MLM) and Fixed and random model Circulating Probability Unification Model (FarmCPU) using R package rMVP and GAPITversion3. The Gramene QTL database and QTL annotation rice online database (QTARO) were searched to identify the physical locations of the previously reported QTLs. The candidate genes were determined using the genome browser of the Rice Annotation Project Database.

RESULTS

Nitrogen shaped the rice plant architecture into three trait groups include architectural, physiological and biomass-related traits, which are successfully captured and quantified using VIS, IR and NIR sensors. Big phenome image data with 72,000 images and 2.88TB data on NUE of rice were generated.At 68DAS, 75DAS and 83DAS, principal component analysis of 104 i-traits showed thatnitrogen have dramatic effects on plant growth and development. Control plants were clearly distinguished from low nitrogen stress plants, but plants of the same genotype or among agronomic groups tended to be grouped together. First principle component gradually decreases from 48.61% at 68DAS to 31.35% at 83DAS suggesting that more phenotypic variance can be observed between control and low nitrogen stress plant at earlier stage. Selection indexMGIDI with10% selection intensity, 30 superior rice genotypes with high grain yield under low nitrogen level were selected. Rice donors with high NUE have grain yield under stress more than 12 grams, contain at least 8 tillers with 100% productive tiller percentage per pot and harvest index no less than 0.4. Major NUE related traits were strongly effected under nitrogen stress condition such as plant height, tiller number, dry weight and grain yield. Various QTLs/genes control NUE related traits also recognized, presented in whole 12 chromosomes. Highest log value was detected in tiller traits and tiller-related derived from i-traits, productive tiller percentage (PTP)traits under both control and nitrogen stress condition using GLM, MLM and FarmCPU model.Major QTL governing nitrogen uptake efficiency (NUpE)were found such as qNUpE2.1 and qNUpE12.1 and nitrogen utilization efficiency (NUtE) such as qNUtE2.1, qNUtE9.1by both FarmCPU and MLM model.

CONCLUSION

Phenomics and high-throughput phenotyping is efficient techniques that can rapidly increase throughput enabling the screening of large numbers of rice genotypes for NUE breeding in rice. It is new



technologies for improvement of rice NUE were developed for screening diverse rice genotype rice NUE. Big phenome image data generated from this study can be used for furtherstrengthen the rice improvement. The donors identified from this study can be used for further field evaluation and utilization in NUE rice breeding program. QTL/genes governing NUE in rice are widely distributed through whole genome highlighted the complicated of the inheritance of NUE and its components. Gene/QTLs identified from this study would be beneficial for breeding for high nitrogen use efficiencyin rice.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/OP-4

MOLECULAR MAPPING OF NOVEL LOW SOIL PHOSPHORUS TOLERANCE LOCI AND MARKER-ASSISTED INTROGRESSION OF *PUP1* INTO ELITE RICE VARIETIES

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Adequate availability of phosphorus (P) is a major production constraint in rice in India and as far as the soils are considered as they are low (49.3% of soils) to medium (48.8% of soils) in terms of actual or available P content. Considering limited P reserves in the world coupled with increasing cost of P fertilizers, it is imperative to develop alternative solutions for this problem, like better crop residue management, adoption of integrated nutrient management and development of low soil P tolerant rice varieties. Tolerance to low soil P is polygenic in rice and so far only one major QTL, *Pup1* has been identified and characterized to be associated with low soil P tolerance and utilized in breeding programs across the world (Chin et a. 2011). Keeping these points in view, this study focused on identification of novel, non-*Pup1* type sources of tolerance, molecular mapping of the genetic loci associated with tolerance and deploy them along with *Pup1* in elite rice varieties.

METHODOLOGY:

A total of 96 north-eastern rice germplasm (Mahadevaswamy et al 2019) along with 56 landraces /rice varieties (Kale et al 2020) were screened in the low soil P plot (Available P <2kg ha^{-1}) at ICAR- IIRR, Hyderabad, India for 14 tolerance associated traits along with the tolerant checks- Swarna, Kasalath and susceptible (i.e. sensitive) checks Improved Samba Mahsuri (ISM) and MTU1010 in augmented RBD in order to identify tolerance rice lines. They were then screened with a set of PCR based markers, specific for *Pup1* to identify novel sources of tolerance. Two RIL populations were developed from two such novel, non-*Pup1* donor lines, Rasi and Wuzuhophek by crossing them with ISM. The RILs were screened in the low soil P plot of ICAR-IIRR and molecular mapping was undertaken with the help of SSR markers. In order to transfer *Pup1* into elite rice varieties, Swarna rice variety (possessing *Pup1*) was crossed with Improved Samba Mahsuri and MTU1010 (which are sensitive to low soil P levels) and marker-assisted backcross breeding approach was adopted to develop NILs (Anila et al.2018). The developed NILs were subjected for testing in the low soil P plot of ICAR-IIRR and also in low phosphorus tolerance trials of AICRIP.

RESULTS:

Screening of 152 rice lines in the experimental low soil P plot revealed that three rice lines/varieties, viz., Rasi, Wuzuhophek and IC21683 possess excellent tolerance to low soil P. These lines showed highest value for stress tolerance index (STI), yield stability index (YSI) and yield index (YI), and the lowest value for tolerance index (TOL), stress susceptibility index (SSI) and percent yield reduction (PYR). Further, the germplasm lines were screened for the presence of *Pup1* QTL using the reported markers- K46-1, K46-2, K46-K1, K452 and K46 cg1 (Chin et al. 2011) and the analysis revealed the complete absence of *Pup1* genomic region in the rice lines, Rasi, Wuzuhophek and IC21683, indicating novel genetic control other than *Pup1* in these three rice lines with respect to low soil P tolerance.

The RIL mapping populations developed from Rasi and Wuzuhophek were analyzed for 14 tolerance associated traits. In the Wuzuhophek derived population, 16 QTLs were identified (6 Major and 10 Minor) with a QTL hotspot identified on the short arm of Chr. 8 harboring five major QTLs for the traits, plant height, shoot length, number of productive tillers, panicle length and plant yield. The other QTLs were identified for the traits root volume, dry shoot weight, total biomass and root to shoot ratio and mapped on Chr.7 and. In the mapping population derived from Rasi, a total of 15 major QTLs were identified, including thoses for days to 50 % flowering are present on Chr. 9 & 12, for Plant height on Chr. 4, for panicle length on Chr. 11, for root volume on Chr. 10, 11& 12, for dry shoot weight on Chr. 5, for dry root weight on Chr. 2, for straw weight on Chr. 2 & 4, plant yield on Chr. 2 & 8 and for test seed weight on Chr. 1 & 7.

With an objective to improve low soil P tolerance of the elite rice varieties- ISM and MTU1010 by targeted introgression of the major QTL, *Pup1*,crosses were made with the two rice varieties with the variety, Swarna (possessing *Pup1*) serving as donor. Backcrossing was restricted to BC_2 generation since there was maximum recurrent parent genome recovery of 85- 89 % among the BC_2F_1 plants. By BC_2F_6 generation, promising, tolerant NILs of ISM and MTU1010 possessing *Pup1*were identified (which were > 95% similar to the recurrent parents) and validated in low soil P plot of ICAR-IIRR. Two best lines each from ISM and MTU1010 are in final year of testing in AICRIP trials.

CONCLUSION:

Varietal improvement and identification of novel sources for low P tolerance helps in reducing the application of P fertilizers, import burdens, and environmental contaminations due to fertilizer run-offs and for getting sustainable yields, thus enhancing the income of farmers. Three novel, non-*Pup1* type donors, viz., Rasi, Wuzuhophek and IC21683 have been identified through the present study. Major and minor QTLs associated with novel low soil P tolerance have been identified from Rasi and Wazuhophek through molecular mapping. Breeding lines of the elite rice varieties, ISM and MTU1010 possessing *Pup1* and showing excellent tolerance to low soil P levels have been developed through MABB approach. The present study highlights the effective use of molecular markers in rapid identification of novel sources of low soil P tolerance and also in improving low soil P tolerance of Indian elite rice varieties through MABB approach.

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IRC/TM-1/OP-5

GENE STACKING FOR SUBMERGENCE TOLERANCE, BACTERIAL BLIGHT RESISTANCE AND YIELD POTENTIAL IN RICE VARIETY SWARNA THROUGH CLASSICAL AND MOLECULAR BREEDING APPROACH

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The rice variety ‘Swarna’ is an extremely popular variety in the eastern region of the country. The farmers of eastern India are mostly cultivating rainfed rice and face the occurrences of ill effects of climate change which are very frequent. Thus, rice production in the region is not stable. This variety is also highly susceptible to different biotic and abiotic stresses like bacterial blight (BB) disease caused by Xanthomonas oryzaepv. oryzae (Xoo) and flash flood which causes a heavy yield loss. Therefore, a superior variety need to be developed with biotic and abiotic stress tolerance and enhanced yield from the previous version.

OBJECTIVE

In this study our objective is to develop a variety with submergence tolerance, bacterial leaf blight resistance and higher yield in the background of mega variety ‘Swarna’.

MATERIAL AND METHODS

Leaves were collected from 15 days old seedlings to extract genomic DNA for molecular screening. Total genomic DNA extraction and PCR were done as per the standard protocol. Genomic DNA was isolated from fresh leaves by CTAB method. The amplification of DNA was performed .Five gene-specific markers namely Gn1a, GW2, gw5, OsSPl14, and SCM2 were used to screen for the presence of yield component QTLs. In 2.5-3% gel PCR amplification products were loaded which is containing 0.8 mg/ml EtBr for the process of electrophoresis in 1X TBE (pH 8.0) for 4 hours. Data scored were analyzed for each genotype-primer combination based on the presence or absence of amplified products.

RESULTS

The molecular marker integrated backcross breeding program has been employed to transfer proposed seven genes/QTLs into Swarna variety. During the backcross generation, direct markers were used for Sub1A, Gw2, OsSPL14, SCM2 and markers closely linked to the genes for xa5, xa13, and Xa21 genes. Three donor parents viz, Swarna Sub1, Swarna MAS (CR Dhan 800) and Swarna-Habataki were first screened for parental polymorphism and validated for presence and absence of the targeted genes. First Swarna Sub1 was crossed with Swarna MAS produced F1. Those seeds were grown, and the next cross was done with our third parent Swarna- Habataki. After completion of the 3-way cross with multiple parents, Swarna-Sub1, Swarna MAS and Swarna-Habataki, the first back cross was done with Swarna, the recipient parent and 796 BC1F1 seeds were produced. The amplification of the genomic DNA was performed using gene-based direct markers for strong culm, wealthy farmers’ panicle, grain width, submergence tolerance and markers closely linked to the BB resistance. We have found 6 plants out of a total 796 progenies which contains all the six genes/ QTLs and total of 446 numbers of seeds were produced for further evaluation and backcrossing. The amplification of the genomic DNA of 446 progenies of BC2F1was performed and 161, 169 and 173 positive plants were detected for GW2, SCM2, OsSPL14 and

159 plants were observed to be positive plants for the Sub1A. In this experiment, 157, 168 and 27 progenies were observed to be positive for xa5, xa13, and Xa21, respectively. Four plants were found to be having 7 gene combinations. Those four BC2F1 plants containing seven gene were selfed and after selfing, a total number of 15570 seeds from the derivative were produced and screened for seven desirable genes / QTLs and we got one plant with all 7 desirable gene. The Screening of BC2F3 progenies for BB disease resistance and Submergence tolerance was performed. The bioassay was conducted for the resistance reaction of the pyramided lines and parental lines against the eight Xoo isolates .The donor parent showed a smaller range of average lesion lengths (0.4 cm to 0.5 cm) while the 'Swarna' had very high lesion length (10.3 cm to 12 cm). A total of 80 genotypes comprising 78 BC2F3 seven gene plants and 4 parents were evaluated in the submergence screening tank under controlled condition. Total submergence stress of 14 days was applied to the pyramided and parental lines. All the 79 plants which are positive for Sub1 exhibited regeneration ability of 62.5 to 87.5% and they regenerated after a week of de-submergence. However, no regeneration was detected in the recipient parent 'Swarna'. The Sub1 pyramided lines have shown similarity of regeneration ability very much with Swarna-Sub1 which is the donor parent while Swarna could not revive and thus decay completely under the submergence stress. The pyramided lines showed better regeneration ability were SSBY-69-584, SSBY-69-868, SSBY-69-27. The evaluation of yield QTLs was performed for SCM2. Culm strength of the pyramided lines were validated by calculating different parameters for culm breaking force. For the 3rd internode, the pyramided lines showed a range of 13.5 cm to 17.9 cm which is very much similar to our donor Swarna-Habataki and higher then Swarna. Here the bending strength is calculated highest in SSBY-69-1063 that is 39 and Swarna-Habataki also displayed similar bending strength. Thirty days old pyramided lines carrying Sub1 and BB resistance genes and yield QTLs with the parents were transplanted in the main field. Plot size of 6 m2 was allotted for each entry with 40 plants per row and 5 rows per entry at 15 × 20 cm spacing in a randomized complete block design with three replications transplanted at NRRI, Cuttack in wet season, 2019. Evaluation of the pyramided and parental lines indicated that the pyramided line SSBY-69-245 showed highest panicle weight of 6.63g followed by 6.35g in SSBY-69-840. The pyramided line SSBY-69-840 also showed highest yield of 7.52 t/ha. The panicle weight was 2.87g in recipient parent Swarna.

CONCLUSIONS

Evaluation results indicated that the pyramided line SSBY-69-840 yielded highest grain yield of 7.52 t/ha followed by 7.34t/ha and 7.02 from SSBY-69-245 and SSBY-69-1063, respectively. The best pyramided line showed 18 % yield advantage over the recipient parent, Swarna and 6.8 % over yield QTLs ,Submergence tolerance and BB resistance.

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IRC/TM-1/OP-6

IDENTIFICATION OF QTLS ASSOCIATED WITH GRAIN YIELD AND RELATED TRAITS UNDER LOW LIGHT IN RICE (*Oryza sativa L.*)

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Low light is one of the important constraints for grain yield and quality of rice in kharif (wet) season. About 40 to 50% yield loss is experienced due to low light intensity during Kharif (wet season) in India and South East Asian countries. It affects all the stages of rice growth. It has pronounced effect on the entire photo-morphogenesis of rice plant resulting reduction in the number of tillers and panicles at vegetative stage, while it causes reduction in spikelet number, grain weight and grain quality at the reproductive stage. Besides, it affects plant height, shoot and root growth. Low light causes varieties of biochemical and physiological disturbances in plants. There is sufficient evidence that low light intensity caused by overcast skies is the major factor impairing grain yield, which averages around 1.2 t ha-1 during the wet season in India. In the present study, a RIL population derived from tolerant cultivar, Swarnaprapbha and susceptible cultivar, IR8 was used to identify QTLs associated grain yield and related traits under low light tolerance.

OBJECTIVE:

Identification of QTLs associated with grain yield and related traits under low light, Normal light and both conditions in rice.

METHODOLOGY:

Field experiments were conducted in the experimental plots of ICAR-National Rice Research Institute (NRRI), Cuttack, Odisha, India (20.4625° N, 85.8830° E) during the *kharif* 2019. Two genotypes, i.e., Swarnaprabha (Tolerant), IR8 (Susceptible) along with their 188 RILs (F_7) were grown in Alpha lattice design with two replications. Low light stress was imposed after 15 days of transplantation up to maturity (active tillering stage to maturity) by using agro shade nets matted on wooden frame (50% and 25% interception of photosynthetically active photon flux density), while no agro shade net was used for normal light condition. The spacing of plants were kept line to line 20cm and plant to plant 15cm. Readings were taken after 45 days of shade treatment from the flag leaves during 50% flowering stage. Data for all the 10 agro-morphological traits (DFF, PH,TN, PN,GN, SN,SFP%,TGW,PW and GY) were taken for phenotypical study. Genotyping has been done by using both SSR and SNP markers. Development of linkage map and QTL analysis has been done by using software ICIMapping- 4.2 under both Low light and normal light conditions.

RESULT:

188 RILs were phenotyped for 10 grain yield and related traits during kharif season and genotyped with polymorphic SSR (77) and SNP (46) markers. Phenotypic traits showed wide variations. Linkage analysis led to the identification of 17, 14 and 4 QTLs associated with grain yield and related traits under low light , normal light and both conditions, respectively. Phenotypic variance explained by any QTL varied from 4.33 to 14.19% (Table 1).

CONCLUSION:

The stable QTLs for grain yield and related traits identified in either seasons would be useful in marker-assisted selection breeding for improving grain

Table 1 : QTLs Identified in RILs of the Cross Swarnaprabha (T)and IR8(S) for Kharif 2019.

						Low Light				Normal Light			
Sl No	Trait	QTL	Chrom#	LeftMarker	RightMarker	Position	LOD	PVE(%)	Add	Position	LOD	PVE(%)	Add
1	PH	*qPH1.1*	1	RM10207	Affx93254811					29	2.40	7.74	6.3052
2	PH	*qPH1.2*	1	RM11738	RM11935	116	3.24	4.53	8.97				
3	PH	*qPH9.1*	9	Affx93244150	NKSSR9-44	120	2.23	2.96	5.36	123	2.67	8.29	6.16
4	PH	*qPH11.1*	11	RM26086	Affx93233829	102	10.12	12.17	22.36				
5	TN	*qTN2.1*	2	RM13861	NKSSR2-54	86	2.00	7.04	0.47				
6	PN	*qPN1.1*	1	Affx93254811	Affx93259142	37	2.30	7.62	0.47				
7	PN	*qPN1.8*	8	NKSSR 8-17	RM556					40	2.04	7.92	-0.39
14	GN	*qGN1.1*	1	RM11738	RM11935	117	2.75	8.04	9.80				
15	GN	*qGN4.1*	4	Affx93242145	Affx93215884	0	2.03	4.34	5.93	1	3.17	5.16	7.69
16	GN	*qGN8.1*	8	RM225565	RM22506					310	3.13	5.48	8.15
17	GN	*qGN8.2*	8	RM22542	RM22674	351	2.04	5.20	7.01				
18	GN	*qGN11.1*	11	Affx93233829	NKSSR 11-3	126	2.67	12.03	-21.18	128	3.11	12.77	-21.27
8	SN	*qSN1.1*	1	RM11738	RM11935	122	2.38	7.00	8.06				
9	SN	*qSN3.1*	3	RM15981	RM15630	291	2.00	8.52	-9.21				
10	SN	*qSN11.1*	11	Affx93233829	NKSSR 11-3					130	2.16	4.69	-21.84
11	SFP	*qSFP1.1*	1	RM12157	RM12182	372	2.55	8.70	4.68				
12	SFP	*qSFP1.2*	1	NKSSR 1-67	RM11738					92	2.51	8.33	3.96
13	SFP	*qSFP8.1*	8	RM6208	RM225565	308	2.61	7.33	4.21				
19	TGW	*qTGW7.1*	7	RM18	Affx93258412					42	3.87	14.19	1.26
20	TGW	*qTGW8.1*	8	NKSSR 8-10	RM6208					293	2.72	4.33	-0.56
21	PW	*qPW4.1*	4	Affx93242145	Affx93260627	0	3.37	5.50	0.20	2	3.017	8.29	0.25
22	PW	*qPW8.1*	8	Affx93230286	Affx93252641					251	2.80	8.82	0.26
23	PW	*qPW8.2*	8	RM6208	RM225565	308	2.36	4.38	0.17				
24	PW	*qPW11.1*	11	Affx93233829	NKSSR 11-3	127	2.45	12.04	-0.54				
25	GY	*qGY1.1*	1	RM11738	RM11935					111	3.53	11.45	1.86
26	GY	*qGY5.1*	5	Affx93248203	Affx93230537					0	3.13	6.35	-1.24
27	GY	*qGY8.1*	8	RM6208	RM225565	308	3.94	11.4036	1.44				

yield under low light prevailing, especially in easter India in susceptible high yield rice cultivars. Further, work is continuing to identify QTL under lowlight in rabi season using same RIL population.

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IRC/TM-1/PP-1

MAS OF SOME RICE GENOTYPES FOR BACTERIAL LEAF BLIGHT (BLB) RESISTANCE

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Bacterial Leaf Blight (BLB) caused by *Xanthomonas oryzae pv. Oryzae,* is an important biotic stress, severely affecting the annual rice production all over the world. The systemic infection of this pathogen results in the wilting and desiccation of leaves causing crop loss. Leaf sheaths and culms are more susceptible to this infection. The pathogen lives on the dead plants and spreads through water. This disease infects the leaf veins as well as the xylem, causing blockage and plant wilting.

BLB can be controlled by the development of Host Plant Resistance (HPR), because it is the most economic and eco-friendly strategy for management of biotic stresses. For developing host plant resistance to BLB, resistance genes must be incorporated into high yielding susceptible varieties. One of the most important resistance genes is *xa13*. Being a recessive gene, *xa13* is very difficult to assess but, can be diagnosed easily using closely linked molecular markers. Major objective of the present study was marker assisted selection of (MAS) of some traditional rice genotypes for *xa13* gene using its linked STS marker RG-136.

METHODOLOGY

Field screening was conducted for forty two traditional rice genotypes obtained from the germplasm collection at the Division of Plant Breeding and Genetics, RARS, Pattambi. Artificial inoculation of BLB culture was conducted for the seedlings of all genotypes on the 30th day of sowing. Symptomless genotypes were selected for molecular characterisation using RG 136, specific for *xa13* gene. Sixteen symptomless and two susceptible check genotypes were used for molecular characterisation. The amplification pattern was viewed by electrophoresis followed by UV trans-illumination.

RESULTS

Artificial screening of forty two taditional rice genotypes reslted in the identification of sixteen symptomless genotypes. Subsequently, these were subjected to molecular characterisation with STS marker RG 136 linked to the recessive gene *xa13*, for BLB resistance. During PCR amplification, specific bands were produced only in ten rice genotypes indicating that these traditional genotypes were having the gene *xa13*. Hence it can be concluded that the resistance in these ten genotypes *viz*., Ponkuruka (TRV 2029**)**, Kalluruli (TRV 2054), Karutha cheera (TRV 2059), Kathikannan (TRV 2062), Pokkalai-II (TRV 2063), O-10 (TRV 2076), Pokkali (TRV 2125), Karutha karuka (TRV 2127), Kachu vithu (TRV 2148), and Punjapurathu (TRV 2154), may due to the presence of *xa13* gene.

Also, the remaining six symptomless rice genotypes identified during the artificial screening in field *viz*., Nithya kalyani (TRV 2001), Kuruva (TRV 2064), Mannuveliyan (TRV 2066), Karutha cheera (TRV 2068), Gendakasala (TRV 2070), and Mangalapuram (TRV 2071) did not show any amplification for RG-136 marker. This indicates the absence of *xa13* gene in these six genotypes. Hence the resistance exhibited by them may be due to the presence of the some other resistance genes. As expected, there was no amplification for the marker in two susceptible check genotypes (TRV 2008-Pandi vella and TRV 2141-Kuruva). Similar marker assisted screening of BLB resistance gene *xa13* was conducted by Phuc *et al*. (2005) using the STS marker RG 136 itself in hundred rice varieties and they found that sixty varieties had the *xa13* gene and also found that it is present in homozygous state.

CONCLUSION

In the present study, a complete recessive BLB resistant gene *xa13* could be successfully diagnosed in ten traditional rice genotypes through marker assisted selection with STS marker RG136, closely linked to this specific gene. Hence, these genotypes can be utilised as donors for marker assisted breeding to develop BLB resistant high yielding rice varieties.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-2

GREEN SUPER RICE – A RECENT DEVELOPMENT

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Rice is the leading food crops globally, and it plays a key role in food security. The conflicts are becoming more and more acute between rice production and environmental capital. For this reason, the Green Super Rice concept was proposed by scientists in China to promote the production of resource-saving and environmentally-friendly rice, which can increase yields and improve quality. Green super rice has been described as one of the world's key agricultural science and crop improvement goals, for the use of important genes associated with superior agronomic characteristics, such as high yield, nutrient use efficiency and biotic and abiotic stress resistance.

***Keywords**: GSR, Rice, Productivity, Food security*

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important food crops and is the principal staple food for almost half of the world's population. The world population is expected to continue growing and hit 9 billion by 2050, which calls for an increase of almost 70 percent in food production (FAO 2013). Therefore, to ensure global food security and living standards, increased rice yields are crucial. In order to boost rice yields, farmers have gradually increased the amounts of fertilizers (Ali et al. 2018). Overuse of nitrogen fertilizers and poor efficiency of fertilizer use, have caused significant residual quantities of nitrogen fertilizer to enter the soil and water bodies around farmlands, resulting in serious contamination of the ecosystem (Ali et al. 2018). Another factor that hinders agricultural production is also the regular occurrence of drought, posing major threats to global food security (Luo 2010). Therefore, the breeding and cultivation of new varieties of rice using China's proposed green super rice technology, with superior resistance to biotic and abiotic stresses, including water and nutrient quality, has become a key objective of improving rice to stabilize the productivity of rice and ensure food security.

The Green Super Rice project

In 2005, a green super rice project was proposed by Chinese scientists to cultivate new rice varieties with different characteristics, including high fertilizer performance, water conservation, drought tolerance, and improved resistance to stress due to increasing resource scarcity, atmospheric pollution, and deterioration of ecological systems. The international cooperation project 'Green Super Rice for Resource-Poor Farmers of Africa and Asia' was sponsored by the Bill and Melinda Gates Foundation in 2009. In 2010, the Ministry of Science and Technology of China granted the project,' Breeding and Development of Green Super Rice,' with extended funding up to 2018 (Zhang et al. 2018).

Major focal points of the Green Super Rice project

i. Production and development of green super rice breeding, through technological systems

ii. Establishment of entire genome selection platforms based on recent developments in worldwide research on rice functional genomics

iii. Production of new germplasm resources by pyramidizing green trait genes (Table 1)

iv. Breeding new green super rice cultivars with different combinations of green features

Table 1. Genes related to green traits in green super rice

Green traits	Gene (Chromosome)	Function
Grain quality and yield	OsAAP6 (1), GL2/GS2/OsGRF4 (2), GNP1 (3), lgy3 (3), GL3.3/TGW3/qTGW3 (3), Chalk5 (5), GW5 (5), GW7/GL7 (7), GLW7/OsSPL13 (7), OsOTUB1 (8)	Change in Expression due to variations in promoter or premature termination or establishment of protein structure
Biotic stress resistance	Bsr-d1 (3), Bph3 (4), BPH6 (4), PigmR (6), IPA1 (8), STV11 (11), Xa10 (11), BPH9 (12)	Amino acid substitution or gene deletion or Change in Expression due to variations in promoter or premature termination
NUE (Nitrogen use efficiency)	DEP1 (9), NRT1.1B (10), GRF4 (2)	Amino acid substitutionor Change in Expression due to variations in promoter or premature termination
Abiotic stress resistance (Cold)	LGS1 (2), COLD1(4), CTB4a (4), bZIP73 (9), HAN1 (11)	Amino acid substitution or gene deletion or Change in Expression due to variations in promoter
Abiotic stress resistance (Heat)	OsTT1 (3)	Substitution of Amino acids

v. Techniques of high-yield production and field management for Green Super Rice

Green genes identified for the breeding of new GSR varieties

At present, 3000 genes have been cloned and dissected in rice affecting a broad variety of phenotypes, with tolerance to biotic stresses and abiotic stresses and high efficacy of nutrient usage, high yield and characteristics of good grain quality (Wing et al . 2018).These can be referred to as green genes. As the templates for green super rice breeding, these green genes were used (Table 1). Several databases and software programmes (Table 2) for rice genomic variations have been developed during the implementation of the Green Super Rice project. For gene functional analysis and rice breeding, such databases provide critical platforms for whole-genome selection (Yu et al., 2020).

Table 2. Databases available for green super rice breeding

Database or software programme available	Information	Web link or references
RFGB (Rice functional genomics and breeding database)	Informations regarding the variation in rice genomic	http://www.rmbre eding .cn/
Rice SNPs Database	Rice breeding by selecting genomic regions	http://varia tion.ic4r.org/
Marker-assisted molecular breeding platform for GSR	Comparing rice breeding materials	http://47.92.174.110
RiceVarMap v2.0	Integratingand annotation of the data sets available for rice	http://ricev armap .ncpgr .cn/ v2/
GS software gblup.jar	genomic variations and genome-wide associationanalysis Identification of additive effect and dominance effects	Covarrubias-Pazaran et al., 2018

CONCLUSION

In 2050, the world population is projected to reach nine billion. Rapid population growth requires a corresponding increase in the production of rice in a sustainable way, which in future decades will be a major challenge for global rice breeders. Green super rice varieties can maintain stable and higher yields with less inputs and higher resistance and recoverability features when facing the regular occurrence of severe climate change-induced stresses. Over the past decade experience has shown that the combination of green super rice varieties and corresponding improved growing techniques will lead to more efficient and higher yields, thereby reducing the use of pesticides and fertilizers in irrigated rice production areas by more than 30 percent as well as irrigation water by at least 30 percent (Yu et al . , 2020). In order to guide the green development of agriculture, green super rice can become a crucial factor and its objectives related to entire genome breeding strategies can provide trends or set examples for other crops to explore with suitable traits.

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IRC/TM-1/PP-3

MARKER ASSISTED INTROGRESSION OF YIELD ENHANCING GENES INTO RESTORER LINE OF RICE (*ORYZA SATIVA* L.)

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Rice (*Oryza sativa* L.) is one of the major staple food crops and is a primary source of food for more than half of the global population. To feed the increasing population, development of climate smart rice varieties/hybrids with a higher yield potential are highly required. Hybrid rice provides yield advantage of 15-25% over current commercial cultivars which requires developing number of diverse parental lines with good restoring ability and specific desirable traits. Therefore, improving parental lines becomes an integral part of hybrid rice breeding programmes.Through quantitative trait loci (QTL) analysis with fine mapping or positional cloning using rice mutants, about 20 genes involved in yield related traits were isolated in rice which are being used for rice breeding programs. Recently, several genes including *Gn1a* and *OsSPL14* which contribute for genetic improvement of yield potential in rice were identified.

METHODOLOGY

The study was carried out at ICAR-Research farm, Indian Institute of Rice Research (IIRR), Hyderabad during wet season (*Kharif*), 2019. In *Kharif*, 2018 hybridization was carried out between an aerobic restorer line AR 9-18 and yield enhancing donor YPK 198 for generating F_1s. True F1 plants were selfed to generate F2 population.These 205 segregating F_2 population derived from the cross between AR 9-18 and YPK 198 possessing *Gn1a* and *OsSPL14* were used for the study. Experiment was conducted in non-replicated trial with thirty days old seedlings of F_2 population along with parents and restorer check KMR-3R. Recommended cultural practices and plant protection measures were taken up for raising a healthy crop.

The leaf samples of 205 segregating F_2 population, parental lines and checks were collected from 20-25 days old seedlings and stored at -20^{o}C to extract genomic DNA for molecular screening of yield enhancing genes in the population. Extraction of total genomic DNA was carried out by using the Cetyl trimethyl ammonium bromide (CTAB) buffer and by chloroform:isoamyl alcohol extraction followed by ethanol precipitation. Agarose gel electrophoresis and nano drop UV spectrophotometer was used to estimate DNA concentration and each sample was then diluted to approximately 40-50 ng/ìl and stored at 4^{o}C for further use. All genotyping markers followed the PCR conditions and PCR products amplified were electrophoresed in 2.5 % agarose gel.

RESULTS

Parental polymorphism and F_2 population screening

In the present study for screening of two yield enhancing genes in F_2 population, parental polymorphism survey was taken up between aerobic restorer AR 9-18 and yield enhancing donor YPK 198.

A total of ten (*Gn1a* - 4 markers) and (*OsSPL14* - 6 markers) gene specific markers were used to study parental polymorphism. Among four gene specific markers, one marker Gn1a-indel3 for *Gnla* and among six gene specific markers, one marker *viz.*, Os08g39950 for *OsSPL14* showed polymorphism between parents AR 9-18 and YPK 198. These polymorphic markers were used for screening of 205 segregating F_2 population for the presence of yield enhancing *Gnla* and *OsSPL14* genes.

Screening of yield enhancing *Gn1a* in F_2 population

Two hundred and five segregating population in F_2 generation were screened for the presence of yield enhancing gene *Gn1a* located on the chromosome 1 with gene specific marker Gn1a-indel3. Out of 205 F_2 population, 48 plants were positive which showed band size similar to yield enhancing donor parent YPK 198, 43 plants were negative which showed band size similar to aerobic restorer AR 9-18 and 114 plants showed the heterozygous band by amplifying both the fragments (Figure1).

Screening of yield enhancing gene *OsSPL14* in F_2 population

The same segregating F_2 population was screened for yield enhancing gene *OsSPL14* located on chromosome 8 with gene specific Os08g39950 marker. Out of two hundred and five F_2 population, 38 plants having yield enhancing gene at homozygous status were taken as positive, which showed band size similar to donor parent YPK 198, 57 plants were negative which showed band size similar to AR 9-18 and 110 plants were heterozygous by amplifying both the fragments (Figure 2). The screening results revealed that out of two hundred and five F_2 population screened, 48 plants had *Gn1a*, 38 plants had *OsSPL14* and 21 plants had both *Gn1a* and *OsSPL14* genes. The plants with homozygous positives for yield enhancing genes showed improved grain number per panicle. Similar results were reported by Huang *et al.* (2018). This demonstrates that marker assisted screening in F_2 segregating populations reduces the time for accelerating parental development with high grain number. With advent of marker assisted breeding, the study resulted in development of improved aerobic restorer lines with yield enhancing genes, which ultimately will be utilized in developing high yielding aerobic hybrids for unfavourable ecologies.

The screening results in F_2 population were subjected to chi-square (÷2) analysis to test their goodness of fit to test for appropriate mendelian ratio 1:2:1. Genetic segregation pattern of yield enhancing genes *Gn1a* and *OsSPL14* in the F_2 population was done using chi-square (÷2) test. The expected number was set based on the normal mendelian segregation

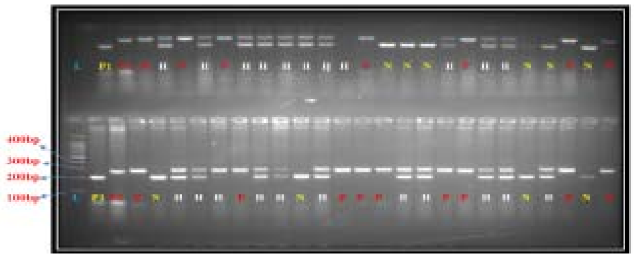

Figure 1: Segregation pattern of F_2 population for the marker Gn1a-indel 3 for yield enhancing gene *Gn1a*.
L=100bp ladder, P1=Aerobic restorer parent (AR 9-18), P2= Yield enhancing donor parent (YPK 198), P= Positive, N=Negative, H=Heterozygous.

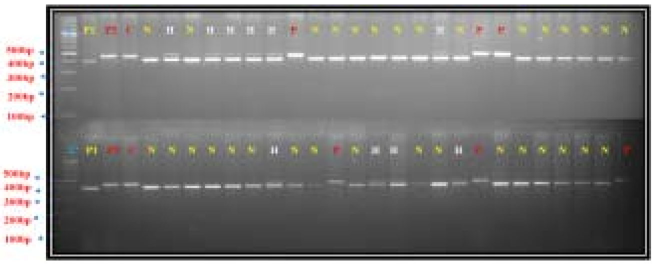

Figure 2: Segregation pattern of F_2 population for the marker DRRM RF3-10 for *Rf3* fertility restorer gene.
L=100bp ladder, P1=Aerobic restorer parent (AR 9-18), P2= Yield enhancing donor parent (YPK 198), C=Check variety (KMR-3R), P= Positive, N=Negative, H=Heterozygous.

pattern of the single gene (homozygous for positive: heterozygous: homozygous for negative = 1:2:1 ratio).

CONCLUSION

Chi square analysis revealed that the table value of ÷2 at 0.05 level of probability at 2 degrees of freedom is 5.99. The calculated ÷2 value was lower than the chi-square table value 5.99 at 2 df. Thus, the difference is non-significant between the observed and expected values for both the yield enhancing genes, indicating that they showed a normal mendelian segregation pattern. Kim *et al.* (2018) reported similar findings for genetic segregation pattern of both yield enhancing gene in BC_3F_2 progenies using the chi-square (÷2) test. The plants with both the yield enhancing genes showed improved grain number per panicle. The heterozygous and homozygous positive plants for yield enhancing genes were further forwarded to the next generation for evaluation.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-4

ELECTRON BEAM AND GAMMA RAYS INDUCED ANNA (R) 4 RICE MUTANTS WITH IMPROVED GRAIN QUALITY

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The directed seeded rice cultivation under rainfed situation needs short duration and drought tolerant rice varieties to mitigate moisture stress and to avoid yield loss. Rice variety Anna (R) 4 has the ability to tolerate moisture stress and is specially released for rainfed tracts of Tamilnadu. Though the plant type of Anna (R) 4 cultivar is suitable for rainfed cultivation, its long slender grain type has not been preferred by the farmers of Tamil Nadu because of low market price. Hence, to meet market demand, altering grain type of Anna (R) 4 will lead to increased adaptation by farmers with good remunerative price. The hybridization and selection in rice is one of the options to alter grain type. This process will generate the variations derived from both parent for all traits and the selection of desirable plant type become complex process. The mutation of Anna (R) 4 cultivar and selecting the desirable grain type from mutants of Anna (R) 4 is a viable option to alter the grain type. Hence, the new mutant source of electron beam and gamma rays were used to induce mutation and generate variability.

METHODOLOGY:

The seeds of Anna (R) 4 rice variety were subjected to electron beam and gamma rays irradiation at different doses from 100 Gy to 400 Gy of 50 Gy intervals. Gamma rays (^{60}Co) treatment of seeds was undertaken at Bhabha Atomic Research Centre, Mumbai and electron beam at 10 MeV at electron beam Accelerator facility of Electron Beam Centre, BARC. The LD_{50} values were estimated from germination percentage of different levels of radiation by Probit analysis. Based on LD_{50}, 200 Gy, 250 Gy, 300 Gy and 350 Gy mutant seeds were raised for M_1 generation during 2017-18 at Agricultural College and Research Institute, Madurai. The M_2 generation was raised from M_1 seeds of 200 individual plants from each dose. A total of 5400 plants and 12240 plants were raised and observed for M_2 generation during *kharif* 2018. The viable mutants were identified and early maturing mutants were tagged and observations on quantitative traits were recorded.

RESULTS:

The viable mutants were generated in Anna (R) 4 rice M_2 population by irradiation in plant habit namely tall, dwarf, grassy and extreme dwarf through macro mutation. Mutants in tillering, leaf shape, flower organisation, awned grains etc. were identified in M_2 population. Based on viable mutants the effectiveness was 0.086 and 0.05, efficiency was 0.54 and 0.723 in electron beam and gamma rays respectively. The micro mutations in quantitative traits generated range of variability through irradiation. The expression of plant height was varied from 67 to 127 cm (electron beam) and 70 to 120 cm (gamma rays) and in number of productive tillers by electron beam was 3 to 29 and gamma rays was 2 to 28 with negative shift in mean performance. The mutants from both radiation caused positive shift in mean from Anna (R) 4 for panicle length and panicle weight. The bidirectional shift in mean performance was observed in number of filled grains per panicle and grain yield per plant in all the doses from 200 to 350 Gy in both radiations.

The frequency of reduced grain length mutants produced from long slender (6.9 mm) Anna (R) 4 rice was 0.0146 by electron beam and 0.0019 by gamma rays. The range of medium slender grain type mutants was recorded in electron beam was from 5.71 to 6.53 mm and gamma rays was from 6.04 to 6.53 mm. Among grain mutants the grain yield per plant was ranged from 6.2 to 45.1 g and 11 to 52 g in electron beam and gamma rays respectively.

CONCLUSION:

The viable **macro** mutants induced by irradiation in M_2 population from Anna (R) 4 rice indicates the electron beam found to be more effective and less efficient than gamma rays. Both ã-rays and electron beams have low LETs of around 0.2KeV/ µm (Magori *et al.*, 2010). However, electron beam irradiation proved to be stronger mutagenic effect as short pulses whereas gamma irradiation at same dose as continuous effect. Hence the electron beam caused more injury in seedling and growth characters and pollen sterility at lesser dose than gamma rays.

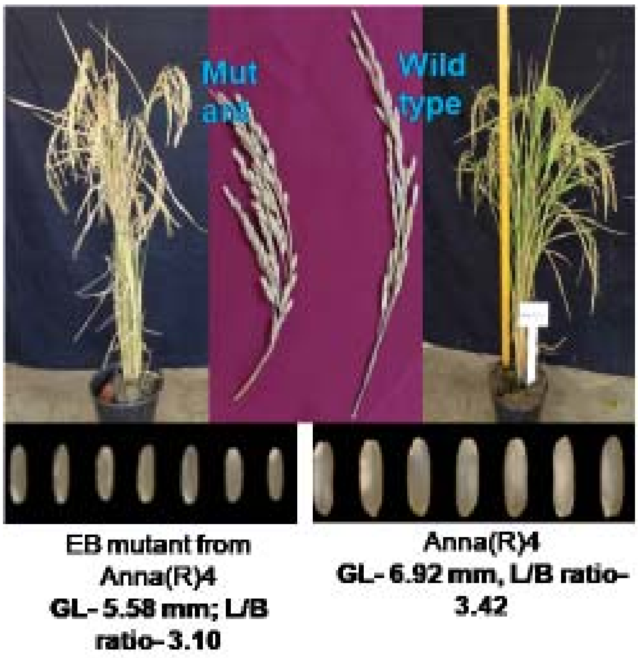

Figure 1. Early maturing medium slender grain type mutant from electron beam mutants from Anna (R) 4 rice in M_2 generation

The irradiations caused wide range of variations for all quantitative traits studied by inducing micro mutations. The radiation caused reduction in mean plant height and number of productive tillers in M_2 population from Anna (R) 4 across doses, whereas increase in mean performance was noticed in panicle length and panicle weight. The electron beam found to efficient in reducing grain length than gamma rays in long slender grain type Anna (R) 4 rice (Fig. 1). More numbers of reduced grain length mutants with medium slender grain type were isolated from electron beam (79) than gamma rays (24) mutants in M_2 generation. Among doses, the 300 Gy of electron beam found more efficient in isolating medium slender grain mutants (63 no.). Huang *et al.* (2013) reported that the QTLs affecting grain length are fine mapped namely qGL-3a, qGL4b, qGL7, GS7, qSS7, qGRL1 and LGS1 are located across chromosome number 3, 4, 7, 1 and 2. This supported that the grain length character are governed by oligogenes and can be altered by mutation. Further the grain mutants in both irradiations produced more variations for single plant yield. This offers more scope for selecting medium slender grain type mutants with improved yield performance. These mutants help to develop drought tolerant rice variety with improved grain quality of Anna (R) 4 rice, to benefit direct seeded rice growing farmers.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-5

STABLE HIGH YIELDING MUTANT RICE VARIETY -TUNGABHADRA SONA (GNV 1801) FOR TUNGABHADRA COMMAND AREA OF KARNATAKA

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Rice (Oryza sativa L.) is a staple food source for nearly 3.5 billion people and has occupied an enviable prime place among the food crops cultivated around the world, which contributes significantly to global food security and with China and India as lead producers. Measurement of G x E interaction has always remained an intriguing problem in the past. Now a day, the use of biplot to quantify the genotype environment interaction (GEI) is widespread since the GE effects can be visualized in a single graph, which facilitates the comparison of genotypes and their interaction with the environments. More recently, Yan et al. (2000) proposed a new technique in the GEI analysis using biplots similar to the AMMI technique, which has the advantage of decomposing the joint effect of genotype (G) and GE (G + GE) by principal component analysis, differing from the original AMMI analysis that decomposes only GE and method was called GGE biplot by Yan et al. (2000). The main objective of this study was to evaluate rice genotypes and to apply GGE biplot to identify better performance and stability on grain yield and hence to recommend the best genotype for rice farmers of tungabhadra command area of Karnataka.

METHODOLOGY:

The experimental material for the present study consisted of twenty-two medium slender rice genotypes used from previous study Prashant et al. (2019) including BPT 5204 based mutants along with local checks BPT 5204 and Gangavati sona, These varieties were evaluated in four locations of Karnataka viz., Agriculture Research Station, Gangavati, Agriculture Research Station, Dhadesugur, Agriculture Research Station, Malnoor and Agriculture Research Station, Kawadimatti of Karnataka state during kharif 2019. Evaluation of these rice genotypes along with four checks was carried out using randomized complete block design with three replications at four locations selected under study. Each genotype was planted in 13 rows of 4 m row length with a spacing of 20 cm between the rows and 15 cm between the plants was followed in all locations and recommended package of practices for rice cultivations in respective locations were followed, AMMI model and GGE bi-plot methodology was used for the stability analysis.

RESULTS:

Analysis of variance as per AMMI model revealed that there was significant contribution for variation by main effects (genotypes and environments) and interaction effects for the trait yield. Significant mean sum of squares due to genotypes indicated that there existed genotypic differences and significance of environment explains that environmental effects differ across different locations and test locations were diverse. Further, G×E interaction effects signify that genotypes behave differently across different environments. Large sum of squares due to environments for yield indicated that differences among environmental means were very high and environments were diverse in nature. It was found in present study that environmental mean variations were very higher than genotypic mean variations for yield. Hence, test locations were diverse. The multiplicative variance of the treatment sum of squares due to G×E interaction was further partitioned into interaction principal component axis (IPCA) as it was significant. IPCA I and IPCA II scores explained 71.92 per cent and 25.06 per cent of the interaction respectively. These two PCA axes cumulatively captured 96.98 per cent of the total GEI for the trait grain yield per hectare. Stability parameters: According to AMMI stability value (ASV) Tungabhadra sona (BPT mutant GNV 1801) was the most stable genotype for yield (8637 kg/ha), since it recorded lowest ASV (0.31) followed by BPT mutant 1804 (8003 kg/ha) and BPT mutant 1811 (8071 kg/ha) with 0.39 and 0.41 ASV respectively. According to genotypic selection index (GSI), BPT mutant 1801 was found to be the best variety since it recorded lower value for it. Pattern of genotype-environment interaction display using graphical tool: A polygon is drawn on the genotypes that are farthest from the bi-plot origin so that all other genotypes fall within the polygon. Locations within the same sector share the same winning genotype and locations in different sectors have different winning genotypes. Thus, polygon view of a GGE bi-plot indicates presence or absence of cross-over GEI. 'Which won where' pattern of GGE biplots for grain yield of selected varieties indicated that genotypes viz., IET-27870, IET-26241, Gangavati sanna, BPT mutant 1809, BPT mutant 1806 and IET-27438 occupied vertices of polygon and unstable for grain yield per hectare, since they were located on vertices of polygon. The four environments were divided into four sub-groups by the radiating lines from the biplot origin to intersect each of the polygon sides at right angle. First sub-group consisted of environment Dhadesugur (E4) in which IET-27438 was winning genotype. Kawadimatti (E3) formed the second sub-group, in which the genotype IET-27870 was winner. Third sub group consisted of environment Malnoor (E2) where IET-26241 was the winner. Fourth sub group consisted of environment Gangavati (E1) where BPT mutant 1809 was the winner. Rest of the genotypes viz., GNV 10-89, Tungabhadra sona (BPT mutant GNV 1801), BPT mutant 1811, BPT mutant 1804, RNR-15048, BPT-5204, Rp Bio 226 and GGV-05-01 were found to be stable according to GGE biplots since they are located near origin and among them Tungabhadra sona (BPT mutant GNV 1801) was most stable genotype because it is located very closer to the origin (number 10) and have high yield potential combined with the better and wide adaptability over different agro-climatic conditions (Fig. 1.).

'Discrimitiveness vs. representativeness' pattern of GGE biplot for grain yield per hectare. Indicated that the environment Kawadimatti (E3) had shortest vector, so this environment was unable to discriminate the genotypes, while the environments Malnoor (E2), Dhadesugur (E4) and Gangavati (E1) were having longer vectors than Kawadimatti (E3) depicting that environments were able to discriminate the genotypes for grain yield per hectare. Low discrimination ability of the location Kawadimatti (E3) could be due to environmental or human effect.

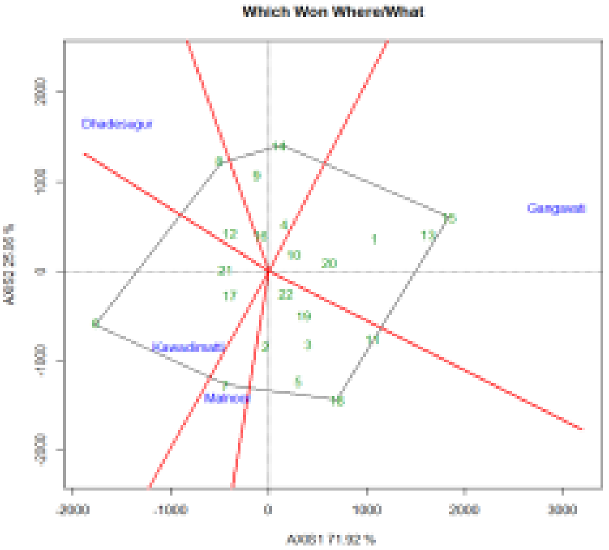

Fig 1. Polygon view of GGE bi-plot based on the symmetrical scaling for 'which won-where' pattern of genotypes and locations for grain yield per hectare.

CONCLUSION:

Genotype-Environment (GE) interaction is a complex phenomenon in nature which needs to be understood by breeders in order to identify locations that are suitable for better yield of a given variety. It was revealed by AMMI analysis in present investigation that there existed significant GE interaction among twenty-two rice varieties evaluated across four different locations. Analysis revealed that Tungabhadra sona (BPT mutant GNV 1801), BPT mutant 1804 and BPT mutant 1811 were found to be most stable varieties. Among these varieties, Tungabhadra sona (BPT mutant GNV 1801) was found to be best variety since it recorded highest grain yield and also it was stable performer for grain yield across four different locations and could be released for commercial cultivation.

The AMMI model and GGE biplots were found to be excellent tool to understand GE interactions. But, GGE biplots could provide more meaning information with reference to relationship between genotypes and environments.

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IRC/TM-1/PP-6

DEVELOPMENT OF HETEROTIC HYBRIDS THROUGH ALLOCYTOPLASMIC RESTORER IMPROVEMENT IN RICE (*ORYZA SATIVA* L.)

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Hybrid rice technology is one of the most promising and sustainable option to break the yield ceiling in rice. Three line system is widely adapted for development of hybrids. The frequency of restorers in germplasm is around 10 – 15 %. Improving potential restorer lines and diversification of CMS source must be an integral part of hybrid rice breeding. Cytoplasmic male sterility (CMS) is a maternally inherited trait and pollen fertility is restored by nuclear encoded genes called fertility restorer (*Rf*) genes and it was discovered that fertility restoration is controlled by two independent dominant nuclear genes *Rf3* and *Rf4*genes located on chromosome 1 and chromosome 10 respectively which have major influence on fertility restoration in many restorer lines for WA-CMS lines. The main objective of allo cytoplasmic restorers development are increasing the magnitude of heterosis through broadening the genetic base, combining the desirable traits and increasing the frequency of restorer genes.

METHODOLOGY:

Single, double and three way crosses were made between restorer lines and handled the breeding material up to F_6 generation by pedigree method. The new Restorer lines developed were evaluated for yield and other ancillary characters like pollen load, plant height and panicle length, restoring ability, quality traits and also biotic stresses for further use in hybrid breeding programme. Subsequently the new restorer lines were screened for fertility restorer genes using functional markers RM 6100 (*Rf4)* and RM 3873 (*Rf*3). Simultaneously these newly developed restorer lines were test crossed with different CMS lines.The resultant test crosses were studied for maintainer / restorer reaction using 1% Iodine potassium iodide solution and confirmed fertility restoration for second time also. Based on fertility restoration percentage, yield, plant type, grain type and other morphological characters 27 hybrids were selected for further evaluation.

RESULTS AND DISCUSSION:

Interestingly the frequency of restoration was high with a range of 90 – 100 % pollen fertility in 153 hybrids and rest of the crosses were partially fertile (<80%) out of 315 test crosses studied. By using restorer lines developed from R x R parental line improvement programme with different CMS lines has resulted in increase of fertility restoration in more number of crosses due to accumulation of *Rf* genes in restorer lines. Forty eight hybrids were studied for confirmation of restoring ability for second time during *Kharif*, 2015. Most of the hybrids were very early to early in duration. The new restorer lines WGL-R15, WGL-R17, WGL-R18, WGL-R23, WGL-R24, WGL-R26, WGL-R44, WGL-R55, WGL-R 65 and WGL-R 66 were found to be good combiners as they have shown restorer reaction in more than four CMS lines. Based on grain yield, grain type and spikelet fertility 27 hybrids were selected and evaluated for three seasons at station level during *Kharif*, 2016, *Rabi* 2016-17 and *Kharif* 2017 along with check PA 6444. Pooled data over three seasons indicated that WGRH-18 (7.27 t/ha) and WGRH-17 (7.18 t/ha) and WGRH-22 (6.90 t/ha) and WGRH-10 (6.87 t/ha) recorded superior yield over check PA 6444 (6.20 t/ha).The hybrid WGRH - 18 (16.31**)has recorded high significant standard heterosis followed by WGRH-17 (14.75**),WGRH-22 (12.10**)WGRH-19 (5.38**), while spikelet fertility recorded was 85.6 % in WGRH-18, 90.5% in WGRH-17, 86.3% in WGRH-22 and 83.17 % in PA 6444. The hybrid WGRH-18 was nominated for AICRP during *Kharif* 2019and Multi location trial (Early) in *Kharif* 2018. The results of pooled data from six rice research centers in Telangana state showed that WGRH-18 has recorded higher yield of 7.43 t/ha over check PA6444(7.08 t/ha). The restorers for these hybrids possessing *Rf3* and *Rf4 f*or WGRH-18 & WGRH-19, while *Rf3* for WGRH-17. Among the restorer lines WGL R-7, WGL R-11, WGLR-13, WGLR-14 and WGLR-15 positive for both *Rf3*and*Rf4* andWGLR-12, WGLR-17 and WGLR-23 for *Rf3* genes were identified as good restorers.

CONCLUSION:

All the conventional breeding strategies along with use of molecular markers linked to *Rf* genes can enhance the selection efficiency to develop better parental lines further which will help in developing highly heterotic hybrids.

IRC/TM-1/PP-7

STUDIES ON GENE ACTION FOR YIELD AND QUALITY COMPONENTS IN RICE

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Rice is life and prince among cereals, belongs to genus *Oryza* of the family poaceae and it is the most diverse cereal crop. Rice offers a great wealth of material for genetic studies because of its wide ecological distribution and enormous variation encountered for various morphological and physiological characters. To breed a genotype with high yielding potential, information on the genetic mechanism controlling various traits in the genetic material being studied is a prerequisite. The detection and estimation of epistasis in the inheritance of various quantitative triats are essential for rapid improvement. Generation mean analysis (Hayman, 1958) is the best method for estimating genetic variance and epistasis

MATERIAL AND METHODS

The present investigation was carried at Agricultural Research Station, Nellore, ANGRAU, AP, India during 2014-2017. Six crosses comprising F1, F2, BC1, BC2, P1 and P2 generations. Generation mean analysis was followed as per the procedure given by Hayman, 1958 for eleven yield and 12 qualitative parameters in rice

RESULTS AND DISCUSSION

A perusal of gene effects in generation mean analysis for six crosses *viz.*, RNR 2465 x NLR 145, BPT 5204 x IR 64, BPT 5204 x IR 36, BPT 5204 x NLR 34449, WGL 48684 x IR 36 and RNR 2465 x IR 64 revealed the presence of significant proportion of epistatic effects besides the major components *viz.*, additive (d) and dominance (h) gene effects for important yield and quality attributes. Partitioning of variance indicating that the mean values (m) for gene effects were highly significant in all the six crosses for all the characters except ear bearing tillers per plant, grain yield, SCMR and kernel L/B ratio in the cross BPT 5204 x IR 64 and filled grains per panicle and gel consistency in RNR 2465 x IR 64.

Additive gene component was significant in all the six hybrids for days to 50 percent flowering, test weight and number of filled grains per panicle suggesting simple selection would be useful for improvement of the traits. Dominance (h) component was significant in all the six hybrids for days to 50 percent flowering, days to maturity, test weight, SCMR, number of filled grains per panicle, harvest index, milling recovery (%), water uptake and volume expansion ratio. Higher magnitude of negative dominance gene effects most of the hybrids indicated the dominance of decreaser alleles in the inheritance of the traits and therefore, selection would be effective only at later generations. Among the interaction effects additive × additive (i) type of epistasis with negative sign was significant in all the six hybrids for days to 50 per cent flowering, days to maturity, plant height, grain yield, SCMR, number of filled grains per panicle and kernel length indicating little scope of improvement through simple pedigree selection.

Dominance x dominance (l) gene effects were significant in all the six hybrids for days to 50 percent flowering, days to maturity, test weight, SCMR, number of filled grains per panicle, kernel length, milling recovery (%) and water uptake indicating that in addition to additive and dominance gene effects, the epistatic interaction effects were also important in the expression of above studied characters in rice. However, the magnitude of epistasis could be biased by the presence of linkage especially (i) and (l) (Kempthorne, 1957). Even though, the effect of epistasis is basic genetic mechanism perhaps cannot be considered as negligible. Hence, biparental mating and recurrent selection especially reciprocal recurrent selection in early segregating generations to break the repulsion phase linkages followed by isolation of pure lines in advanced generation would be the correct strategy as compared to pedigree breeding alone.

In the present investigation, the results of dominance (h) and dominance × dominance (l) type interactions revealed prevalence of duplicate type of epistasis in most of the traits in all the six hybrids except in WGL 48684 x IR 36 for plant height, effective bearing tillers per plant and kernel breadth; in RNR 2465 x NLR 145 for effective bearing tillers per plant and grain yield; in RNR 2465 x IR 64 for number of filled grains per panicle and BPT 5204 x NLR 34449 (for kernel breadth and kernel elongation ratio), BPT 5204 x IR 64 (for head rice recovery) and BPT 5204 x IR 36 (for harvest index) where complementary gene action played a vital role in the inheritance of the traits. It was evident from the results that the duplicate type of epistasis was common, except in few hybrids for some characters limiting the pace of progress through selection. Therefore, few cycles of recurrent selection followed by pedigree method would be effective and useful to utilize all types of gene effects by maintaining considerable heterozygosity through mating of selected plants in early segregating generations.

Significance of additive components besides duplicate epistasis indicated the scope for recovering the transgressive plants effect for the characters governed by non additive gene actions and epistasis recurrent selection methods can be recommended. But these methods have certain limitations in self pollinated crops like rice, due to difficulty in crossing and seed sterility. Repeated back crossing is more rewarding to pool up the desired genes into single line. Hence biparental mating in early generation followed by selection besides repeated back crossing will give fruitful results.

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IRC/TM-1/PP-8

STUDY ON STABILITY OF GRAIN YIELD IN LONG DURATION RICE CULTURES

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Rice is a wonder crop and it is the staple food of more than two third of worlds population, rice has wide adaptability to grow well in different types of agroclimatic conditions. Varietal adaptability to environmental fluctuations is important for the stabilization of crop production over both the region and years. An information on genotype x environment interaction leads to successful evaluation of stable genotype, which could be used for general cultivation. Yield is a complex quantitative character and is greatly influenced by environmental fluctuation; hence selection for superior genotype based on yield per se at a single location in a year may not be very effective. Thus, varietal stability is of paramount importance for stabilizing the production over region and seasons especially in decreased farm holdings and resource poor farmer conditions. This lays a heavy emphasis on developing technologies while keeping sustainability of small farmer and his resources as the top priority. In subsistence agricultural system, yield *per se* may be less important than reaching a certain yield level (Fox *et al*., 1997). Therefore, development of varieties and hybrids with stable performance is gaining ground to help achieve sustainability in agricultural production. To achieve this, first concept is to select the genotype with the smallest deviation from its production potential. In view of this, the present investigation was carried out with eight rice genotypes.

MATERIALS AND METHODS

Eight elite genotypes viz., NLR 3548, NLR 3637, NLR 3638, NLR 3644, NLR 3634, NLR 3635, NLR 3640, NLR 3545 and three checks, NLR 33892, NLR 3041and BPT 5204 were taken for study for three consecutive years to study the stability of the performance with respect to grain yield, the present experiment was conducted a Agricultural Research Station, Nellore, ANGRAU during 2017-18, 2018-19 and 2019-20 kharif season. The genotypes were planted in three replications with a spacing of 20x15cm^2 and having a plot size of 12m^2 every year.Fertilizers wereapplied @ 120:60:40 kgha-1 N, P and K, respectively.Plant protection measures were taken as and whenrequired. Data was recorded on days taken for 50% flowering, grain yield and its attributing characters. The sustainability was calculated based on the formula given below: (Average performance of the genotype in terms of yield/better performance among the years)x 100.

RESULTS AND DISCUSSION

High performance regarding grain yield was recorded by NLR 3548 (6.23t/ha) followed by NLR 3634 (5.89t/ha). The culture NLR 3634 possessed fine grain and it also performed better when compared to the medium slender grain types like NLR 33892 (5.5t/ha) and NLR 3041 (3.63t/ha0. High sustainability index indicates the little effect on environmental factors on the yield of a genotype. In the present study high sustainability index was recorded by NLR 3644 (9058) followed by NLR 33892 (90.48), NLR 3548 (88.7) and NLR 3545 (85.4) indicating the stable performance of the genotypes over the years tested. High mean performance coupled with high sustainability index was observed with the genotypes viz., NLR 3644 (GY: 5865, SI:90.5) followed by NLR 3548 (GY:5530, SI:9048), NLR 33892 (GY:5530, SI:90.48) and NLR 3635 (GY:5780, SI:82.2) indicating the best

S.No	Genotype	Grain yield			Average performance	Standard devation	Best score	Sustainability index
		2017-18	2018-19	2019-20				
1	NLR 3548	6.47	7.02	5.19	6.23	0.94	7.02	88.7
2	NLR 3637	6.88	5.29	5.02	5.73	1.01	6.88	83.2
3	NLR 3638	6.8	4.93	4.79	5.51	1.13	6.80	80.9
4	NLR 3644	6.47	6.51	4.60	5.86	1.09	6.47	90.5
5	NLR 3634	7.75	5.36	4.56	5.89	1.6	7.75	76
6	NLR 3635	7.03	5.87	4.43	5.78	1.3	7.03	82.2
7	NLR 3640	6.77	5.60	4.37	5.58	1.2	.77	82.4
8	NLR 3545	5.79	6.10	3.75	5.21	1.2	6.12	85.4
9	NLR 33892	2.79	2.49	4.43	3.24	1.04	4.43	73.1
10	NLR 3041	6.11	5.90	4.57	5.53	0.84	6.1	90.4
11	BPT 5204	4.32	2.72	3.84	3.63	0.82	4.32	83.8

performance of the genotypes and it could be taken as an indication of proximity between best performance and the average performance over the years. These genotypes can be used a parents in the future breeding programmes for evolving genotypes with high sustainability of grain yield.

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IRC/TM-1/PP-9

PS-II EFFICIENCY OF QTL INTROGRESSED LINES OF HYBRID RICE RESTORER, KMR-3R UNDER HIGH TEMPERATURE STRESS

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Climate change resulted in high temperature episodes and altered precipitation levels. According to IPCC, the global mean temperature was expected to rise by 2.5 ºC - 5.8 ºC by the end of the present century. In order to sustain global rice production and to meet the estimated demand of growing population, breeding rice for high temperature stress remains a major priority. In this regard, hybrid rice technology could be a great opportunity for its heterosis. Hybrid rice technology contributed a major share in global rice production. In India, hybrid rice is cultivated in 3 million hectares and provides 3–4 million tons of rice grain. Rice hybrids consistently noted 10-13% yield advantage over conventional varieties withstanding various biotic and abiotic stresses. However, yield of hybrids was effected due to low seed setting under high temperatures (38 ºC). Usually in India, rice hybrid seed production was followed in dry (summer) season. The high temperature at anthesis stage effects the pollen viability, anther dehiscence, pollen tube elongation and stigma receptivity which eventually results in low spikelet fertility rate and reduced grain yield.

In order to produce high temperature tolerant rice hybrids, heat tolerant parents can play key role and moreover, the association between rice hybrids and their heat tolerant parental lines can be understood. Thus, the emphasis was given to the improvement of heat tolerant hybrid rice parents. KMR-3R is promising restorer line employed in the development of a hybrid KRH-2. Nagina22 (N22) is a potential genetic resource for heat tolerance and widely used in the heat tolerance studies.

To achieve this, the restorer line (KMR-3R) was introgressed with *qHTSF1.1* and *qHTSF4.1* for heat tolerance through Marker-Assisted Backcross Breeding (MABB) approach at Indian Institute of Rice Research (IIRR).

OBJECTIVE

The developed heat tolerant lines and their parents were subjected to chlorophyll and fluorescence screening studies to identify the relation between PSII efficiency and heat tolerance.

METHODOLOGY

Eight BILs (BC_2F_6) derived from the KMR-3R/Nagina22 were evaluated for heat tolerance in terms of physiological traits such as chlorophyll fluorescence during 2018. The trait chlorophyll fluorescence can be used as an effective tool to evaluate the photosynthetic performance of plants under high temperature. Marker-Assisted Backcross Breeding (MABB) approach was followed to succeed the introgression of *qHTSF1.1* and *qHTSF4.1* into the KMR-3R. The SSR makers associated with QTLs - RM431, RM11943 and RM12091 for *qHTSF1.1* on chromosome 1 and RM5757 for *qHTSF4.1* on chromosome 4 were employed for genotypic confirmation of QTL positive plants. In addition, the derived BILs were also screened for fertility restoration.

As in AICRIP plant physiology high temperature trial, high temperature stress was imposed by enclosing the crop with a poly cover tent just before the anthesis stage. It was assembled with a transparent polythene sheet (>92% transmittance) of 1 mm thickness (~19 gauge) and supported over a metal framework. An increase in the temperature (4ºC – 5ºC) over the ambient conditions was noticed inside the poly cover tent. A standard thermo hygrometer was employed to record the minimum and maximum temperatures and relative humidity (RH) inside the poly cover tent throughout the experiment period.

Chlorophyll fluorescence was measured at reproductive stage (1 week after anthesis) using a portable fluorometer (PAM-210, Walz, Effeltrich, Germany). The fluorescence parameters *viz.*, maximum efficiency of PSII photochemistry (Fv/Fm), Electron transport rate (ETR), effective PSII quantum yield (ÖPSII), coefficient of photochemical quenching (qP) and coefficient of non-photochemical quenching (qN) were measured in dark adapted (30-45 min.) leaves collected from genotypes under ambient and high temperature stress. The data was analysed statistically using two-way ANOVA in *Statistix 8.1*.

RESULTS

Significant differences were observed between treatments (T), genotypes (G) and the interaction between T X G. The mean Fv/Fm reduced from 0.782 in control to 0.722 under high temperature. All the QTL positive ILs noted with higher Fv/Fm value (IL8 is on par) than N22 (0.736) except QTL negative line, IL1 (0.588). This is due to the effect of introgressed QTLs which not only controls spikelet fertility under high temperature, also the photosynthetic traits.

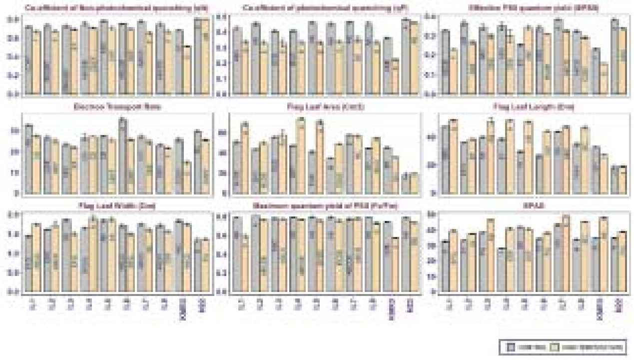

Figure 1. **Mean values of Chlorophyll Fluorescence Traits under ambient and high temperature stress.**

ETR for all the genotypes was decreased by 16% under high temperature stress. QTL positive ILs and N22 were observed with higher ETR than recurrent parent, KMR-3R (14.55) and QTL negative IL1 (21.65). The IL8 (27.3) and IL4 (27.08) were observed with higher ETR.

The ÖPSII was reduced significantly under high temperature stress by 22.5% over the control. All the QTL positive ILs were observed with higher values after the N22 (0.335). Conversely, KMR-3R (0.156) and QTL negative IL1 (0.229) were observed with lower values.

Further, there was a reduction in qP and qN in all the genotypes. The mean qP under control was 0.436 which reduced to 0.337. N22 was observed with maximum qP for both the experimental conditions (*i.e.*, 0.483 in control and 0.460 in high temperature stress). Among the ILs, IL7 (0.353) was observed with highest qP value next to the N22. QTL negative IL1 was observed with the qP value of 0.259. N22 (0.801) and IL4 (0.705) were observed with high qN values under high temperature stress. IL1 (0.652) was observed with lower qN value among the ILs in stress environment.

CONCLUSION

The fluorescence parameters recorded a significant reduction under high temperature stress. However, heat tolerant QTL introgressed positive lines noted better performance under high temperature stress.

IRC/TM-1/PP-10

GENETIC ANALYSIS OF YIELD AND QUALITY ATTRIBUTES IN MOLAKOKULU RICE CULTURES

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Rice is the major staple food crop in India and Andhra Pradesh as well. Nellore is popular for rice cultivation and it is named for its rice cultivation. Molakolukulu rice was indigenous to Nellore and traditionally it was cultivated in the districts of Nellore, Chittoor, Prakasam, Kadapa and Guntur districts up to 1947. They were famous for their good cooking, eating and keeping quality. But they were of very long durationed (160-180 days) and highly photo sensitive and can be grown only during kharif season. They grow very tall (130-150 cms), susceptible to lodging and low yielders. Though the molakolukulu and molakolukulu derived rice varieties possess good cooking, eating and keeping quality, due to their very long duration, tall with lodging habit, photo sensitive and suitable for only kharif season the area under these varieties is reduced drastically and now being grown in only about 45000 acres in Prakasam, YSR Kadapa, parts of Guntur and Krishna districts (Ramesh Babu et al., 2016). Hence it is time to transfer the good characters of molakolukulu in to medium and short duration rice varieties which are widely cultivated by farmers in kharif as well as rabi seasons.

METHODOLOGY

To improve molakolukulu rice varieties one has to study the major chemical components which made them superior in terms of cooking quality and the exact features of the varieties interms of yield and yield components. In view of that the present study was conducted with 25 molakolukulu rice genotypes during 2017 kharif season at agricultural research Station, Nellore to study the variability, heritability, genetic advance, genetic advance as percent of mean for 25 yield and quality attributes. The genotypes were plated with a spacing of 20x15cm, 5x5m plot using RBD design with three replications. Relavant agronomic practices were followed to raise a good crop. Analysis was done as per the standard procedures.

RESULTS AND DISCUSSION

The present study revealed that the estimates of PCV and GCV were high for Alkali spreading value, Gel consistency, Oil content and Zinc content. Moderate PCV and GCV were observed for Plant height, Number of productive tillers per plant, Flag leaf length and Protein content. High PCV and Moderate GCV were observed for Filled grains per panicle, Water uptake and Iron content. Moderate PCV and low GCV were observed for Flag leaf breadth and Grain yield per plant. While, low PCV and GCV were observed for Days to 50 % flowering, Test weight, Kernel length, Kernel breadth, Kernel length/breadth ratio, Hulling %, Milling %, Head rice recovery, Amylose content, Kernel elongation ratio, Volume expansion ratio and Gel consistency.

PCV values were close to GCV for the traits, Days to 50% flowering, Plant height, Flag leaf length, Filled grains per panicle, Test weight, Kernel length, Kernel breadth, Kernel length/breadth ratio, Hulling%, Milling%, Head rice recovery, Gel consistency, Amylose content and Protein content

exhibiting little or no influence of environment on these traits, while for the traits, Panicle length, Flag leaf breadth, Number of productive tillers per plant, Grain yield per plant, Water uptake, Volume expansion ratio, Kernel elongation ratio, Alkali spreading value, Iron content, Zinc content and Oil content, PCV was higher than GCV indicating the effect of environment in expression of these traits.

The estimates of heritability and genetic advance as per cent of mean were high for the characters viz., plant height, filled grains per panicle, flag leaf length, oil content, gel consistency and iron content indicating the influence of additive gene action in the inheritance of these traits hence simple selection would be rewarding. High heritability coupled with moderate genetic advance as per cent of mean was observed for Panicle length, Test weight, Kernel length/breadth ratio, Head rice recovery, Protein content, Volume expansion ratio and Amylose content. Moderate heritability coupled with high genetic advance as per cent of mean observed for Zinc content, Alkali spreading value and Water uptake. Moderate heritability coupled with moderate genetic advance as per cent of mean observed for Flag leaf breadth and Productive tillers per plant. High heritability coupled with low genetic advance as per cent of mean was observed for Days to 50% flowering, Kernel length and Milling%.

Involvement of both additive and non additive gene action in the inheritance of all these traits thus simple selection may not be effective instead population improvement for these traits would be desirable. The traditional molakolukulu rice varieties were of tall statured plants, having more productive tillers, less number of grains per panicle. The advanced cultures developed from traditional varieties were of comparatively short stature, less tillers with more productive ones, more filled grains per panicle, medium lengthy panicle and non lodging in nature. Similarly, the traditional ones are of bold grain types whereas the advanced lines were of medium slender types. The trend was greatly evidenced in the present study.

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IRC/TM-1/PP-11

PERFORMANCE OF DIFFERENT CROP ESTABLISHMENT METHODS AND NUTRIENT MANAGEMENT PRACTICES ON RICE IN RICE-*PAIRA* PEA CROPPING SYSTEM

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The productivity and sustainability of rice-based systems are threatened because of the inefficient use of inputs (fertilizer, water, labor); increasing scarcity of resources, especially water and labor; changing climate; the emerging energy crisis and rising fuel prices; the rising cost of cultivation; and emerging socioeconomic changes such as urbanization, migration of labor, preference of non-agricultural work, concerns about farm-related pollution (Ladha *et al*., 2009). Farmers of Odisha are cultivating paddy by manual transplanting and broadcasting. Delayed onset of monsoon and shortage of labour during the peak time of planting paddy are the main problem to complete timely transplanting. Mechanical transplanting with self propelled transplanter and direct seeding of rice by tractor drawn seed drill could be an alternative for paddy cultivation. Similarly, nutrient management plays a vital role in successful crop production. Balance and site specific nutrient management is the need of the hour. Keeping this in mind, the experimental was conducted with the objective to evaluate the “Effect of different crop establishment methods and nutrient management practices of rice in rice - paira pea system” on yield attributes, yield and economics of the rice-pea cropping system.

MATERIALS AND METHODS

The experiment was conducted at Regional Research and Technology Transfer Station (OUAT), Bhawanipatna during 2017-18 and 2018-19 to evaluate the different crop establishment methods and nutrient management practices on *kharif* rice followed by pea sown as *paira* crop. The experiment was conducted in *split plot* design with twelve treatment combinations, consisting of three crop establishment methods *viz.* M_1: Mechanical transplanting (MTP), M_2: Direct seeding of rice with seed drill (DSR) and M_3: Manual transplanting (TP) in main plot and four nutrient management practices *viz.* N_1: Rice Crop Manager (RCM)-95.2:29.9: 35.4:25.0 kg N: P_2O_5: K_2O: Zn SO_4 ha^{-1}, N_2: State recommendation (SR)- 80:40:40 kg N: P_2O_5: K_2O ha^{-1}, N_3: Soil test based fertilizer Recommendation (STBFR)100:30:40:25 kg N: P_2O_5: K_2O: Zn SO_4 ha^{-1} and N_4: Farmers’ Practice (FP)- 100:50:30 kg N: P_2O_5: K_2O ha^{-1} in sub plot replicated thrice.

The soil of the experimental site was claey loam having pH 6.4, medium in organic carbon content (0.60%), low in available N (214.0kg ha^{-1}), high in available P (34.1 kg ha^{-1}), medium in available K (264.0kg ha^{-1}) and low in Zinc content (0.38mg kg^{-1}). Medium duration paddy variety MTU-1010 was used for direct seeding of rice by seed drill and nursery raising on 30th June 2017 and 25th June 2018, respectively, for mechanical transplanting and manual transplanting. Pea (Kalahandi local) was sown fifteen days prior to harvest of paddy.

RESULTS

The number of effective tillers/hill and grains/ panicle were significantly higher in mechanical transplanting (MTP) than direct seeding of rice by seed drill (DSR) but remained at par with manual transplanting (TP). Higher number of effective tillers hill^{-1} and grains panicle^{-1} (9.5 and 117, respectively) were observed in fertilizer applied plot using RCM

Table 1: Effect of crop establishment methods and nutrient management on yield attributes, yield and economics of rice under rice- *paira* pea cropping system (Pooled over 2017-18 and 2018-19)

Treatment	No. of effective tillers hill $^{-1}$	No. of grains Panicle^{-1}	Grain Yield of Paddy (kg ha^{-1})	Straw yield of Paddy (kg ha^{-1})	Seed Yield of Pea (kg ha^{-1})	REY (kg ha^{-1})	System Gross return (Rs.ha^{-1})	System Net return (Rs.ha^{-1})	Return Rupee^{-1} invested (Rs.ha^{-1})
	Crop establishment methods(Main Plot)								
MTP	8.7	116	4117	4510	317	4951	79233	36228	1.84
DSR	7.8	102	3818	4299	448	4995	80061	44792	2.27
TP	8.6	109	3906	4319	402	4961	79495	32559	1.69
SEm±	0.2	2.4	67.9	50.9	8.9	76.5	1231	1231	0.03
CD at 5%	0.7	7.5	214.0	160.5	27.9	NS	NS	3880	0.10
	Nutrient management (Sub Plot)								
RCM	9.5	117	4480	4846	412	5561	89023	45758	2.08
SR	7.0	101	3052	3567	354	3981	63836	22999	1.59
STBFR	8.8	110	4290	4684	426	5408	86654	45517	2.15
FP	8.1	107	3967	4408	365	4925	78873	37164	1.92
SEm±	0.3	2.5	111.8	122.3	14.6	128.7	2053	2053	0.05
CD at 5%	0.7	7.3	320.7	350.7	41.8	369.2	5889	5889	0.15

During 2017-18, cost of Paddy =Rs.14.5/kg, straw=Rs.1.00/kg, pea=Rs.40.00/kg and during 2018-19, cost of Paddy = Rs.17.70/kg, straw=Rs.1.00/kg and pea=Rs.45.00

which remained at par with STBFR (8.8 and 110, respectively) but significantly higher from FP (8.1 and 107, respectively) and SR (7.0 and 101, respectively).

Amongst different establishment methods, maximum grain yield was obtained in MTP (4117 kg ha^{-1}) which was at par with manual transplanting (3906 kg ha^{-1}) and significantly more from DSR (3818 kg ha^{-1}). Paddy straw yield followed the same trend as that of grain yield. Maximum grain yield (4480 kg ha^{-1}) of paddy was recorded in the nutrient management practice using RCM, (Sharma *et.al*., 2019) which was at par with STBFR (4290 kg ha^{-1}) and remained statistically superior from FP (3967 kg ha^{-1}) and SR (3052 kg ha^{-1}). The grain yield in RCM and STBFR nutrient management practices were 46.8 and 40.5% higher than fertilizer application as per state recommendation, respectively. Straw yield followed the same trend as that of grain yield.

Seed yield of pea was significantly influenced by different crop establishment methods. Higher pea seed yield (448 kg ha^{-1}) was obtained in DSR plot, which was significantly higher from TP (402 kg ha^{-1}) and MTP (317 kg ha^{-1}). The seed yield of pea in DSR plot was 11.4 and 41.3% higher than manual transplanting and mechanical transplanting, respectively. STBFR produced higher pea seed (426 kg ha^{-1}) which was at par with RCM (412 kg ha^{-1}) and significantly superior from FP (365 kg ha^{-1}) and SR (354 kg ha^{-1}). Nutrient management using STBFR produced 16.7 and 20.3% higher pea seed than FP and SR fertilizer application, respectively.

Crop establishment by DSR produced maximum Rice equivalent yield REY (4995 kg/ha) followed by TP (4961 kg ha^{-1}) and MTP (4951 kg ha^{-1}). However, nutrient application using RCM produced higher REY (5561 kg ha^{-1}), which was at par with

STBFR method (5408 kg ha^{-1}) but significantly more than FP (4925 kg ha^{-1}) and SR (3981 kg ha^{-1}). REY in RCM and STBFR approach was 39.7 and 35.8% higher in comparison to SR, respectively (Table 1).

System net return was higher in DSR method of crop establishment (Rs.44792 ha^{-1}) which was significantly higher than mechanical transplanting (Rs.36228 ha^{-1}) and manual transplanting (Rs.32559 ha^{-1}). Among the nutrient management practices, RCM fetched higher net return (Rs.45758 ha^{-1}) which was at par with STBFR approach (Rs.45517 ha^{-1}) and significantly higher from FP and SR.. DSR recorded significantly higher return per rupee invested (2.27) followed by MTP (1.84) and TP (1.69). Among the nutrient management approaches STBFR recorded higher return per rupee invested (2.15) followed by RCM (2.08), FP (1.92) and SR (1.59).

CONCLUSION

For higher production, profit and better utilization of resources under changing climatic situation, direct seeding of rice using seed drill fertilized with soil test based fertilizer application (100:30:40:25 kg N, P_2O_5, K_2O, $ZnSO_4$ ha^{-1}) followed by *paira* pea is advisable over manual transplanting with state recommended fertilizer application in Odisha.

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IRC/TM-1/PP-12

FERTILITY RESTORATION STUDIES OF PROMISING GENOTYPES IN RICE (*ORYZA SATIVA* L.)

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Rice is the principal food crop cultivated throughout the world. However, yield plateaus have been observed in the crop in recent years. Siddiq (1997) reported hybrid rice to be a potent technological option for breaking the yield plateaus. Further, Akhter *et al.* (2008) identified the establishment of test cross nursery to identify restorer and maintainer lines as the initial step for any successful three-line hybrid rice breeding program. In this context, the present study was undertaken with the objective of identification of potential restorers and maintainers for the popular and widely used CMS lines of rice.

MATERIALS AND METHODS

The experimental material comprised of 50 hybrids obtained from the mating of two CMS lines (APMS 6A and APMS 8A) with 25 genotypes (BPT 5204, RP6112-MS-128-5-2-3-1-4-5, MTU 2244-128-18, MTU 2201-34-3-1, MTU 2049-5-2-1, MTU 2247-55-2, BPT 2659, JMP 16, MTU 1061, RM 168-28-1-1-1, MTU 2336-70-46-25-44, MTU 2347-158-3-1-1, MTU 2336-62-25-39-16, MTU 2284-103-1-7, HR L4, NLR 5815-10-1-1-1, UTR 51, NLR 3445 and BPT 2782). These hybrids were evaluated at Regional Agricultural Research Station, Maruteru. A standard spacing of 20 x 15 cm was adopted for planting and 30 plants were maintained in a single row. Spikelet fertility (%) was recorded on five randomly selected plants in each hybrid.

Pollen sterility studies were carried out in the F1 plants. For this purpose 15-20 spikelets from just emerged panicles of three randomly selected plants of each hybrid were collected separately in a vial containing 70% ethanol. A glass slide was taken with a drop of 1% Iodine Potassium Iodide (IKI) stain. All the anthers were taken out with the help of a forceps and placed in the stain. These were gently crushed by using a needle head to release the pollen grains. After removing the debris, a cover slip was placed and observed under microscope. Pollen sterility per cent was obtained as ratio of the sterile pollen to the total pollen in three microscopic fields and was expressed in percentage. For spikelet fertility, five panicles of each hybrid were covered with butter paper bags to avoid foreign pollen contamination and were harvested at maturity. The genotypes were classified as maintainers or restorers as per the procedure described by Virmani *et al*. (1997) based on pollen sterility per cent and spikelet fertility per cent.

RESULTS AND DISCUSSION

Pollen sterility percentage was observed to range from 2.06 (APMS 8A x NLR 3445) to 60.23 (APMS 8A x MTU 2049-5-2-1) with an average value of 21.11 per cent (Table 1). Based on the classification for pollen sterility provided by Virmani *et al.* (1997), 16 genotypes were classified as fully fertile with 0-20 per cent pollen sterility (BPT 5204, MTU 2244-128-18, MTU 2049-5-2-1, BPT 2659, MTU 2336-62-25-39-16, NLR 5815-10-1-1-1, MTU 2067-9-1-1-2, MTU 2345-98-3, BPT 2782, NLR 3445, MTU 2331-216-1-1, JMP 16, UTR 51, MTU 2336-70-46-25-44, RP6112-MS-128-5-2-3-1-4-5 and MTU 2201-34-3-1), four as fertile with 21-30 per cent pollen sterility (MTU 2247-55-2, MTU 2284-103-1-7, RM 168-28-1-1-1 and RM 138-80-3-1-1-1) and five as partially fertile with 31-70 per cent pollen sterility (MTU 2284-103-1-9, MTU 1061, MTU 2347-158-3-1-1, MTU 2337-216-1-1 and HR L4) for APMS 6A. For APMS 8A, 11 genotypes, (NLR 3445, MTU 2247-55-2, MTU 2337-216-1-1, MTU 2067-9-1-1-2, JMP 16, BPT 2659, MTU 2345-98-3, RP 6112-MS-128-5-2-3-1-4-5, BPT 5204, MTU 2244-128-18 and MTU 2331-216-1-1) were classified as fully fertile, while six genotypes (MTU 2336-70-46-25-44, MTU 2347-158-3-1-1, BPT 2782, MTU 2336-62-25-39-16, NLR 5815-10-1-1-1 and MTU 2284-103-1-7) were classified as fertile and eight genotypes (HR L4, MTU 2201-34-3-1, RM 138-80-3-1-1-1, MTU 2284-103-1-9, UTR 51, MTU 1061, RM 168-28-1-1-1 and MTU 2049-5-2-1) were classified as partially fertile. However, none of the genotypes studied had recorded maintainer reaction (100 per cent pollen sterility) for the CMS lines studied.

Spikelet fertility for the 50 hybrids studied in the present investigation was observed to range from 46.24 per cent (APMS 8A x MTU 2049-5-2-1) to 92.30 per cent (APMS 8A x MTU 2337-216-1-1) with a mean value of 75.61 per cent (Table 1). Based on the classification for spikelet fertility percentage given by Virmani *et al.* (1997), 17 genotypes were classified as restorers with more than 75 per cent spikelet fertility (BPT 5204, MTU 2049-5-2-1, MTU 2336-62-25-39-16, MTU 2244-128-18, BPT 2659, NLR 3445, MTU 2067-9-1-1-2, MTU 2331-216-1-1, JMP 16, BPT 2782, NLR 5815-10-1-1-1, MTU 2336-70-46-25-44, MTU 2345-98-3, UTR 51, RP 6112-MS-128-5-2-3-1-4-5, MTU 2201-34-3-1 and MTU 2247-55-2), six as partial restorers with 50.1 -75 per cent spikelet fertility (MTU 2284-103-1-7, RM 168-28-1-1-1, RM 138-80-3-1-1-1, MTU 2284-103-1-9, MTU 2337-216-1-1 and MTU 2347-158-3-1-1) and two as partial maintainers with 0.1 to 50 per cent

Table 1. Identification of maintainers and restorers based on pollen sterility and spikelet fertility percentage

S. No.	Cross combination	Pollen sterility (%)	Spikelet fertility (%)
Crosses with APMS 6A			
1	APMS 6A x BPT 5204	12.50	83.92
2	APMS 6A x RP6112-MS-128-5-2-3-1-4-5	17.50	78.31
3	APMS 6A x MTU 2244-128-18	6.34	90.37
4	APMS 6A x MTU 2201-34-3-1	19.98	77.52
5	APMS 6A x MTU 2049-5-2-1	7.62	91.83
6	APMS 6A x MTU 2247-55-2	22.34	76.49
7	APMS 6A x BPT 2659	8.62	90.18
8	APMS 6A x JMP 16	15.34	86.45
9	APMS 6A x MTU 1061	31.88	48.01
10	APMS 6A x RM 168-28-1-1-1	27.82	69.68
11	APMS 6A x MTU 2336-70-46-25-44	15.60	84.03
12	APMS 6A x MTU 2347-158-3-1-1	31.88	63.12
13	APMS 6A x MTU 2336-62-25-39-16	8.63	90.77
14	APMS 6A x MTU 2284-103-1-7	24.70	70.77
15	APMS 6A x HR L4	55.62	44.26
16	APMS 6A x NLR 5815-10-1-1-1	9.45	85.25
17	APMS 6A x UTR 51	15.53	81.97
18	APMS 6A x NLR 3445	12.20	88.88
19	APMS 6A x BPT 2782	11.50	85.27
20	APMS 6A x MTU 2284-103-1-9	30.93	65.57
21	APMS 6A x MTU 2345-98-3	10.60	83.75
22	APMS 6A x MTU 2067-9-1-1-2	9.62	88.09
23	APMS 6A x RM 138-80-3-1-1-1	28.23	69.27
24	APMS 6A x MTU 2337-216-1-1	35.25	64.75
25	APMS 6A x MTU 2331-216-1-1	13.40	87.59
Crosses with APMS 8A			
26	APMS 8A x BPT 5204	14.55	82.95
27	APMS 8A x RP6112-MS-128-5-2-3-1-4-5	14.30	79.49
28	APMS 8A x MTU 2244-128-18	16.46	81.04
29	APMS 8A x MTU 2201-34-3-1	32.77	63.73
30	APMS 8A x MTU 2049-5-2-1	60.23	46.24
31	APMS 8A x MTU 2247-55-2	4.26	91.25
32	APMS 8A x BPT 2659	8.14	87.15
33	APMS 8A x JMP 16	7.26	90.95
34	APMS 8A x MTU 1061	37.89	47.11
35	APMS 8A x RM 168-28-1-1-1	39.73	58.77
36	APMS 8A x MTU 2336-70-46-25-44	20.43	77.08
37	APMS 8A x MTU 2347-158-3-1-1	22.50	72.00
38	APMS 8A x MTU 2336-62-25-39-16	27.45	70.05
39	APMS 8A x MTU 2284-103-1-7	29.12	68.38
40	APMS 8A x HR L4	32.62	63.79
41	APMS 8A x NLR 5815-10-1-1-1	28.42	69.06
42	APMS 8A x UTR 51	37.49	58.01
43	APMS 8A x NLR 3445	2.06	92.08
44	APMS 8A x BPT 2782	23.80	70.95
45	APMS 8A x MTU 2284-103-1-9	37.38	58.12
46	APMS 8A x MTU 2345-98-3	11.46	88.45
47	APMS 8A x MTU 2067-9-1-1-2	6.85	91.92
48	APMS 8A x RM 138-80-3-1-1-1	33.49	63.01
49	APMS 8A x MTU 2337-216-1-1	6.82	92.30
50	APMS 8A x MTU 2331-216-1-1	16.93	87.07

spikelet fertility (MTU 1061 and HR L4) for APMS 6A, while 12 genotypes (MTU 2337-216-1-1, NLR 3445, MTU 2067-9-1-1-2, MTU 2247-55-2, JMP 16, MTU 2345-98-3, BPT 2659, MTU 2331-216-1-1, BPT 5204, MTU 2244-128-18, RP 6112-MS-128-5-2-3-1-4-5 and MTU 2336-70-46-25-44) were identified as restorers, 11 as partial restorers (MTU 2347-158-3-1-1, BPT 2782, MTU 2336-62-25-39-16, NLR 5815-10-1-1-1, MTU 2284-103-1-7, HR L4, MTU 2201-34-3-1, RM 138-80-3-1-1-1, RM 168-28-1-1-1, MTU 2284-103-1-9 and UTR 51) and two as partial maintainers (MTU 1061 and MTU 2049-5-2-1) for APMS 8A. However, none of the genotypes studied had recorded maintainer reaction (0 per cent spikelet fertility) for the CMS lines studied.

A perusal of the results on pollen sterility and spikelet fertility percentage revealed 17 genotypes (BPT 5204, MTU 2049-5-2-1, MTU 2336-62-25-39-16, MTU 2244-128-18, BPT 2659, NLR 3445, MTU 2067-9-1-1-2, MTU 2331-216-1-1, JMP 16, BPT 2782, NLR 5815-10-1-1-1, MTU 2336-70-46-25-44, MTU 2345-98-3, UTR 51, RP 6112-MS-128-5-2-3-1-4-5, MTU 2201-34-3-1 and MTU 2247-55-2) to be potential restorers for APMS 6A; and 12 (MTU 2337-216-1-1, NLR 3445, MTU 2067-9-1-1-2, MTU 2247-55-2, JMP 16, MTU 2345-98-3, BPT 2659, MTU 2331-216-1-1, BPT 5204, MTU 2244-128-18, RP 6112-MS-128-5-2-3-1-4-5 and MTU 2336-70-46-25-44) for APMS 8A.

CONCLUSION

Seven genotypes (BPT 5204, NLR 3445, MTU 2331-216-1-1, MTU 2067-9-1-1-2, MTU 2336-62-25-39-16, MTU 2049-5-2-1 and NLR 5815-10-1-1-1) were identified as potential restorers for both, APMS 6A and APMS 8A. However, none of the genotypes studied had recorded maintainer reaction for the CMS lines studied.

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GREEN SUPER RICE – A RECENT DEVELOPMENT

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Rice (*Oryza sativa* L.) is one of the most important food crops and is the principal staple food for almost half of the world's population. The world population is expected to continue growing and hit 9 billion by 2050, which calls for an increase of almost 70 percent in food production (FAO 2013). Therefore, to ensure global food security and living standards, increased rice yields are crucial. In order to boost rice yields, farmers have gradually increased the amounts of fertilizers (Ali et al. 2018). Overuse of nitrogen fertilizers and poor efficiency of fertilizer use, have caused significant residual quantities of nitrogen fertilizer to enter the soil and water bodies around farmlands, resulting in serious contamination of the ecosystem (Ali et al. 2018). Another factor that hinders agricultural production is also the regular occurrence of drought, posing major threats to global food security (Luo 2010). Therefore, the breeding and cultivation of new varieties of rice using China's proposed green super rice technology, with superior resistance to biotic and abiotic stresses, including water and nutrient quality, has become a key objective of improving rice to stabilize the productivity of rice and ensure food security.

THE GREEN SUPER RICE PROJECT

In 2005, a green super rice project was proposed by Chinese scientists to cultivate new rice varieties with different characteristics, including high fertilizer performance, water conservation, drought tolerance, and improved resistance to stress due to increasing resource scarcity, atmospheric pollution, and deterioration of ecological systems. The international cooperation project 'Green Super Rice for Resource-Poor Farmers of Africa and Asia' was sponsored by the Bill and Melinda Gates Foundation in 2009. In 2010, the Ministry of Science and Technology of China granted the project,' Breeding and Development of Green Super Rice,' with extended funding up to 2018 (Zhang et al. 2018).

MAJOR FOCAL POINTS OF THE GREEN SUPER RICE PROJECT

i. Production and development of green super rice breeding, through technological systems

ii. Establishment of entire genome selection platforms based on recent developments in worldwide research on rice functional genomics

iii. Production of new germplasm resources by pyramidizing green trait genes (Table 1)

iv. Breeding new green super rice cultivars with different combinations of green features

v. Techniques of high-yield production and field management for Green Super Rice

GREEN GENES IDENTIFIED FOR THE BREEDING OF NEW GSR VARIETIES

At present, 3000 genes have been cloned and dissected in rice affecting a broad variety of phenotypes, with tolerance to biotic stresses and abiotic stresses and high efficacy of nutrient usage, high yield and characteristics of good grain quality (Wing et al . 2018).These can be referred to as green genes. As the templates for green super rice breeding, these green genes were used (Table 1). Several databases and software programmes (Table 2) for rice genomic variations have been developed during the implementation of the Green Super Rice project. For gene functional analysis and rice breeding, such

Table 1. Genes related to green traits in green super rice

Green traits	Gene (Chromosome)	Function
Grain quality and yield	OsAAP6 (1), GL2/GS2/OsGRF4 (2), GNP1 (3), lgy3 (3), GL3.3/TGW3/qTGW3 (3), Chalk5 (5), GW5 (5), GW7/GL7 (7), GLW7/OsSPL13 (7), OsOTUB1 (8)	Change in Expression due to variations in promoter or premature termination or establishment of protein structure
Biotic stress resistance	Bsr-d1 (3), Bph3 (4), BPH6 (4), PigmR (6), IPA1 (8), STV11 (11), Xa10 (11), BPH9 (12)	Amino acid substitution or gene deletion or Change in Expression due to variations in promoter or premature termination
NUE (Nitrogen use efficiency)	DEP1 (9), NRT1.1B (10), GRF4 (2)	Amino acid substitutionor Change in Expression due to variations in promoter or premature termination
Abiotic stress resistance (Cold)	LGS1 (2), COLD1(4), CTB4a (4), bZIP73 (9), HAN1 (11)	Amino acid substitution or gene deletion or Change in Expression due to variations in promoter
Abiotic stress resistance (Heat)	OsTT1 (3)	Substitution of Amino acids

databases provide critical platforms for whole-genome selection (Yu et al., 2020).

CONCLUSION

In 2050, the world population is projected to reach nine billion. Rapid population growth requires a corresponding increase in the production of rice in a sustainable way, which in future decades will be a major challenge for global rice breeders. Green super rice varieties can maintain stable and higher yields with less inputs and higher resistance and recoverability features when facing the regular occurrence of severe climate change-induced stresses. Over the past decade experience has shown that the combination of green super rice varieties and corresponding improved growing techniques will lead to more efficient and higher yields, thereby reducing the use of pesticides and fertilizers in irrigated rice production areas by more than 30 percent as well as irrigation water by at least 30 percent (Yu et al ., 2020). In order to guide the green development of agriculture, green super rice can

Table 2. Databases available for green super rice breeding

Database or software programme available	Information	Web link or references
RFGB (Rice functional genomics and breeding database)	Informations regarding the variation in rice genomic	http://www.rmbre eding .cn/
Rice SNPs Database	Rice breeding by selecting genomic regions	http://varia tion.ic4r.org/
Marker-assisted molecular breeding platform for GSR	Comparing rice breeding materials	http://47.92.174.110
RiceVarMap v2.0	Integratingand annotation of the data sets available for rice genomic variations and genome-wide associationanalysis	http://ricev armap .ncpgr .cn/v2/
GS software gblup.jar	Identification of additive effect and dominance effects	Covarrubias-Pazaran et al., 2018

become a crucial factor and its objectives related to entire genome breeding strategies can provide trends or set examples for other crops to explore with suitable traits.

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VARIATION IN GI OF PROMISING EMS SAMBAMAHSURI MUTANTS

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Rice is the most important cereal crop of the world's population. Carbohydrates are the major source of energy in human diet. It is easily digestible, rich source of starch(contains two polysaccharides, amylose and amylopectin) and contains proteins(albumins, globulins, prolamines and glutelins etc.), lipids as major metabolites.& Minerals, vitamins and simple sugars are present in traces. The glycemic index (GI) concept was introduced by Jenkins et al. in 1981 for Diabetes patients. GI is defined as the area under the blood glucose response curve that is measured two hours after a fixed amount of available carbohydrate is consumed compared to a control food, which is either white bread or glucose.

Glucose, a monosaccharide, induces a large glycemic response and is often used as the reference food (GI of glucose is 100). Food factors influencing glycemic responses :Amount of carbohydrate, nature of carbohydrate or starch, amylose, amylopectin, starch-nutrient interaction , resistant starch, cooking/ food processing , degree of starch gelatinization, particle size , food form, cellular structure, other food components, fat and protein, dietary fibre, antinutrients, organic acids. The GI concept has been extended to also take into account the effect of the total amount of carbohydrate consumed. Thus glycemic load (GL), a product of GI and quantity of carbohydrate eaten provides an indication of glucose available for energy or storage following a carbohydrate containing meal. The time required for digestion of starch and release of glucose are the major physiological properties of starch. It has been used as the key clinical marker in characterizing starchy food and assessing dietary carbohydrate quality. GI is influenced primarily by the structure and composition of starch.

Although over thousand rice varieties were released so far, only few of them became mega varieties like Swarna, Samba mahsuri, IR-64, Pusa basmati-1121, etc. Most of the released varieties are high yielding, but, these mega varieties possess desirable or acceptable cooking quality. Among these, in non-aromatic rice category, Samba mahsuri is considered and well accepted across the various rice stake holders as best in cooking quality. Hence, many breeding programmes aimed to reach similar cooking quality by using Samba mahsuri as one of the parents or subjecting it to mutagenesis to get better yield with same cooking quality.

OBJECTIVE

Samba mahsuri is low in GI. Hence, GI was estimated in the promising EMS mutants to further categorize these mutants based on GI value.

METHODOLOGY

Samba Mahsuri is highly popular in Southern and Eastern parts of India. It holds highest acres in the states of Andhra Pradesh, Telangana, Tamilnadu and Karnataka. Consequently, around 10,000 EMS Samba Mahsuri mutant lines were developed by IIRR and CCMB. Of these, some(98) promising mutants were selected based on morphological as well as yield parameters and were screened for GI by widely followed invitro method(Goni et.al 1992). Compared with *invivo*, this invitro method is less costly, simple,easy, etc., and it can be used for initial screening of the varieties.

RESULTS

Among the 98 **promising lines** , 43 were low in GI; only two lines were high in GI and the remaining 53 were medium in GI; and it ranges from 46.23

(lowest) to72.27 (highest).GI is influenced primarily by the structure and composition of starch. A GI classification system is in common use in which foods are categorized as having low (0-55), medium (55–69) or high GI (70^) (BrandMiller et al., 2003a).Starch hydrolysis is the key factor in the estimation. The rice kernel Starch is divided into three fractions based on the enzymatic hydrolysis, readily digestible (RDS), slowly digestible (SDS), and resistant starch (RS) (Englyst and Hudson, 1996).Mutation in starch biosynthetic enzymes produce altered amylopectin chain length distribution in rice endosperm(Fujita et al., 2007) and the suppression of both *SBEIIb* and *SBEI* in rice led to high AC (Zhu et al., 2012). Hence, reasons for the variation in GI in mutant lines in comparison with Samba mahsuri is underway.

Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-15

FUNCTIONAL GENOMICS STUDY IN RICE

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Rice (Oryza *sativa*) has been well known as a model for plant functional genomics research due to its petite genome size. The accurate genome sequences were characterized by co-linearity with the sequences of other distantly related cereal crops, high-efficiency transformation technology, and abundant germplasm resources (Jiang *et al*., 2012). In the last few decades, remarkable advancement has been achieved in rice functional genomics research, such as: (1) construction of resource platforms for high-throughput gene identification; (2) functional genomics analysis of gene sequences for important agronomic traits and biological processes; and (3) development of novel tools for categorization of desirable genes.

Our aim is to focus on the main improvement achieved during the last 10 years as well as present our prospects for future studies of rice functional genomics research and possible challenges in applying the findings to the development of green super rice (GSR).

RECENT DEVELOPMENT OF PLATFORMS FOR RICE FUNCTIONAL GENOMICS RESEARCH

Many of the functional genomics platforms have been established in the past decade, as the completion of whole-genome sequencing in rice, together with collection of germplasm resources and generation of mutant libraries, full-length cDNA libraries, gene expression microarrays, and RNA-sequencing (RNA-seq) technologies for expression profiling. Vast platforms of proteomics, metabolomics, and phenomics have also been gradually established and improved, and corresponding platforms of bioinformatics analysis and databases have also been set up in rice.

GENE EXPRESSION PROFILES

The tool Knowledge-Based Oryza Molecular Biological Encyclopedia (KOME) database collects information for about 38, 000 full-length cDNAs of *japonica* cv. Nipponbare. The Rice *indica* cDNA Database (RICD) database contains 10, 081 and 12, 727 full-length cDNA sequences from Minghui 63 and Gaunglui 4, respectively. Affymetrix GeneChip Rice Genome Array was used for the analyses of specific expression profiles in various tissues under different stress conditions in elite hybrid rice Shanyou 63 and its parents Zhenshan 97 and Minghui 63, which were in the information platform of the Collection of Rice Expression Profiles (CREP).

HIGH-THROUGHPUT PHENOTYPING FACILITY

CropDesign (Belgium) developed the TraitMill platform, which can be used to measure the Quantitative traits. LemnaTec Scanalyzer 3D suits best for fully automatic analysis of plant phenotypes. The Australian Plant Phenomics Facility has fruitfully applied this technology in the studies of salt stress, drought tolerance, toxicity (boron) tolerance , as well as modeling and prediction of crop yield and root development. In 2011, KeyGene (Netherlands) and LemnaTec (Germany) announced the initiation of commercial operation of a plant phenomics platform (PhenoFab), which has been officially useful in commercial crop breeding.

EPIGENOMICS

Epigenomes are a collection of whole-genome chromatin profiles of cells under specific internal and environmental conditions, such as DNA methylation, histone modification, and arrangement of nucleosomes on genomic DNA. Compared with Arabidopsis, the features of DNA methylation in rice include the following. (1) The average methylation levels of CG, CHG, and CHH and the total cytosine methylation density in rice genome are much higher. (2) The methylations of CG and CHG occur mainly in the heterochromatin regions, which modify the transposable elements and related genes.

METABOLOMICS

In recent years, with the development of metabolomics analytical technologies, particularly the advance in metabolic profiling based on mass spectra and magnetic resonance imaging, the research fields of metabolomics have been continuously expanded. Progress has been made in the application of plant metabolomics to the identification of functional genes, dissection of metabolic pathways, and genetic analysis of natural variations through integration with other omics technologies. The metabolomic analysis of samples from 210 RILs derived from a cross between two elite indica rice varieties, Zhenshan 97 and Minghui 63, and detected approximately 1000 metabolites, which were resolved to over 2800 metabolic QTLs.

PROTEOMICS

Proteomics research focuses on protein identification, quantification, activity, stability, localization, and function, which play essential roles in cell signaling events. In the last decade great advances have been achieved in rice proteomics, which provide comprehensive snapshots on the understanding of rice development, stress tolerance, organelle, secretome, and protein post-translational modification (PTM). Proteomics studies in rice have been performed mostly using gel-based (1DE, 2DE, and 2DIGE) and gel-free (LC-MS/MS or MudPIT) approaches. Scientists reviewed and summarized the progress in rice proteomics studies from 2010 to 2013, with major focus on rice under diverse abiotic and biotic stress conditions.

BIOINFORMATICS AND DATASETS IN RICE

Along with the advances in rice functional genomics research and the widespread application of various high-throughput technologies, there have been explosive increases in various kinds of omics datasets. A large number of bioinformatics databases have been constructed in rice, including the databases of genomes, transcriptomes, proteomes, and metabolomes.

NEWLY DEVELOPED TOOLS FOR GENE IDENTIFICATION

1. Genome-Editing Technology through use of CRISPR/Cas9
2. Genome-wide Association Studies

FUNCTIONAL GENOMICS OF IMPORTANT AGRONOMIC TRAITS

Functional genomic understanding of an agronomic trait refers to characterization of the genes (including non-coding sequences) and their regulatory networks, which collectively determine the formation and development of the trait. The formation of any trait involves a large array of genes, and the majority of the genes that participate in many processes thus affect the development of many traits (or pleiotropic effects). Data and literature accumulated to date have already clearly depicted such a ‘‘net-like’’ structure between genes and traits.

CONCLUSION

The knowledge, genes, germplasms, and genomic data obtained presently are already enough to lead a revolutionary change in strategies and technologies in rice breeding, which can be termed ''designed genomic breeding.'' Such breeding may include the following components:

1) Specifications of the traits (yield, quality, resistances to biotic and abiotic stresses, NUE) for cultivars adaptive to specific cropping systems, especially emphasizing resource saving and environment-friendly agriculture for green development;

2) Lists of the genes and germplasms for the traits;

3) Technologies for whole-genome selection and gene-specific introgression;

4) Breeding programs for implementation. The progress in rice research may also provide models for other crops, thus transforming the norm of crop breeding.

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MARKER ASSISTED INTROGRESSION OF SEMI-DWARFING GENE IN *KATARNI* RICE

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'Katarni' is geographical indication tagged scented rice landrace of Bihar. However, it is low yielder (25-30 Qtls/ha) due to its tall and lodging tendency at the time maturity. Marker assisted introgression of semi-dwarfing (*sd1*) gene from rice varietiesRajendra Sweta and BPT5204 into Katarni was attempted and present study is framed for assessing the background recovery in the backcross lines.

METHODOLOGY

Assessment of background recovery in133 BC_4F_1plants of Katarni x R.Sweta and 80 BC_3F_1plants of Katarni x BPT5204 was performed.Foreground selection was performed using *sd1* gene specific primer (Speilmeyer*et al.*, 2002) while recombinant and background selection was performed using parental polymorphic SSR markers. Presence of aroma gene in the selected progenies was confirmed through gene specific primer for *badh2* gene (Bradbury *et al.*, 2005).

RESULTS

Average Recurrent Parent Genome (RPG) % recovery of BC_4F_1 plants in Katarni x R. Sweta was 90.26% with a maximum recovery of 94.68% in plant number BCKRS-79. In case of BC_3F_1 plants of Katarni x BPT5204, the average RPG % was 91.89 with maximum recovery of 94.44% in BCKBT-50.Phenotypic performances of the plant number BCKRS-79 and BCKBPT-50 were in congruity with the results of background selection. Except plant height, the morphological features of both these plants were similar to recipient parent Katarni (Table 1). Evaluation of yield of selected semi-dwarf, early maturity aromatic backcross derivative of Katarni rice is being done through multi location testing.

CONCLUSION

Previous attempts through conventional breeding to reduce the height of Katarni and to make it

Table 1. Phenotypic performance of the plants identified through background markers

Plant / parent	Plant height (cm)	Days of flowering	1000 grain wt. (gm)	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Leaf aroma score
Katarni	164.90	125	12.50	7.40	1.49	4.99	3
R.Sweta	110.20	109	12.00	7.92	1.51	5.19	0
BPT5204	98.20	112	14,50	7.89	1.63	4.77	0
BCKRS-79	128	121	12.50	7.17	1.64	4.37	2
BCKBPT-50	128	122	13.75	8.57	1.76	4.86	3

non-lodging with high yielding ability were failed due loss of its various exquisite quality traits. In the present study, the functional molecular markers of aroma and semi-dwarfism gene had provided a convenient way to screen the progenies and background selection increased the accuracy and reduced the duration of the breeding process to improve the traditional Katarni rice for yeild and various agronomic traits.

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IRC/TM-1/PP-17

GENITIC DIVERSITY ANALYSIS OF RICE (*ORYZA SATIVA* L.) GENOTYPES FOR YIELD ATTRIBUTING CHARASTERS

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Rice is the main staple food for 50% population of the world and its production has to be increased to 880 million tonnes by 2025 to meet the global demand. But the area under rice cultivation cannot be increased due to urbanization and population growth, breeding of rice varieties with high yielding ability, tolerance to biotic and abiotic stresses and adoption to varied climatic conditions is need of the hour. Development of novel varieties through hybridization programme depends on the selection of parents from the divergent germplasm which are well characterized.

The present investigation was taken up with the objective of studying genetic divergence and quantitative characterization of fifty germplasm lines of rice.

METHODOLOGY

Fifty rice genotypes collected from different sources were raised at Regional Agriculture Research Station Nandyal during kharif 2019 to identify diverse genotypes. The experiment was laid in randomize block design with three replications. The genotypes were raised in a row length of 5 meters in 6 rows with a spacing of 30 cm X 20cm and recommended agronomic practices were followed. They were evaluated for six yield and yield attributing characters like days to 50% flowering, plant height, panicle length, number of productive tillers per plant, test weight and grain yield per plant. Ten random plants per genotype in each replication were selected and tagged to record observations. The genetic distance between the genotypes was worked out using Mahalnbobis D^2 analysis (1936) and grouping of varieties into clusters was done following the Tocher's method (Rao, 1952). This is the most effective method of quantifying the degree of genetic divergence among the genotypes taken for the study.

RESULTS

Analysis of variance showed significant differences for all the six character studied among 50 genotypes based on D^2 analysis. 50 genotypes were divided into seven clusters (Table 1). Maximum number of genotypes (33 genotypes) were grouped in cluster I followed by cluster II with seven genotypes. Cluster IV have four genotypes followed by cluster VI with three genotypes while the remaining clusters were represented by one genotype each. Clustering pattern represented that genotypes collected from the same geographic origin were distributed in different clusters (Vennila *et al*.2011).

Table 1. Clustering pattern of 50 genotypes.

Cluster	No. of genotypes	Name of genotypes
I	33	MTU 2077,MTU 1064, MTU 1075, MTU 4850, Tellahamsa, Indursamba,JGL 17004,MTU 3626, JGL 11727, AdityaNLR 40024, WGL 678, Tulasi,NLR 33057, Vardhan ,Vasumathi,NLR 34449,NLR 3041, NLR 145, NLR 3358, NLR 34242, NLR 33359, NLR 33641, NLR 33671,NLR 30491, MAS 26, NLR 4001, Taramathi, NLR 40065,RNR 2354, RNR 15048, NLR 2064,NLR 4002, NLR 3217
II	7	MTU 1061, C-148,NLR 9674, NLR 28600,NLR 27999,NLR 33892,NLR 33365
III	1	Shireen
IV	4	Varsha, NLR 40065, Triguna, Govind
V	1	NLR 28523
VI	3	Kalabhatty, Rakthashali, Kalakar
VII	1	Swarnasub

Table 2. Intra and inter cluster average of yield traits in 50 rice genotypes.

	I	II	III	IV	V	VI	VII
I	233.45	915.93	469.19	614.8	518.71	446.32	448.31
II		231.87	1755.53	1028.96	447.18	1121.59	708.31
III			0.00	1378.44	787.87	458.97	1056.94
IV				312.93	813.54	676.32	958.71
V					0.00	345.81	924.45
VI						210.34	1163.15
VII							0.00

The inter and intra cluster distances are presented in Table 2. Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among genotypes. The maximum inter cluster distance was observed between cluster II and cluster III (1755.53) followed by cluster III and cluster IV (1378.44), cluster VI and cluster VII (1163.15), cluster III and cluster VII (1056.94) and cluster II and cluster IV (1028.96) indicating wider genetic diversity of the genotypes between the groups. The hybrids developed by selecting parents from these groups would produce high variable segregating populations with improved grain yield through transgressive breeding. The minimum inter cluster distance was recorded between cluster V and cluster VI (345.81) and cluster I and cluster VI (446.32) indicating the genotypes in these cluster are genetically very close and hence hybridization between these groups is not desirable.

The maximum intra cluster distance was observed in cluster IV (312.93) followed by cluster II (231.87). Hence selection within these clusters maybe exercised based on the highest areas of desirable traits by making use the method of improvement through inter varietal hybridization. Minimum intra cluster distance was observed for clusters III (0.00), V (0.00) and VII (0.00). Similar results reported by Kumari *et al* (2016).

The cluster means presented in Table 3 revealed that cluster IV with four genotypes recorded highest mean value for panicle length (35.58 cm) , number of productive tillers per plant (47) , test weight (21.42g) and grain yield per plant (106.83g). Cluster II and cluster VII were characterized by recording more number of days to percent flowering (125 and 120 days respectively) and cluster V with more plant height (159.67 cm) followed by cluster II (143.52). Early flowering genotypes were grouped in cluster III (83 days) and cluster VI (90 days) and tall genotypes in cluster V (159.67 cm) and cluster II (143.52 cm). Cluster III has recorded minimum values for number of days to 50 percent flowering (83 days), panicle length (22 cm), number of productive tillers per plant (21) , test weight (12g) and grain yield per plant (23g).

None of the clusters contained the genotypes with all the desirable characters which can be directly selected and utilized. All the minimum and maximum

Table 3. Cluster means of different yield characters in 50 rice genotypes.

Cluster	Days to 50% flowering	Plant height	Panicle length	Productive tillers	Test weight (g)	Yield /plant (g)
I	100.82	99.03	24.23	31.30	16.7	49.83
II	125.14	143.52	24.71	27.33	15.24	52.43
III	83.33	105.0	22.00	20.67	12.00	23.0
IV	105.42	109.58	35.58	46.92	21.42	106.83
V	103.33	159.67	26.33	30.33	16.67	43.33
VI	90.33	136.33	27.78	41.44	14.22	67.89
VII	120.0	71.67	21.33	22.00	14.33	34.00

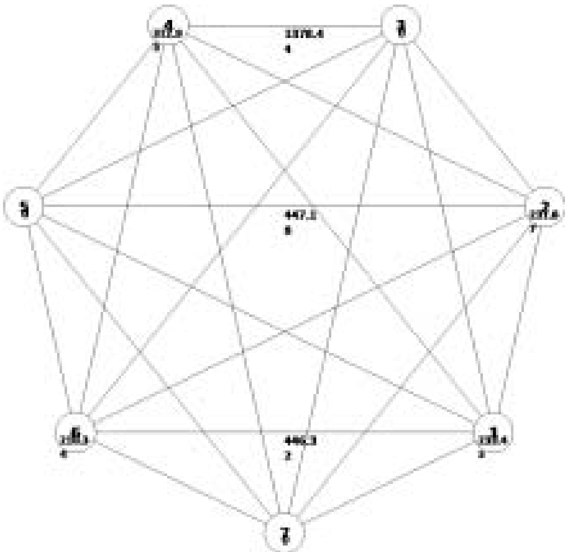

Fig 1 : Mahlnbobis Euclidean^2 Distances of genotype clusters

cluster mean values were distributed in relatively distinct clusters. However the cluster IV recorded relatively desirable mean values for panicle length (35.58 cm) ,maximum number of productive tillers per plant (47) , test weight (21.42g) and grain yield per plant (106.83g). Similar results were reported by Bhanumurthy et al (2010) indicating hybridization between divergent cluster genotypes is necessary to develop desirable genotypes. Based on the performance of the genotypes within the cluster better genotypes can be neither directly selected nor used as potential parents in hybridization programme .

Table 4. Percentage of contribution of each character towards total divergence.

Character	No.of first rank	Contribution (%)
Days to 50% flowering	523	42.69
Plant height	281	22.94
Panicle length	2	0.16
Productive tillers	5	0.41
Test weight (g)	149	12.16
Yield /plant (g)	265	21.63

Percent contribution of each character to total divergence is presented in Table 4. Among six traits number of days to 50 percent flowering contributed maximum divergence (42.69%) followed by plant height (22.94%), yield per plant (21.63%) and test weight (12.16%). The minimum percentage of contribution was by number of productive tillers per plant (0.41%) followed by panicle length (0.16%). The traits like number of days to 50 percent flowering, plant height , yield per plant contributed 87.26% toward total divergence. Hence these traits should be given importance in hybridization and selection in segregating populations to develop novel genotypes.

CONCLUSION:

The hybridization between parents selected from cluster II and cluster III, cluster III and cluster IV, cluster VI and cluster VII, cluster III and cluster VII and cluster II and cluster IV with the importance to traits like number of days to 50 percent flowering, plant height , yield per plant in the segregating populations can be suggested for development of better varieties from these fifty genotypes.

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IRC/TM-1/PP-18

MARKER ASSISTED PYRAMIDING OF MAJOR ABIOTIC STRESSES OF COASTAL RICE AREAS

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Rice is important staple food crop for south Asia. Rice productivity has to be improved enormously to meet demands of ever growing population with shrinking resources. Occurrence of transient flash floods to prolonged stagnant flooding of rice crop from germination to harvesting stage coupled with lodging of the crop at reproductive phase due to unpredicted cyclonic rains in monsoon is causing drastic yield reduction in coastal areas. Simultaneously increase in coastal salinity is another abiotic stress dampening the rice productivity. Large scale adoption of direct seeding is limited during wet season due to lack of anaerobic germination in the coastal ecosystem. Precise molecular breeding for major biotic stresses of coastal rice areas would enhance the productivity under changed climatic conditions. Present study aimed to pyramid major abioitc stresses *viz*., submergence, lodging resistance, salinity and anaerobic germination in the back ground of Swarnasub1 using marker assisted selection.

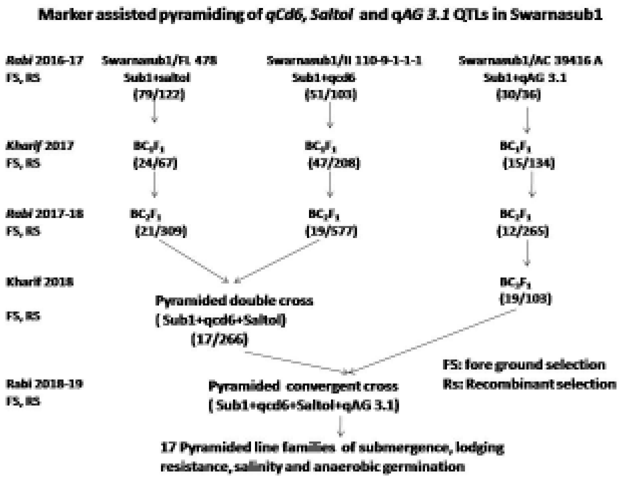
METHODOLOGY

Marker assisted pyramiding of major abioitc stresses in the background of Swarnasub1 was carried out using II110-9-1-1-1-1 as donor for lodging resistance (Girija Rani *et al.* 2019) , FL478 for Saltol , AC 39416A for anaerobic germination for three weeks (Sandya *et al.* 2017) at Regional Agricultural Research Station(RARS), Maruteru of Acharya NG Ranga Agricultural University (ANGRAU) from the years 2016 to 2018. Two successive back crosses were performed using Swarnasub1 as female parent and II110-9-1-1-1-1 for *qCd6* for culm diameter (Girija Rani *et al* 2019) with foreground (RM 20557) and recombinant markers (RM 340, RM 30) on chromosome 6 for two trait Introgressed Lines (ILs) of submergence and lodging resistance. Simultaneously two cycles of back crosses of swarnasub1/ FL 478 was generated for pyramiding of submergence and salt tolerance using fore ground (RM 10694) and recombinant markers (RM 10793, AP 3206) on chromosome 1. Whereas three cycles of back crosses were adopted for incorporation of identified QTL *qAG3.1* for anaerobic germination from AC39416A at RARS, Maruteru for getting two trait ILs of submergence and anaerobic germination using fore ground marker (RM15561) and recombinant markers (RM 15576, RM15441) on chromosome 3. Three traits (submergence, lodging resistance and salinity) pyramided lines were developed by crossing BC$_2$F$_1$ two trait ILs of *sub1+qCd6* with two trait ILs of BC$_2$F$_1$ of *sub1+saltol*. Three trait pyramided line (*Sub1+qCd6+saltol*) F$_1$ confirmed line were crossed with BC$_3$F$_1$ lines of *Sub1+qAG 3.1* to get final targeted traits pyramided lines of submergence, lodging resistance, salinity and anaerobic germination. In each generation, fore ground and recombinant markers for targeted traits were used apart from *Sub1* foreground marker sub1BC2 and recombinant markers (RM 8303, RM 23887) for Swarnanasub1/ II110-9-1-1-1 and Swarnasub1/FL 478 and RM 23788 as fore ground marker and RM 316, RM23917 as recombinant markers for back cross of Swarnasub1/AC 39416A. All the genotyping work is performed as per Girija Rani *et al* 2019 and electrophoresis was carried out using 3% high resolution metaphor Agarose.

RESULTS

The details of development of pyramided lines of major abioitc stresses submergence, lodging resistance, salinity and anaerobic germination was depicted in the following schematic representation.

For the development of two trait ILs of submergence and salinity, 79 positive plants conferring *Sub1+Saltol* were identified at F_1 generation out of 122 plants genotyped in Rabi 2016. Generated sixty seven BC_1F_1 plants of Swarnasub1/FL 478 were genotyped to identify 24 positive plants for further development of BC_2F_1 using trait specific fore ground and recombinant markers and finally identified 21 positive two trait ILs of submergence and salinity out of 309 plants at BC_2F_1 generation in 2017 for further use in pyramided double cross. Submergence and lodging resistant ILs were developed by selection of 51 positive plants for *Sub1* +*Cd6* at F_1 generation of Swarnasub1/II110-9-1-1-1-1 among 103 plants tested using trait specific fore ground and recombinant markers in 2016. Generated 208 BC_1F_1 plants were screened using fore ground and recombinant markers of *Sub1* and *qCd6* and identified 47 positive plants for further use in the development of second back cross during kharif 2017. Identified 19 confirmed ILs of submergence and lodging resistance out of 577 plants by fore ground and recombinant selection at BC_2F_1 generation during Rabi 2017. Three trait pyramided double cross 266 plants were generated by crossing 21 two trait ILs of *Sub1+Saltol* as female with 19 two trait ILs of *Sub1+qCd6* as male during Rabi 2017.



Simultaneously 30 positive plants of *Sub1+qAG3.1* were identified at F_1 in 2016 and generated 134 BC_1F_1 plants of Swarnasub1/ AC39416A for the development of two trait ILs of submergence and anaerobic germination. Fore ground and recombinant selection resulted in identification of 15 confirmed lines of *Sub1+ qAG3.1 at* BC_1F_1 generation for further use in development of 265 BC_2F_1 plants during kahrif 2017. Generated 103 BC_3F_1 plants by using 12 positive BC_2F_1 plants during Rabi 2017.

To converge all the four targeted traits viz., submergence , lodging resistance, salinity and anaerobic germination, 17 identified three trait ILs of *Sub1+qCd6+ Saltol* in kharif 2018 were used as female plants and 19 two trait ILs of *Sub1+ qAG3.1 at* BC_3F_1 generation as male plants. Finally developed 17 marker assisted pyramided lines (PILs) of *Sub1+qCd6+ Saltol+qAG3.1* for submergence , lodging resistance, salinity and anaerobic germination to combat adverse effects of climate changed condition out of 548 plants genotyped by respective target trait fore ground and recombinant selection.

CONCLUSION

The developed 17 marker assisted pyramided introgressed lines of submergence, salinity , lodging resistance and anaerobic germination would serve as climate resilient lines in coastal ecosystem after thorough phenotypic evaluation for yield under targeted environments. Nonlodging high yielding submergence and salt tolerant rice varieties having three weeks anaerobic germination would help the farmers in realizing sustained yields by overcoming labour shortage.

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IRC/TM-1/PP-19

TROMBAY KARJAT KOLAM- FINE RICE VARIETY

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The rice cultivation in Konkan region is carried out on three types of soils classified as upland, midland and lowland requiring early, midlate and late varieties respectively. The proportion of area under early, midlate and late varieties is about 40, 40 and 20 percent respectively. There is a need for fine and midlate duration rice variety for *Kharif* season in Konkan region of Maharashtra state with higher yield. Accordingly, the efforts were made to develop and release the Trombay Karjat Kolamto fulfill the requirement of fine grain type, midlate duration, high yielding rice variety for the farmers of the Konkan region of Maharashtra state collaboration with BARC, Mumbai.

OBJECTIVE:

In the peri urban areas of Maharashtra there is a huge demand of fine rice to evolve midlate duration, dwarf stature, non-lodging, high yielding, short slender grain type rice variety

METHODOLOGY:

Pusa Basmati1 mutant (early duration) was crossed with Pusa Basmati1 (midlate duration) and midlate duration, dwarf stature, non-lodging, high yielding, short slender grain type rice variety Trombay KarjatKolam (IET 27100) is evolved through pedigree method followed by selection

RESULT:

The rice variety Trombay Karjat Kolam (IET 27000) exhibited 30.50%, 20.7% and 18.95% higher grain yield over the checks in station, state and adaptive trials respectively. It showed excellent milling (73.7%), head rice recovery (67.98%) andacceptable amylose content (23.09%) with translucent grains and excellent cooking quality. It has been observed moderately resistant to stem borer with an average yield of 4.0 to 4.5 t/ha. Therefore, this rice variety is released for Konkan region of Maharashtra state.

CONCLUSION:

Trombay Karjat Kolam high yielding rice variety having dwarf stature with short slender grain type with good grain quality, mid late duration is release for commercial cultivation in Konkan region of Maharashtra State has been notified vide S.O3482(E) 20, dt 7th October 2020

REFERENCE:

Sanjeev Singh (2006)., Gamma rays induced mutations in Basmati rice, Indian J. Genet., 66(2): 143-144

Maharashtra State Rice Workshop 2017 pp : 21& 70

IIRR Annual Progress report 2017 Vol.1- Varietal Improvement pp. 1.386 to 1.390

ILLUSTRATION:

Trombay Karjat Kolam (BARCKKV 13) IET 27000is release for commercial cultivation and notified vide S.O3482(E) 20, dt 7th October 2020

Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-20

KARJAT SHATABDI –RICE VARIETY FOR SCENTED BEATEN RICE (*POHA*)

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Rice (Oryza sativa L.) is the world's most important crop and staple food for more than half of the population. It continues to hold the key to sustain food security in India for more than half of the total population. The local rice cultivar "Botvel" is popular for beaten rice. It is tall and long duration. There is need to develop high yielding, dwarf and short bold grain type rice variety suitable for beaten rice (Poha). Accordingly, the efforts were made to develop rice variety to fulfill the requirement of Konkan region farmers. Induction of mutations with radiation has been the most frequently used method for directly developed mutant varieties. The prime strategy in mutation-based breeding has been to upgrade the well-adapted plant varieties by altering one or two major traits, which improve their productivity.

OBJECTIVE:

To develop high yielding, dwarf and short bold grain type rice variety suitable for beaten rice (Poha).

METHODOLOGY:

The traditional landrace of rice viz., Botvel was subjected to gamma irradiation at different doses (50 Kr,100Kr, 150Kr and 200Kr). The M2 seeds collected from M1 were space planted to evaluate for desirable traits. A total of 350 plants were selected based on plant type and productivity per se from 50Kr dose of irradiation in Botvel M2 population and were advanced to M3. These M3 families were evaluated for yield parameters and further selected BM 4 stable population was evaluated in Station and multilocation trialsalong with check.

RESULT:

The rice variety Karjat Shatabdihas translucent grains and excellent cooking qualityfor beaten rice (Poha) with scent, is dwarf in stature and non-lodging, 125 to 130 days to maturity (Midlate duration), having Short bold grain typeexhibited 51.53 %, 22.5% and 16.22 % higher grain yield over the checks in station, state and adaptive trials respectively. It showed excellent milling (67.09%), head rice recovery (63.56%) andacceptable amylose content (20.08%) It has been observed Moderately resistant to stem borer and bacterial leaf blight and Leaf blastwith an average yield of 3.8 to 4.0 t/ha. Therefore, this rice variety is released for beaten rice (Poha) with scentfor Konkan region of Maharashtra state

CONCLUSION:

Karjat Shatabdi medium duration, dwarf stature, short bold grain type high yielding rice variety suitable for beaten rice (Poha) with scentis recommended for cultivation in Konkan region of Maharashtra State

REFERENCE:

Singh, Sanjeev, Richharia A. K. and Joshi A. K. 1998. An assessment of gamma ray induced mutations in rice (Oryza sativa L.). Indian J. Genet., 58: 455-463.

Maharashtra State Rice Workshop 2015 pp : 158 and 2016 pp : 138

ILLUSTRATION:

Karjat Shatabdi rice variety suitable for beaten rice (Poha) with scentis recommended by Jt. AGRESCO 2019

IRC/TM-1/PP-21

BPT 2841- A HIGH YIELDING BIOFORTIFIED BLACK RICE GENOTYPE WITH EXCELLENT COOKING QUALITY

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Rice (*Oryza sativa* L.) is the predominant staple food crop for more than half of the world's population and is playing a pivotal role in providing human nutrition, energy supply and food security of Asian countries. Change in income levels and self sufficiency induced rice availability for consumption has brought a shift in the consumer as well as market preferences for better rice grain quality. Although, white rice is the most widely consumed rice, pigmented rice is considered as enriched rice for taste and health benefits due to the presence of anthocyanin. The brown rice possess higher concentration of Total Phenol Content (TPC) and antioxidant activity than white rice in both pigmented and non-pigmented varieties (Isnaini *et al.*, 2019). Hence, consumption of whole grain has a major role for the overall health improvement and management of chronic disorders. Colored rice possess unique color, flavor therefore they are used as an ingradient in many dishes and pigmented rice is becoming popular among health-conscious food consumers for its antioxidants mainly because it is a good source of bioactive compounds.

Due to increased health consciousness and demand for colored rice, farmers in Andhra Pradesh and Telangana states are growing black rice varieties like Burma black, Kalabhatt and Chakhao amudi which are popular in North eastern states of India. Eventhough, all these varieties are popular for their nutritional properties, these black glutinous rice is mainly used for the preparation of sweet snacks and desserts in Asia and is not suitable for consumption as plain cooked rice. Especially in South India, the consumers of Andhra Pradesh, Telangana, Karnataka and Tamilnadu prefer to eat varieties like Samba Mahsuri, Telangana Sona and White Ponni *etc.*, which possess medium slender grain with excellent cooking quality *i.e.* soft and flaky texture of cooked rice. In addition, all the traditional black rice varieties are tall in stature, low yielding, possess bold grain and had low amylose content with poor cooking quality. Hence, for the development of high yielding colored rice genotypes possessing medium slender grain type coupled with good cooking quality, a breeding programme was initiated at Agril. Research Station, Bapatla by utilizing the breeding material supplied by ICAR-IIRR, Hyderabad.

BPT 2841 is a derivative of a three way cross between MTU 7029/IRGC 18195 and MTU 1081 and matures in 130-135 days during kharif season & 125 days in rabi season. It is a semi-dwarf genotype with 100-110cm plant height and has a yield potential of 5.5 to 6.0 t/ha. It also exhibited moderate resistance to blast and BPH. Unlike other traditional black rice varieties, BPT 2841 has straw colour hull and the unpolished rice is black. BPT 2841 possess medium slender grain with a test weight of 14.0 to 14.5g and also recorded more than 60% head rice recovery. Alkali spreading value (ASV) and amylose content (AC) are the important cooking quality traits which determine the texture of cooked rice. Li *et al.*, (2016) also stated that the amylose content of the rice variety has culinary implications because it has an influence on the organoleptic qualities of rice once cooked. BPT 2841 recorded intermediate amylose content (23.5%) and alkali spreading value (4.0), hence the cooked rice will be soft and flaky. Majority of desi black rice varieties possess low amylose content, hence may not be included in daily diet, particularly in South India where rice consumers prefer soft and flaky texture of cooked rice.

The unpolished rice of BPT 2841 was utilized for analysis of nutritional and functional properties by following standard procedures at Post Harvest Technology Centre, Bapatla (Table 1). BPT 2841 recorded 11.08% protein content whereas BPT 5204 brown rice recorded 8.0% protein content. The total phenol content and total antioxidant activity of BPT 2841 are much higher when compared with BPT 5204. The antioxidant activities of pigmented rice were compared with those of non pigmented rice in several studies and the results demonstrated that the extracts from pigmented rice displayed higher antioxidant activity than the non pigmented rice (Finocchiaro *et al*.,2007). It is always better to consume the pigmented rice as whole grain to get the maximum nutrients available. If the pigmented/non pigmented paddy grain is slightly polished (1-2%), then it will be cooked easily as normal polished rice which increases the palatability also and the consumers will get the available nutrients without much loss. The analysis of antioxidant activity was also carried out on 5% polished rice of BPT 2841 which recorded 90.19 mg/100g as compared to 39.0 mg/100g antioxidant activity in non pigmented unpolished BPT 5204. Due to it’s high yield potential, nutritional properties and excellent cooking quality, BPT 2841 was recommended for minikit testing in farmer’s fields in Andhra Pradesh state. BPT 2841 completed first year of minikit testing and the results are quite encouraging. Farmers are very much interested and there is huge demand for the seed of BPT 2841 not only in Andhra Pradesh but also from the farmers of Telangana and Karnataka states. More research and publicity on the relationship between antioxidants and disease risk mechanisms would increase consumption of the anthocyanin rich pigmented rice in near future

Table 1: Physico-chemical and bio-chemical quality parameters of BPT 2841

Quality parameter	BPT 2841	BPT 5204
Hulling(%)	76.8	75.8
Milling (%)	66.6	66.6
Head Rice Recovery (%)	62.1	63.4
Kernel length (mm)	4.72	4.91
Kernel breadth (mm)	1.80	1.81
Length/breadth ratio	2.56	2.71
Amylose content (%)	23.5	22.9
Alkali spreading value	4.0	5.0
Gel consistency (mm)	22	22
Total phenols in unpolished rice (mg/100g)	90.52	59.4
Antioxidant activity in unpolished rice (mg/100g)	110.52	39.0
Antioxidant activity in 5% polished rice (mg/100g)	90.19	-
Protein content in unpolished rice	11.02	8.0
Zinc content in unpolished rice	24.3	18.8
Fe content in unpolished rice	15.6	8.7

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IRC/TM-1/PP-22

CHARACTERIZATION OF COLORED RICE GENOTYPES FOR NUTRITIONAL TRAITS AND FUNCTIONAL PROPERTIES

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Rice is the only cereal cooked and consumed as a whole grain and quality considerations are much more important than any other food crops. In addition to common white rice varieties, there are some speciality rices such as pigmented rice (black also known as purple, brown and red) and the colors in rice are due to the deposition of large amounts of anthocyanin or proanthocyanidin pigment in the rice coat. The commonly consumed white rice is a highly refined staple cereal, which is devoid of almost all minerals and nutrients. The pigmented rice, enriched with anthocyanin is known for it's taste & health benefits and are being consumed since immemorial in most of South Asian countries. Recently, colored rice varieties have received greater attention from consumers for their higher bioactive compounds, antioxidant activity, anti-inflammatory and other health benefits associated with them (Alves *et al.*,2016). Eventhough, many studies elucidating the variability and associations among physical and chemical quality parameters were reported earlier, the studies on biochemical quality parameters of rice and their relationship with other quality traits are meager. Hence, an attempt was made in the present investigation to study the variability and inter-relationships among nutritional traits and phenolic compounds.

METHODOLOGY

The experimental material consisted of 9 black pericarp colored rice genotypes (BPT 2841, BPT 2848, BPT 3136, BPT 3341, BPT 3144, BPT 3145, BPT 3137, BPT 3173, BPT 3344) 6 red pericarp colored genotypes (BPT 2858, BPT 3111, BPT 3137, BPT 3141, BPT 3143 and BPT 3178) and one non pigmented popular rice variety BPT 5204 as control. All these genotypes were grown in an experiment conducted at ARS, Bapatla in randomized block design with 3 replications during kharif,2019. Each genotype was grown in 3.0 m^2 plot with a spacing of 20x15cm. After harvesting, the paddy was sun-dried to a moisture content of about 12% stored in an air-tight plastic bag at room temperature for three months and then stored at 4° C in the dark before analysis. Each sample per genotype per replication (three replicates per genotype) was dehusked and the unpolished rice was utilized for estimation of 13 physico-chemical (kernel length, kernel breadth, L/B ratio, water uptake, volume expansion ratio, amylose content, alkali spreading value), nutritional (protein content, iron and zinc content) and bio-chemical quality parameters (total phenol content, flavonoid content, anti-oxidant activity) by following standard procedures. The mean data was utilized for calculation of GCV, PCV, heritability, genetic advance percent over mean and the association between nutritional and functional properties by adopting standard statistical analysis.

RESULTS

All the colored rice genotypes used in the present study flowered earlier when compared with the non pigmented control variety BPT 5204 and recorded 120-135 days duration. With medium slender grain type, all the colored rice genotypes under study recorded 5.5 -6.5 t/ha grain yield. Alkali spreading value (ASV) and amylose content (AC) are the important cooking quality traits which determine the texture of cooked rice. Among the genotypes under study, BPT 2841, BPT 2848, BPT 2858, BPT 3136, BPT 3140 and BPT 3144 manifested intermediate alkali spreading value and amylose content, hence the cooked rice of all these genotypes will be soft and flaky which is mostly preferred by the consumers. In the present study, the protein content ranged from 8.0% to 14.2% and the black rice genotypes *viz.*, BPT 3136, BPT 3141, BPT 3143, BPT 3346, BPT 3144 and BPT 2848 recorded >10% protein content. Among red pericarp colored genotypes, BPT 2858 (12.82%) followed by BPT 3111 (10.97 %) recorded high protein content where as the check variety BPT 5204 recorded 8.0% protein content in brown rice. In addition, BPT 2848 and BPT 3136 were nominated and evaluated in IVT- Biofortification trial under AICRIP testing during *kharif* 2019-20. Among all the entries tested in this trial over 10 locations spread over 7 states in the country, BPT 2848 recorded maximum mean protein content of 10.5% in polished rice sample followed by BPT 3136 which recorded a mean protein content **of 9.36%** whereas the check DRR Dhan 45 recorded 6.43% and BPT 5204 recorded 7.36% protein content which confirms the results of present study. The genotypes *viz.*, BPT 3141 (27.8ppm) followed by BPT 3136 (27.0ppm), BPT 2858 (26.8ppm) and BPT 3145 (26.1ppm) recorded high Zn content while BPT 2858, BPT 3111, BPT 3145 and BPT 3143 recorded Fe content of more than 10ppm in unpolished rice samples. The control BPT 5204 recorded 16.8 ppm Zn and 8.7 ppm Fe content in unpolished rice. Maximum total phenol content (TPC) was exhibited by BPT 2858 (174.48mg/100g) followed by BPT 3141 (156.31 mg/100g), BPT 3144 (150.82mg/100g) and BPT 3344 (148.65mg/100g). Total antioxidant activity (AOA) and total flavonoid contents (TFC) are higher in colored rice genotypes when compared with non pigmented control variety BPT 5204. Yuehan *et al.*, (2018) also reported that the free TPC of whole grain red rice and black rice had significantly higher values than that of white rice.

The analysis of variance of two way classification revealed significant differences among the genotypes for all the characters studied. The results of various genetic parameters revealed that maximum phenotypic and genotypic coefficients of variation was observed for total phenol content (51.2 and 49.3 respectively), while protein content (%) manifested the least values (6.18 and 5.46 respectively). All the characters studied manifested high estimates for heritability ranging from 89.70 (flavonoid content) to 95.6 (total phenol content). Additive genetic variance is required for the estimation of heritability and response to selection is directly proportional to narrow sense heritability. The maximum value for genetic advance as percent of mean was observed for total anti-oxidant activity (78.5) followed by flavonoid content (62.4). High GCV and PCV coupled with high heritability and genetic advance as percent of mean were observed for total phenol content, total antioxidant activity, flavonoid content, zinc content, iron content, protein content and grain yield/plant suggesting an additive type of gene action. The choice of appropriate breeding procedure depends on the type of gene action involved in the expression of these characters in a genetic population and additive genetic variance is a pre-requisite for genetic gain under selection, because this is the only genetic variance which responds to selection. Hence, all these traits will be improved by simple selection.

The correlation coefficients calculated between functional properties (total phenol content, flavonoid content, antioxidant activity) and nutritional parameters revealed that total phenol content manifested significant and positive association with total antioxidant activity (0.625) (Fig.1). It also manifested positive and significant relationship with flavonoid content (0.763), Zn (0.574), Fe (0.545) and protein content (0.589) suggesting that the colored genotypes used in the present study are rich in micronutrients and protein

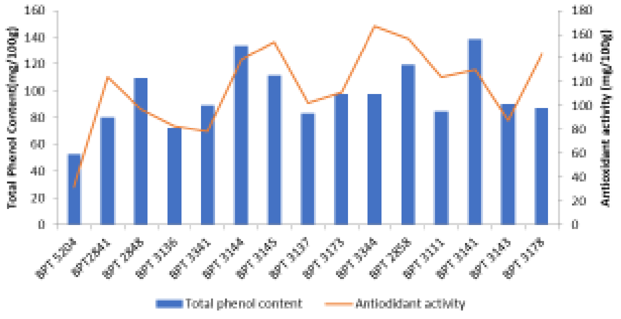

Fig 1: Correlation between total phenol content and anti-oxidant activity

content. High correlation between phenolic contents and antioxidant activity were reported earlier in different rice samples by Yuehan *et al.*,, (2018). The correlation of Fe content with another micro nutrient Zinc (0.531) is also positive and significant while the relationship of protein content with Fe and Zn is positive. The results of this study suggest that total phenol content, flavonoid content, total antioxidant activity are positively associated with each other and also with protein content, Zn and Fe content, hence simultaneous improvement of all these traits is anticipated which is useful for isolation of genotypes with beneficial health effects.

CONCLUSIONS

The traditional glutinous black rice varieties of North Eastern India are popular for their nutritive value but possess tall plant stature, prone to lodging and are low yielding types. Hence, the colored rice genotypes reported in the present investigation *viz.*, BPT 2841, BPT 2848, BPT 2858, BPT 3136, BPT 3140 and BPT 3144 which had semi-dwarf stature, early to medium duration (90-105 days for 50% flowering), high yield potential (5.5 t/ha – 6.5t/ha), medium slender grain type coupled with good cooking and nutritional quality parameters may be exploited commercially.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-23

BREEDING SUPERIOR HYBRID RICE PARENTAL LINES THROUGH INTER SUB-SPECIFIC HYBRIDIZATION

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Successful hybrid rice breeding programme necessitates continuous development of diversified parental lines and their genetic improvement for multiple traits of importance. The yield advantage in the current generation *indica* x *indica* hybrid rice lines is 15-20 % (1-1.5 $t.ha^{-1}$) whereas, in *indica* x *japonica* hybrids, it is around 25-30%. In three-line system of hybrid rice breeding, identification of stable parental lines from diverse *indica*, tropical *japonica* and lines derived from *indica* x tropical *japonica* crosses is important with respect to increasing the heterosis levels. Breeding parental lines from inter-sub specific crosses i.e. exploitation of heterosis using *indica* and tropical *japonica* germplasm is one of the strategies to increase the yield potential of hybrids. The major objective of this study was to breed intermediate superior and diverse hybrid parental lines for the development of heterotic rice hybrids in India.

METHODOLOGY

Crosses were made using promising *indica* parental lines as female parents with tropical *japonica* lines as male parents. Segregating materialswere advanced by pedigree method of breeding and 106 promising, stablegenotypes were developed by selecting for important characters like *indica* plant type and grain type with medium height and strong culm. These promising *indica*x tropical *japonica* derivatives were screened for restorer (*Rf4 and Rf3*) and wide compatibility (*S5n*) genes using reported candidate gene specific markers. For molecular screening, reported candidate gene specific markers viz.,RMS-PRR9-1 (Pranathi *et al*. 2016) for *Rf4*, RMS-SF21-5 (Pranathi *et al*. 2016) for *Rf3* and *S5n* INDEL (Sundaram*et al*. 2010) for *S5n* were used. Based on molecular screening, 50 genotypes with various allelic combinations of *Rf4*, *Rf3 andS5n* were selected and test crossed with one WA-CMS line i.e. APMS6A during *kharif* 2018 to validate their fertility restoration ability at field level.

RESULTS

Out of 106promising *indica* x tropical *japonica* derivative lines, 2 % were identified with three gene combination (*Rf3*/*Rf4*/*S5*n), 15 % of genotypes were identified with both *Rf3* and *Rf4*, 14% of genotypes possessed only *Rf4*, 10 % of genotypes carried *Rf4* and *S5n* gene combination and 13% of genotypes were observed to be completely devoid of any of the genes tested through marker analysis. Test crossed F_1s were analysed for pollen and spikelet fertility percent to identify restorers and maintainers. Out of two genotypes with *Rf4*, *Rf*3 and *S5n* gene combination, one (IJD38) behaved as restorer and the other genotype (IJD34) behaved as partial maintainer. Out of 16 genotypes with both *Rf3* and *Rf4*, 11 genotypes were proved as restorers and remaining genotypes behaved as partial restorers. Out of 6 genotypes with only *Rf4*, four genotypes behaved as restorers and two behaved as partial restorers. Four genotypes with only *Rf3* behaved as partial maintainers. Of 7 genotypes with *Rf4* and *S5n* gene combination, 6 genotypes behaved as potential restorers. From the present study, it can be concluded that *Rf4* has a stronger influence on fertility restoration ability than *Rf3*. It has been observed thatpresence of *S5n* with either of the *Rf3* or *Rf4* has increased the spikelet fertility per cent. However, the confounding effect of *S5n* gene on both the fertility restoration genes needs to be studied further.

CONCLUSION

Breeding intermediate superior parental lines by introgressing the tropical *japonica* genome segments possessing wide compatibility genes into the *indica* genetic background offers a new opportunity for increasing heterosis levels in hybrid rice breedingprogammes. The heterosis levels between selected *indica* WA-CMS lines and *indica* tropical *japonica* derivatives lines are being evaluated. Development of superior parental lines through intersubspecific hybridization may broaden the genetic base of parental pool in hybrid rice.

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IRC/TM-1/PP-24

CAUSE AND EFFECT RELATIONSHIP AMONG YIELD AND QUALITY ATTRIBUTES IN RICE

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With the advent of dwarf genes a spectacular improvement of yield was noticed in rice. We could able to meet the food requirement of the country's population but also reached to a phase of export to other countries. Due to the concerted efforts of many breeders, many high yielding rice varieties were developed which were suitable for different agro climatic conditions. Both yield and quality traits in rice were not easily amenable to selection due to its complex nature and are polygenic traits. Before formulation of any breeding programme a better understanding of the relationship between the yield and its attributing traits, quality parameters is a prerequisite. Hence, the present study was formulated to study the association among yield and quality traits in rice for selected crosses.

MATERIAL AND METHODS

The experimental material consists ofseven parents viz., Erramallelu, IR 72, IR 64, sambamahsuri, Swarnamukhi. Bharani and NLR 33637, its 21 F_1s and F_2s derived through diallell mating (Griffing 1956). The interrelationships among yield and yield components and cooking attributes in parents , F_1s and F_2s along with direct and indirect contribution of yield and its component characters towards yield , quality traits towards protein content were studied (According to Wright, 1921; Deway and Lu , 1959).A total of twenty four characters were taken for study.

RESULTS AND DISCUSSION

Simple correlation coefficients were computed among different character pairs i.e., yield and yield components for three sets includes seven parents, 21 F_1s and 21 F_2s to study the nature and magnitude of interrelationships among different character pairs. The results indicated that there was positive association between grain yield and days to 50% flowering, ear bearing tillers per plant and primary branches per plant in parents. In F1s yield was positively correlated with plant height, ear bearing tillers per plant, panicle length, primary branches per panicle, filled grains per panicle and kernel breadth. The association in F_2 generation between yield and days to 50% flowering, plant height, ear bearing tillers per plant and filled grains per panicle was positive.

Correlation of protein content was studied for grain dimensions, milling and cooking characters for the three sets revealed that test weight was positively associated with kernel length, L/B ratio in parents, while in F_1s it was associated with kernel length, L/B ratio and in F_2 it was correlated with kernel length and kernel breadth only indicating the importance of kernel length, breadth and L/b ratio in isolating rice varieties with fine grain quality.

Chalkiness percentage , an undesirable trait was associated with kernal length, L/B ratio and test weight in F1 and with kernel breadth only in F_2 generation, suggesting that the characters viz., kernel length, breadth, L/b ratio and test weight can be used as selection criteria, while selecting genotypes with low chalkiness percentage.

Hulling percentage was correlated with kernel breadth in parents and F_1s, while milling % was associated with hulling percentage in parents. The positive association was also observed with hulling percent in parents. The positive correlation was also observed between head rice recovery and hulling percent, kernel length in parents only. Kernel breadth after cooking was positively associated with kernel length, L/B ratio in parents and with water uptake, volume expansion in F_1 generation. The positive relationship was also observed between the traits kernel length after cooking and water uptake in parents, F_1 and F_2 generations and between kernel length after cooking and volume expansion in F_1 generation.

GT score was also associated with amylose content, kernel length and milling percentage, head rice recovery and kernel breadth in F_2s. Protein content was correlated with test weight, hulling percentage, head rice recovery, kernel breadth in parents and it was correlated only with head rice recovery in F_1s and with L/B ratio in F_2s.

The path analysis revealed that in parents, F_1s and F_2s ear bearing tillers per plant and filled grains per panicle were the major direct contributing factors for grain yield followed by test weight warranting their inclusion during selection of genotypes with high grain yield.For protein content the major contributing factors were head rice recovery followed by kernel breadth and L/b ratio both directly and indirectly through other characters suggesting the importance of these traits, while selecting lines with high protein content.

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IRC/TM-1/PP-25

CHARACTERIZATION OF ELITE TEMPERATE RICE (*ORYZA SATIVA*. L) OF KASHMIR HIMALAYAS

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Rice (*Oryza sativa* L.) is one of the few crops endowed with rich genetic diversity**.** Rice in the state is grown across diverse agro-ecological conditions ranging from subtropical zone of Jammu (>200m amsl) to temperate high altitudes region of Kashmir (2300m amsl) spread between 30.4°N to 34.38°N latitude and 74.0°E to 75.25°E longitude. Rice cultivation is an integral component of rich cultural heritage of the state and is a primary source of calories in the people's diet compared to wheat and maize (Najeeb *et al*., 2017). Agro-morphological parameters of the rice cultivars determine their yield potential, local agronomic suitability and ability to escape from or to tolerate biotic and abiotic stresses. Rice grain quality traits encompass the totality of all characteristics and features of rice or the rice products that meets the consumer demands and preference (Siddiqui and Kammamaru, 2007). A number of rice varieties are being grown across Kashmir valley belonging to two subspecies of rice such as *indica* and *japonica* due to their suitability under different ecotones of the valley.

METHODOLOGY

The experimental material consisted of 51 genotypes and was evaluated in randomized block design (RBD) with three replications at Mountain Research Centre for Field Crops (MRCFC), Khudwani. Net plot size was 5m² with row to row and plant to plant distance of 20cm x 15cm. The main aim of this study was to characterize elite rice germplasm for various agro-morphological and quality traits. Grain and cooking quality characteristics and other post harvest features were recorded as per DUS guidelines following Standard Evaluation System of IRRI.

RESULT

Significant amount of genetic variability was observed for all agro-morphological and cooking

Table-1: Frequency distribution of the genotypes into different classes for important traits

Characteristics	States	No.	Frequency
Days to 50 % flowering			
	Early (80-90)	14	27.5 %
	Intermediate (90-100)	28	54.9 %
	Late (>100)	9	17.6 %
Panicle length (cm)			
	Short (16-20 cm)	14	27.5 %
	Medium (21-25 cm)	35	68.6 %
	Long (26-30 cm)	2	3.9 %
No. of effective tillers per plant			
	Very high (>25)	0	0 %
	Good (20-25)	2	3.9 %
	Medium (10-19)	49	96.1 %
	Low (5-9)	0	0 %
Days to maturity			
	Very early (<120)	1	1.96 %
	Early (120-125)	10	19.61 %
	Intermediate (125-135)	29	56.86 %
	Late (>135)	11	21.57 %
Plant height (cm)			
	Semi dwarf (<90 cm)	13	25.5 %
	Intermediate(110-130 cm)	35	68.6 %
	Tall (>130 cm)	3	5.9 %
Grain yield (q/ha)			
	High (>90 q/ha)	8	15.7 %
	Medium (70-90 q/ha)	23	45.1 %
	Low (50-70 q/ha)	8	15.7 %
	Very low (<50 q/ha)	12	23.5 %

Table-2: Classification of genotypes on the basis of some important cooking quality traits.

Name	Amylose (%)	ASV	Aroma	GC (mm)
China-1007	Intermediate	Intermediate	Non scented	Hard
China-1039	Low	Intermediate	Non-scented	Hard
Chenab	Intermediate	Intermediate	Non-scented	Hard
Jhelum	Intermediate	Intermediate	Non-scented	Medium
SR-1	Intermediate	Intermediate	Non-scented	Hard
SR-2	Intermediate	Intermediate	Non-scented	Hard
SR-3	Intermediate	Intermediate	Non-scented	Hard
SR-4	Intermediate	Intermediate	Low-scented	Hard
SKUA-292	Intermediate	Intermediate	Non-scented	Hard
SKUA-403	Intermediate	Intermediate	Non-scented	Hard
SKUA-406	Intermediate	Intermediate	Non-scented	Hard
SKUA-410	Intermediate	Intermediate	Non-scented	Medium
SKUA-412	Low	Intermediate	Non-scented	Medium
SKUA-415	Low	Intermediate	Non-scented	Hard
SKUA-420	High	Intermediate	Mild-scented	Soft
SKUA-478	Intermediate	Intermediate	Non-scented	Soft
SKUA-483	Intermediate	Intermediate	Non-scented	Medium
SKUA-484	Intermediate	Intermediate	Non-scented	Hard
SKUA-485	Low	Low	High-scented	Medium
SKUA-486	Low	Intermediate	Non-scented	Hard
SKUA-487	Low	Intermediate	Non-scented	Hard
SKUA-488	Intermediate	Intermediate	Non-scented	Medium
SKUA-491	Intermediate	Intermediate	Non-scented	Medium
SKUA-494	Intermediate	Intermediate	High-scented	Medium
SKUA-495	Intermediate	Intermediate	Non-scented	Hard
SKUA-496	Intermediate	Intermediate	Non-scented	Soft
SKUA-497	Intermediate	Intermediate	Non-scented	Hard
SKUA-499	Low	Intermediate	Non-scented	Medium
SKUA-500	Intermediate	Intermediate	Non-scented	Hard
SKUA-501	Intermediate	Intermediate	Non-scented	Medium
SKUA-502	Low	Intermediate	Non-scented	Soft
SKUA-521	Low	Low	Non-scented	Hard
SKUA-522	Low	Intermediate	Non-scented	Hard
SKUA-523	Low	Low, intermediate	Non-scented	Hard
SKUA-524	Intermediate	Low, intermediate	Non-scented	Hard
SKUA-525	Low	Intermediate	Non-scented	Hard
SKUA-526	Low	Low, intermediate	Non-scented	Hard
Purple rice	Low	Intermediate	Non-scented	Soft
Heera	Low	Intermediate	Non-scented	Medium
Koshihikari	Low	Low, intermediate	Low-scented	Medium
K-332	Low	Low	Non-scented	Medium
Name	Amylose	ASV	Aroma	GC
Kohsar	Low	Low	Non-scented	Soft
SR-5	Low	Intermediate	Non-scented	Medium
Mushkbudji	Low	Low, intermediate	High-scented	Medium
Kamad	Low	Low, intermediate	Low-scented	Hard
Pusa Sughand-3	High	Intermediate	High-scented	Medium
SKUA-514	Low	Low	Non-scented	Soft
SKUA-505	Low	Low	Non-scented	Hard
Nunbouel	Low	Low, intermediate	Low-scented	Medium
Tangdar zag	Low	Low, intermediate	Non-scented	Hard
Aromatic zag	Low	Low	Mild-scented	Hard

ASV=alkali spreading value, GC= gel consistency (mm).

quality traits. Further the genotypes could also be differentiated on the basis of morphological traits such as plant height, days to 50 % flowering, panicle length, number of effective tillers/plant and days to maturity etc and frequency distribution given in Table-1. Also cooking quality characteristics of each genotype is mentioned in Table-2.

CONCLUSION

The genotypes have recently been developed, therefore their characterization for various traits shall help their use in future rice breeding programme for improvement of most popular types lacking one or other traits. Also characterization shall help in registration process with PPV&FRA and ICAR-NBPGR after their release and notification.

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IRC/TM-1/PP-26

DISSECTION OF GENETIC VARIABILITY AND DUS CHARACTERIZATION IN ELITE TEMPERATE GERMPLASM OF RICE (*Oryza sativa* L.)

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Existence of baseline genetic variability in rice (*Oryzasativa* L.) or in any other cereal crop isessential that holds a key in improving both production and productivityfor both subsistenceas well as to meet ever increasing demand of global rice supply. The improvement of rice production in India is more crucial in view of foodsecurity concerns due to growing population. Essentially variability denotes the existence of differences between the individuals of plant population due to their genetic configuration and the environment in which they are raised up. The magnitude of phenotypic distribution signifies the range of flexible selection with reference to particular and potential trait for improvement(Sumanth*et al.*, 2017). Classifying genetic variability traits are both quantitative and qualitative in nature, which manifests differentially under diverse climatic conditions due to cross interactions of genotypes with environmental features i.e. for yield and yield attributing traits.Rice genotypes have a greater genetic diversity than elite cultivars (commercial cultivars)and represent an intermediate stage in domestication between wild rice and elite cultivars and this facilitates rice breeding while simultaneously maintaining most of the diversity in rice germplasm repository. Once the variety or novel genotype is developed and identified, its novelty or uniqueness has to be critically evaluated through characteristic descriptor guidelines. The concept of distinctness, uniformity and stability are fundamental to the characterization of a variety as a unique creation (Raut, 2003). Agro-morphological and quality characterization of germplasm is fundamental in order to provide information for plant breeding programmes.In the present investigation a set of rice genotypes including elite and pipeline advanced rice materials were tested across diverse ecological niches for the assessment of existing genetic variability and further characterized for their agro-morphological and grain quality parameters to ascertain the benchmark values and descriptor features for their unique identification.

METHODOLOGY

The experiment was carried out at three locations i.e. Mountain Research Centre for Field Crops (MRCFC), Khudwani (34° N latitude and 74° N longitude at 1560m amsl) (E1), Faculty of Agriculture (FoA), Wadoora (34° N latitude and 74° Elongitude at 1580m amsl) (E2) and Pombay, Kulgam (33.6° N latitude and 75.0° Elongitude at 1739m amsl) (E3) of Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, during *kharif* season of 2018.The investigation was laid out in randomized block design with three replications at each location with spacing 15 × 20 cm.

RESULT

A wide range of genetic variability was observed for all the traits that varied differentially across diverse environments as evident from the ridge distribution pattern**.** The observed distribution is more conspicuously non-overlapping with respect to significant number of traits. This ascertains that phenotypic range distribution pattern changes with changing environment specifically either in increased or decreased manner defining a classified existence of variation among genotypes for different traits at different locations. It is also observed that the distribution and spread of the data is different in case of days to maturity, flag leaf width, days to 50 per cent flowering and tiller count. It was also observed that these yield and yield attributing traits exhibited a linear and non-linear associations with each other as depicted in. It is revealed that total grains per panicle showed linear relationship (direct effect) with filled grains per panicle, grain yield showed linear relationship with biological yield. Also, among the quality traits, grain length showed linear relationship (direct effect) with grain length breadth ratio, decorticated kernel length and kernel length after cooking.

To establish distinctiveness genotypes were characterized for agro-morphological traits and quality traits **(Fig. 1).**

CONCLUSION

The tested genotypes hold a colossal amount of variability for most of the traits at each location. Also the genotypes were diverse therefore, the systematic characterization of these genotypes is pivotal to recognize desired traits. It will pave the approach to widen their utilization strategies.

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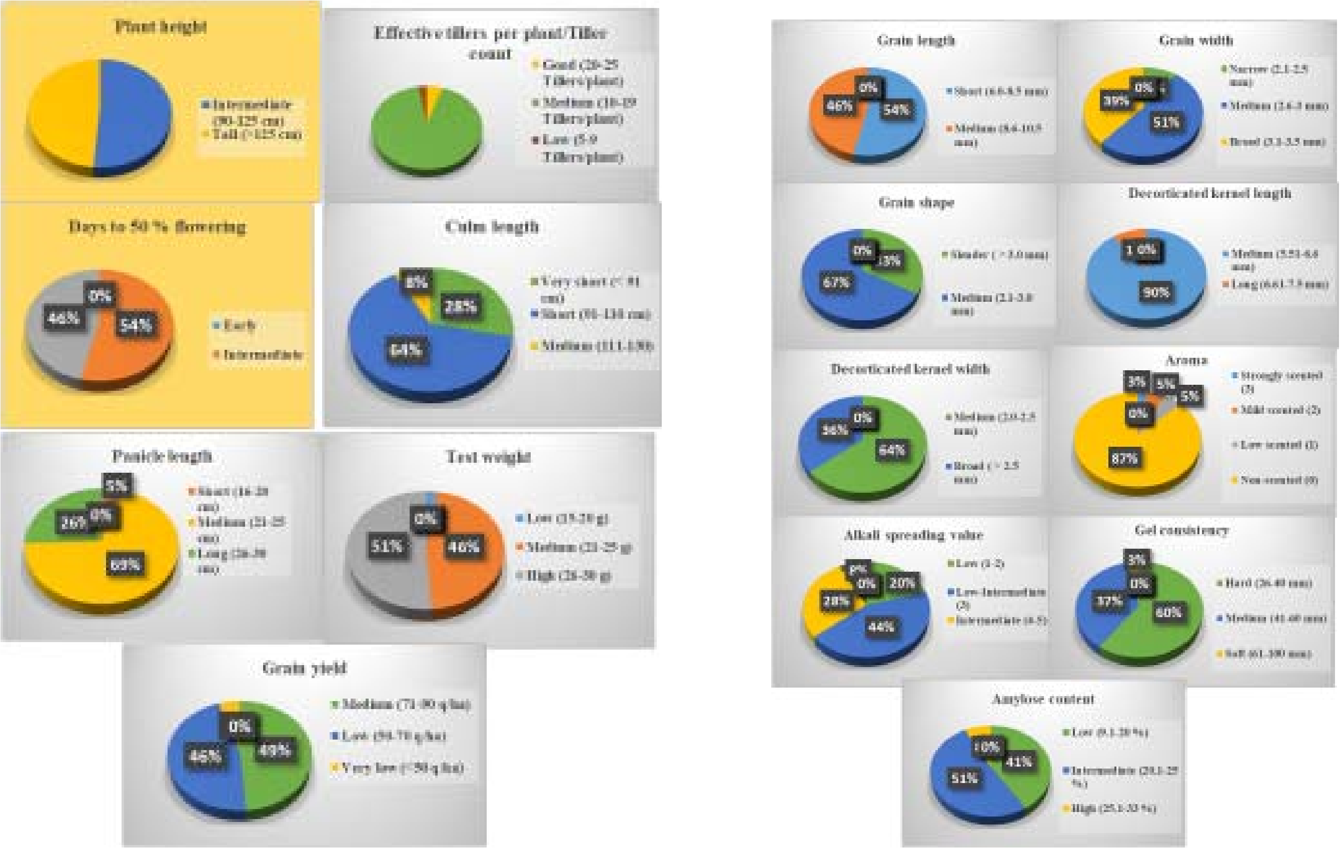

Fig. 1: Frequency distribution for different agro-morphological and quality traits

IRC/TM-1/PP-27

PBNR 03-2 : HIGH YIELDING VARIETY OF PADDY RELEASED FOR MARATHWADA REGION OF MAHARASHTRA STATE

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Rice is staple food of two third of world population. India ranks first in acreage and second in production at global level. Rice is cultivated in two ecosystems in Marathwada region as rain fed Upland and irrigated Upland. The seeds are sown by drilling method in black cotton soils. Previously released rice varieties were resistant to lodging (Prabhavati and Parag) but those varieties are low in quality parameters. These varieties also showed grain shattering at maturity stage. Hence there is urgent need to develop semi dwarf stature, non shattering, early maturity and high yield potential variety of Paddy with resistance to stem borer. Stem borer is the major pest of upland paddy cultivation in Marathwada. The variety PBNR 03-2 was developed by adopting pedigree method of breeding from a cross of PBNR 52 X IET 12077 at Upland Paddy Research Scheme, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. The variety PBNR 03-2 was tested in preliminary station trial during *kharif* 2006 at Parbhani. In one station trial conducted during kharif 2006 at Parbhani location the variety has recorded 35.11 percent and 23.98 percent higher yield over Parag and Avishkar (checks) respectively. On an average five advanced varietal trials over multilocations were conducted during 2007 to 2011 in Maharashtra (Basmathnagar, Somnathpur, Parbhani and Rahuri) (Table No. 2). The variety PBNR 03-2 recorded 13.71 percent and 31.89 percent higher yield over Parag and Avishkar (checks) respectively in advanced varietal trial during *Kharif* 2007. The variety PBNR 03-2 recorded 25.26 percent and 14.53 percent higher yield over Parag and Avishkar (checks) respectively in advanced varietal trial during *Kharif* 2008. The variety PBNR 03-2 recorded 23.76 percent and 16.67 percent higher yield over Parag and Avishkar (checks) respectively in advanced varietal trial during *Kharif* 2009. The variety PBNR 03-2 recorded 13.62 percent and 0.34 percent higher yield over Parag and Avishkar (checks) respectively in advanced varietal trial during *Kharif* 2010. The variety PBNR 03-2 recorded 20.05 percent and 32.47 percent higher yield over Parag and Avishkar (checks) respectively in advanced varietal trial during *Kharif* 2011. The overall increase in yield at all locations in advanced varietal trials during 2007 to 2011 was 19.20 percent and 19.18 percent higher yield over Parag and Avishkar (checks) respectively.

IRC/TM-1/PP-28

COMPARATIVE STUDY OF RICE CULTURES AT UPLAND PADDY RESEARCH SCHEME, PARBHANI

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Rice is consumed as major source of calories in Asian countries. Rice is a staple food for more than half of the world's population, and 90% of the world's rice comes from Asia. Rice is a main staple in more than 100 countries worldwide. In some households, rice is included with more than one meal a day. This starchy high-calorie grain is generally low cost, making it accessible to all and a vital base of many diets. Each country showcases a rice specialty to reflect local spices and taste preferences: risotto in Italy, paella in Spain, jambalaya in the southern U.S., coconut rice in Colombia, steamed rice in China, rice and beans in Mexico, and sweet rice in Portugal. It is also regarded as life. Rice is cultivated in two ecosystems in Marathwada region as rain fed Upland and irrigated Upland. The seeds are sown by drilling method in black cotton soils. The experiment was conducted at Upland Paddy Research Scheme, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. The experiment was laid down in randomized block design by using 10 cultures of rice. The experiment was sown during Kharif 2018. All the recomonded package of practices were followed to raise good crop. The culture PBNR 11-23 (3846 kg/ha) recorded highest grain yield followed by PBNR 11-22 (3590 kg/ha) over check PBNR 03-2 (2872 kg/ha) and Avishkar (3265 kg/ha). The remaining rice cultures were found non significant over both the checks. The maximum plant height of 88 cm was recorded in rice culture PBNR 11-25. The rice culture PBNR 11-23 was found early in 50 per cent flowering (76 days). The rice culture PBNR 11-23 recorded maximum panicle length (30 cm). Maximu number of tillers were noted in rice culture PBNR 11-23 (290). The rice culture PBNR 11-25 recorded maximum number of spikelets. The overall performance was found promising in case of culture PBNR 11-23 at Parbhani location.

IRC/TM-1/PP-29

DYNAMICS OF STARCH FORMATION AND GENE EXPRESSION DURING GRAIN FILLING AND ITS POSSIBLE INFLUENCE ON GRAIN QUALITY.

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After yield, grain quality is important for the large-scale adoption of a variety. Grain quality is assessed to determine milling yield, grain type, chalkiness and cooking quality before selecting desirable rice varieties. Cooking quality includes aroma, alkali spreading value (ASV), gel consistency (GC) and apparent amylose content (AC). Aroma of cooked rice is examined by trained panel members and is prescribed for basmati and aromatic short grains.ASV indirectly represents the gelatinization temperature of starch granule during cooking. GC gives the tenderness or hardness information of the cooked grain. AC is considered as chief cooking quality indicator and it indicates the presence or absence of stickiness of cooked grains. Generally, low or waxy (0%) amylose form sticky cooked grains while cooked grains are well separated in intermediate to high amylose rice.However, the interrelationships between amylose and other quality and rheological parameters exhibited variations among similar amylose containing varieties and the predicted cooking quality is not realized always and it is still elusive.

OBJECTIVE

As starch is the major component of rice grain, quality analysis is being done on 3 months aged paddy and amylose quantity is inadequate to explain these variations. Hence, this study focused on starch biosynthesis during grain filling.

METHODOLOGY

Twenty varieties along with improved Samba mashuriwere used for quality. Panicles were collected at each five-day interval during grain filling period for phenotypic and gene expression analysis.

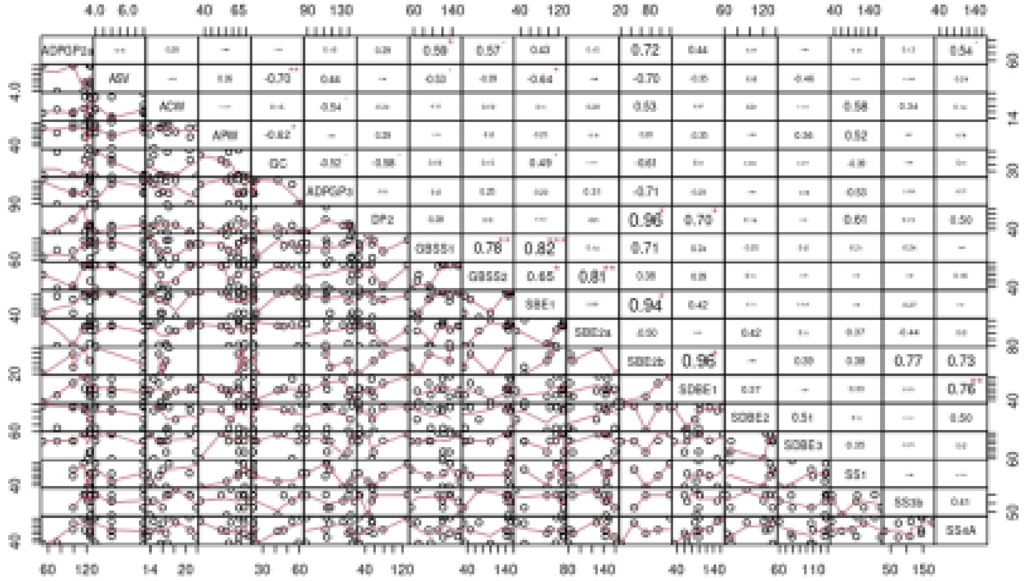

Figure Correlation between grain quality parameters and gene expression of starch metabolizing enzymes

Photosynthetic rate of flag leaf was measured. Grain weight was measured in brown rice grains. AC and amylopectin (AP) content were estimated in individual grains under non-interfering conditions by measuring the intensity of respective iodine complexes at 620 and 520 nm wavelengths. Gene expression (real-time-PCR analysis)was analyzed using fourteen reported primers, GBSSI and II and SBEI, IIa and IIb, ADPGP2a, ADPGP3, SDBE1, SDBE2, SDBE3, DP2, SS1, SS3b & SS4A in the grains of upper branches.

RESULTS

Grain filling was initiated in multiple branches of panicle. Grain weight indicates the stage of development before its characteristic weight is reached. Amylose increased while amylopectin decreased with increase in grain weight. Amylopectin to amylose ratio and expression of four genes were similar for ISM and Tellahamsa. All the genes (except SDBE2) were expressed on all intervals in ISM. Expression of all genes were observed at some intervals in Jaya, MTU 1010 and Vikramarya. ADPGP2a, ADPGP3 and SS3b genes in Tellahamsa, ADPGP3 alone in Swarnadhan, ADPGP2a and SDBE3 in DRRDhan 39, ADPGP2a and SS1 in Rasi, ADPGP2a, SDBE3 and SS4A in Varadhan, ADPGP2a, ADPGP3 & SDBE3 in Nidhi and ADPGP2a, ADPGP3 & SDBE1 in Sampada were expressed at all intervals. Multiple correlation analysis indicates significant negative correlation between ASV and GC, amylopectin content (AP) and GC, ASV and SBE1 and ASV and SBE2b. Chain length variations in branching appears as the reason for the variation in grain quality among similar AC containing varieties.

CONCLUSION

Absence of SBEIIb expression in some varieties indicates the absence of short chains in amylopectin. Variation in expression can produce variation in branching density leading to variation in cooking quality. This indicates that process (grain filling) can dictate product (harvested grain).

IRC/TM-1/PP-30

PYRAMID BREEDING OF THREE DROUGHT TRAIT YIELD QTL THROUGH MAB IN RICE (*ORYZA SATIVA* L.)

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Rice yield stability requires an attenuation of the reduction of yield losses caused by environmental stresses such as drought. More than 44 per cent of India's areas were under various degrees of drought conditions (abnormally dry to exceptionally dry) as of June 10, 2019 — that is nearly 11 percentage point over a year ago, according to the Drought Early Warning System (DEWS).Drought is one of the major constraints to rice production in rain fed areas. Worldwide, drought affects approximately 23 million ha of rainfed rice. The increased frequency of drought in rainfed areas threatens rice production and demands the development of rice varieties which are capable of high yield under stress. Rice is highly susceptible to water stress during the reproductive stage, leading to significant reduction in grain GY (Kamoshita et al., 2008). The yield loss magnitude depends on the growth stage and duration, the severity of Drought Stress (Gana et al., 2011). Using grain yield under stress as the primary selection criterion, several QTLs contributing to yield under drought stress at the reproductive stage have also been identified, such as $qDTY_{1.1}$ (Vikram et al. 2011; Ghimire et al. 2012), $qDTY_{2.1}$ (Venuprasad et al. 2009), $qDTY_{2.2}$ (Venuprasad et al. 2007; Swamy et al. 2013), $qDTY_{3.1}$ (Venuprasad et al. 2009), $qDTY_{4.1}$ (Swamy et al. 2013), $qDTY_{6.1}$ (Venuprasad et al. 2012), $qDTY_{10.1}$ (Swamy et al. 2013), and $qDTY_{12.1}$ (Bernier et al. 2007). According to Arvind et al (2018)., researchers will need introgression the combination of 13–15 genes/QTLs through cost-effective MAS strategy breeding program to develop climate resilient and better rice varieties. To understand the interactions among genetic loci QTL pyramiding is required. In rice breeding programs QTL pyramiding also improve the efficiency of marker-assisted selection for desirable loci.

A major QTL for grain yield under reproductive stage, *qDTY1.1*, was identified and this is the first reported QTL in rice with a major and consistent effect in multiple elite genetic backgrounds (Vikram *et al*., 2011). Another QTL, *qDTY2.2*, also linked with grain yield under reproductive stage drought stress was identified from a cross of drought *qDTY* parent Aday sel and IR64 at IRRI (Swamy *et al*., unpublished). $qDTY_{3.1}$ to be the largest and most consistent QTL affecting yield under drought conditions(Dixit et al., (2017). Shamsudin *et al*. (2016) identified positive digenic interactions of $qDTY_{2.2}$ and $qDTY_{3.1}$ with $qDTY_{12.1}$ enhancing overall expression of drought-related traits. Interaction of $qDTY_{3.2}$ with $qDTY_{1.1}$ and $qDTY_{12.1}$ reduces the flowering duration and subsequently increases GY under stress (Vikram et al., 2016). Similar interaction of *qDTY*2.3 and *qDTY*3.2 with *qDTY*12.1 in a Vandana background (Dixit et al. 2012b); *qDTY*2.2 and *qDTY*3.1 with *qDTY*12.1 in an MRQ74 background (Shamsudin et al. 2016); and *qDTY*2.2 + *qDTY*4.1 in an IR64 background (Swamy et al. 2013) was observed.

*qDTY*1.1 showed positive interactions with *qDTY*2.1, *qDTY*2.2, and *qDTY*3.1, whereas *qDTY*2.2 showed positive interactions with *qDTY*4.1, *qDTY*12.1, and *qDTY*3.1. *qDTY*3.1 showed positive interactions with *qDTY*1.1, *qDTY*2.2, *qDTY*12.1, *qDTY*6.1, and *qDTY*6.2 (Arvind et al., 2018).

OBJECTIVE

The aim of this study was to pyramid drought QTLs, *qDTY3.1*, *qDTY2.2*, and *qDTY1.1* in variety having submergence QTL *SUB1* to develop high yielding drought and submergence *qDTY* variety through marker assisted backcross breeding approach.

METHODOLOGY

Two drought *qDTY* breeding lines developed at IRRI, Philippines, IR102784:2-42-47-2-1-4 (P1) and IR 102796-14-77-2-1-2 (P2) were used in the study for crossing which have already drought QTL *qDTY2.2* and submergence QTL *SUB1*.Breeding line, P74-41(P3) which has QTL *qDTY3.1* developed at Central Rainfed Upland Rice Research Station Hazaribag, Jharkhand used as donor of *qDTY3.1*. P1 and P2 were crossed with P3 plant. DNA isolation of F1 plants done by modified CTAB method (Murray and Thompson, 1980).Foreground selection of F1 plants for the QTLs *qDTY1.1*, *qDTY2.2* and *qDTY3.1* was done by QTL linked RM markers *qDTY1.1* (RM11943, RM 431 and RM3825), *qDTY2.2* (RM279, RM236) and *qDTY3.1* (RM520) respectively.

RESULT

15 F1s have found with the crossing between parents P1 , P2 and P3.Among 15 F1s only 13 F1s have QTL *qDTY2.2*, 11 F1s have QTL *qDTY3.1*. Among 15 F1 plants only 10 F1 plants have both drought QTLs *qDTY2.2* and *qDTY3.1*. We have crossed these F1s with *qDTY1.1* donor lines (102796-14-77-2-1-2 and IR102784 -2-118-22-1-1-2). We have get crossed seeds and now sown these seeds in phenotype.

CONCLUSION

In this study, we are trying to pyramid high yielding drought tolerant QTLs into high yielding drought susceptible variety which have already submergence QTL through MAB approach. Marker assisted backcross provide a unique opportunity to combine multiple trait specific QTLs with other stress-tolerant traits in very short time. May be these varieties serve as valuable genetic material and reduce the yield losses due to drought and flood prone areas.

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IRC/TM-1/PP-31

DECIPHERING GENE ACTION FOR SOME QUANTITATIVE CHARACTERS IN RICE (*Oryza sativa* L.)

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Rice is the premier food crop of the world, contributing to 73 percent of the total calorie intake of the population. Yield traits are dependent on their expression on several morphological and developmental traits, which are interrelated with each other. Generation mean analysis is a very useful technique used to estimate gene action for a polygenic trait. Therefore the study was carried out to estimates the gene actions, i.e., additive, dominance and epistatic effects by using five parameter model (generation mean analysis).

MATERIALS AND METHODS

The experiment was carried out at the Instructional Farm, Bidhan Chandra Krishi Viswavidyalaya, Jaguli, Nadia, West Bengal during 2017-18. The Crossing was made between different rice varieties i.e, Mahsuri × Bhutmuri and IR 36 × Bhutmuri during Kharif season to obtain the F_1 seeds of the said crosses. The experiment was laid in RBD with four replications. Observations were recorded on 10 plants in case of parents and F_1, 30 plants of F_2 and 60 plants in F_3 for different characters.

The analysis of variance was worked out to test the differences among genotypes by F-test. The Scaling test as described by Mather (1949) and Hayman & Mather (1955) was used to check the adequacy of the additive-dominance model for different characters in each cross. Five parameter model was estimated by the Hayman (1958) and Jinks & Jones (1958) model.

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the parents, F_1 hybrids and F_2 generation against all characters studied. The Generation mean analysis for eighteen quantitative characters of different generations for Cross I and Cross II have been presented in Table I respectively. The C and D scaling test for all the characters in the two crosses showed that at least one or both were found significant indicating the presence of non-allelic interaction in the inheritance of the characters under study. Both the crosses exhibiting non-allelic interaction for the inheritance of almost all the traits studied. However the characters number of grains per panicle and harvest index percent(%) in cross I and 1000 grains weight (g) in cross showed nonsignificant values for both C and D scales indicating the non-interacting mode of inheritance. From the table 1, Simple additive-dominance model was found to be inadequate which shows the presence of non- allelic interaction for days to 50 percent flowering, days to maturity, number of panicles per plant, number of primary branches per panicle, number of secondary branches per panicle in Cross I and for plant height(cm), number of tillers per plant, number of panicles per plant, number of grains per panicle, number of filled grains per panicle, and fertility percentage (%) in cross II. Similarly, Simple additive-dominance (3-parameters) model was found to be adequate which shows the absence of non- allelic interaction for plant height(cm), number of tillers per plant, panicle length, number of grains per panicle, number of filled grains per panicle, fertility percentage(%), 1000 grain weight(g), grain length(mm), grain breadth(mm), grain L/B ratio, straw weight(g),

Table I: Different scales for yield components and component of generation means for different characters in cross I and cross II as suggested by Hayman (1958)

Crosses	Scaling test	Three parameter mode			joint scaling test	Five parameter model						Epistasis
	C	D	m	d	h	÷^{2} at 3 d.f.	m	d	h	i	l	
Days to 50% Flowering												
I	1.25	11.75***	_	_	_	8.82*	117***±0.43	15.63***±0.25	0.50±1.36	23.63*** ± 1.53	14**± 4.93	C
II	-9	-14**	79.18***±1.17	-12±0.79	6.5±1.81	0.45	_	_	_	_	_	_
Days to Maturity												
I	-4*	15.00***	_	_	_	55.68***	147.5***±0.34	14.75** ± 0.37	-3.67*** ± 0.83	18.83***± 1.16	25.33***± 1.16	D
II	-1.25	-4.75	116.25***±0.52	-13.89±0.87	10.73***±0.70	2.42	_	_	_	_	_	_
Plant Height (cm)												
I	-27.25***	-25.50***	126.56***±0.32	2.88**±0.41	17.96***±0.547	1.04	_	_	_	_	_	_
II	28.01***	-17.49***	_	_	_	125.62***	130.75*** ±0.23	-20.63*** ± 0.55	30.83*** ±0.85	-24.93*** ±1.25	-60.67*** ±2.52	D
Number of tillers per Plant												
I	-10.37***	-1.13	19.88***±0.25	-2.19±0.20	0.88±1.21	3.63	_	_	_	_	_	_
II	-21.88***	14.38***	_	_	_	91.81***	24.37***±0.21	-5.43*** ± 0.14	12.08*** ± 0.69	-24.10*** ±0.68	48.33*** ± 1.99	C
Number of panicles per plant												
I	27.90***	15.40***	_	_	_	13.59***	29.88***± 0.21	-2.80*** ±0.13	1.33 ± 1.33	-11.21*** ±1.10	-16.66***± 3.07	D
II	-0.6	8.9**	_	_	_	0.08**	25.63*** ± 0.22	-2.80*** ± 0.18	6.67***± 1.89	-11.63*** ±1.46	12.67**± 4.18	C
Panicle Length (cm)												
I	-11.25***	-11.50***	21.80***±0.44	2.13***±0.13	3.33±0.66	0.01	_	_	_	_	_	_
II	1.5	-5.75***	22.52***±0.39	-1.88±0.24	2.64±0.54	8.8	_	_	_	_	_	_
Number of primary branches per panicle												
I	7.13***	-6.12***	_	_	_	21.76***	17.25***± 0.19	1.06*** ± 0.11	11.58***± 0.90	7.39*** ± 0.79	-17.67***± 2.26	D
II	-8.40***	-7.79***	6.88***±0.144	-0.38±0.22	2.96*±1.81	3.14	_	_	_	_	_	_
Number of secondary braches per panicle												
I	-8.13*	79.13***	_	_	_	308.58***	39.13***± 0.61	7.81*** ± 0.24	-15.41***± 1.77	-38.47*** ±1.93	116.3***± 6.06	D
II	-11.13*	-24.13***	27.47***±0.45	2.063*±0.27	10.66***±0.48	3.74	_	_	_	_	_	_
Number of grains per panicle												
I	4.88	7.88	95.17***±0.56	18.61***±0.59	15.23*±1.75	3.42	_	_	_	_	_	_
II	16***	-143***	_	_	_	1109.33***	34.87***±1.09	2.06*** ± 0.27	15.17*** ± 2.38	18.35*** ± 2.80	-17.33 ± 8.96	D
Number of filled grains per panicle												
I	-4.13	17.88**	61.17***±0.41	14.41***±0.43	26.76***±0.60	0.15	_	_	_	_	_	_
II	-4.88	-120.38***	_	_	_	496.34***	133.50*** ± 0.74	40.63*** ± 0.56	123.50***±1.78	179.25*** ± 2.14	-212***±6.36	D
Fertility percent (%)												
I	9.52***	15.48***	66.62***±0.49	-0.89±0.45	-0.13±0.71	6.69	_	_	_	_	_	_
II	4.74***	-11.57***	-	-	-	99.06***	67.60***± 0.22	7.29***± 0.36	4.32*** ± 0.62	23.09*** ± 0.99	-21.75***±1.98	D
1000 Grain Weight (g)												
I	-6.97***	1.75	19.77***±0.23	-3.04±0.233	-7.89±1.54	1.28	_	_	_	_	_	_
II	-1.93	-0.27	18.74***±0.22	-1.52±0.28	-1.47±0.34	2.49	_	_	_	_	_	_

Contd....

Contd....

Crosses	Scaling test	Three parameter mode			joint scaling test	Five parameter model						Epistasis
	C	D	m	d	h	χ^2 at 3 d.f.	m	d	h	i	l	
Grain Length (mm												
I	-1.57***	-1.46***	7.28***±0.09	-0.46±0.04	0.26±0.18	2.27	—	—	—	—	—	—
II	-1.38***	-1.53***	7.18***±0.05	-0.04±0.03	0.09±0.71	3.54	—	—	—	—	—	—
Grain Breadth (mm)												
I	-1.65***	-1.60***	2.01***±0.05	-0.4±0.03	0.64**±0.05	0.027	—	—	—	—	—	—
II	-0.73*	-1.23***	2.35***±0.07	0.34**±0.03	0.23±0.07	1.17	—	—	—	—	—	—
Grain Length/ Breadth (L/B) ratio												
I	1.21***	1.20***	3.57***±0.06	0.32*±0.045	-0.72±0.07	0	—	—	—	—	—	—
II	0.57	1.03***	3.24***±0.08	-0.36±0.03	-0.62±0.14	0.97	—	—	—	—	—	—
Straw Weight (g)												
I	12.23***	10.92***	47.29***±0.45	3.84**±0.38	-10.57±0.72	0.3	—	—	—	—	—	—
II	4.32***	2.59	37.25***±0.16	3.31***±0.06	-0.84±3.14	0.071	—	—	—	—	—	—
Harvest Index percent (%)												
I	-3.82	0.96	40.65***±0.34	3.39**±0.39	4.79±0.62	2.93	—	—	—	—	—	—
II	-1.18	7.89*	40.34***±0.33	0.86±0.51	-6.64±5.56	4.32	—	—	—	—	—	—
Grain Yield Per Plant (g)												
I	8.01**	10.17***	32.28***±0.75	7.86***±0.43	-1.32±1.23	1.44	—	—	—	—	—	—
II	0.75	9.67**	27.72***±1.34	2.94*±0.48	-8.15±4.54	3.22	—	—	—	—	—	—

* indicate significant at 5% level, ** indicate significance at 1% level, **indicates significant at0.01% level, Where D: Duplicate epistasis and C: Complimentary epistasis

harvest index (%) and grain yield per plant(g) in Cross I. Furthermore, additive-dominance model is adequate for days to 50 percent flowering, days to maturity, panicle length(cm), number of primary branches per panicle, number of secondary branches per panicle,1000 grain weight(g), grain length, grain breadth, grain L/B ratio, straw weight(g), harvest index (%) and grain yield per plant(g) in Cross II. In Cross I all gene effects for days to maturity, number of primary branches per panicle and number of secondary branches per panicle were significant except dominance gene effect in days to 50 percent flowering and number of panicles per plant. Roy and Senapati (2011) also reported that the dominance effect was not significant for the days to 50% flowering. In the case of the adequacy of the Simple additive-dominance model, only additive gene effects were significant in panicle length, grain L/B ratio, straw weight (g) and grain yield per plant(g). Similarly, Only dominance gene effect was significant in grain breadth (mm). In plant height(cm), number of grains per panicle, number of filled grains per panicle and harvest index (%) both additive and dominance gene effects were significant. In Cross II all gene effects for plant height, number of tillers per plant, number of panicles per plant, number of filled grains per panicle and fertility percentage were significant except dominance x dominance gene effect in number of grains per panicle. In the case of the adequacy of the simple additive dominance model, only additive gene effect was significant in grain breadth (mm), straw weight (g) and grain yield per plant(g). Similarly only dominance gene effect was significant in, days to maturity and number of primary branches per panicle.

CONCLUSION

From this experiment all the different types of interactions were observed for most of the traits in Cross I and Cross II. It is worth noting that the presence of an additive, dominance, additive × additive and dominance × dominance interaction effects were present along with either duplicate dominant epistasis or complementary recessive epistasis for most of its traits in cross I and cross II. Selection may be delayed to later segregating generations followed by recurrent selection. Selection procedures i.e, pureline selection, mass selection, progeny selection, hybridization and selection with pedigree breeding is sufficient to harness the additive gene action. Heterosis breeding and recombinant breeding with the postponement of selection at latter generations are effective in harnessing dominance gene action to the full extent. So, biparental mating design, reciprocal recurrent selection and diallel selective mating system might be profitable in exploiting both additive and non additive gene action to obtain desirable recombinants.

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GENERATION MEAN ANALYSIS (FIVE PARAMETER MODEL) FOR SOME QUANTITATIVE CHARACTERS IN RICE(*ORYZA SATIVA* L.)

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Rice is the major cereal food crop of the world,contributing to 73 percent of the total calorie intake ofthe population.Yield traits are dependent on their expression on several morphological and developmental traits, which are interrelated with each other. Generation mean analysis is a very useful technique used to estimate gene action for a polygenic trait. Therefore the study was carried out to estimates the gene actions, i.e., additive, dominance and epistatic effects by using five parameter model(generation mean analysis).

MATERIALS AND METHOD

The experiment was carried out at the Instructional Farm, Bidhan Chandra KrishiViswavidyalaya, Jaguli, Nadia, West Bengal during 2017-18.The Crossing was made between different rice varieties i.e,Mahsuri × Bhutmuri and IR 36 × Bhutmuri during Kharif season to obtain the F_1 seeds of the said crosses. The experiment was laid in RBD with four replications. Observations were recorded on 10 plants in case of parents and F_1, 30 plants of F_2 and 60 plants in $F_3$for different characters.The analysis of variance was worked out to test the differences among genotypes by F-test. The Scaling test as described by Mather (1949) and Hayman & Mather (1955) was used to check the adequacy of the additive-dominance model for different characters in each cross. Five parameter model was estimated bythe Hayman (1958) and Jinks & Jones (1958) model.

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the parents, F_1 hybrids and F_2 generation against all characters studied. The Generation mean analysis for eighteen quantitative characters of different generations for Cross I and Cross II have been presented in Table I respectively.The C and D scaling test for all the characters in the two crosses showed that at least one or both were found significant indicating the presence of non-allelic interaction in the inheritance of the characters under study. Both the crosses exhibiting non-allelic interaction for the inheritance of almost all the traits studied.However the characters number of grains per panicle and harvest index percent(%) in cross I and 1000 grains weight (g) in cross showed nonsignificant values for both C and D scales indicating the non-interacting mode of inheritance. From the table, Simple additive-dominance model was found to be inadequate which shows the presence of non- allelic interaction for days to 50 percent flowering, days to maturity, number of panicles per plant, number of primary branches per panicle, number of secondary branches per panicle in Cross I and for plant height(cm), number of tillers per plant, number of panicles per plant, number of grains per panicle, number of filled grains per panicle, and fertility percentage (%) in cross II.Similarly, Simple additive-dominance (3-parameters) model was found to be adequate which shows the absence of non- allelic interaction for plant height(cm), number of tillers per plant, panicle length, number of grains per panicle, number of filled grains per panicle, fertility percentage(%), 1000 grain weight(g), grain length(mm), grain breadth(mm), grain L/B ratio, straw weight(g), harvest index (%) and grain yield per plant(g) in Cross

Table I: Different scales for yield components and component of generation means for different characters in cross I and cross II as suggested by Hayman (1958)

Crosses	Scaling test	Three parameter mode			joint scaling test	Five parameter model						Epistasis
	C	D	m	d	h	÷^{2}at 3 d.f.	m	d	h	i	l	
Days to 50% Flowering												
I	1.25	11.75***	0	0	0	8.82*	117***±0.43	15.63***±0.25	0.50±1.36	23.63*** ± 1.53	14**± 4.93	C
II	-9	-14**	79.18***±1.17	-12±0.79	6.5±1.81	0.45	0	0	0	0	0	-
Days to Maturity												
I	-4*	15.00***	0	0	0	55.68***	147.5***±0.34	14.75** ± 0.37	-3.67*** ± 0.83	18.83***± 1.16	25.33***± 1.16	D
II	-1.25	-4.75	116.25***±0.52	-13.89±0.87	10.73***±0.70	2.42	0	0	0	0	0	-
Plant Height (cm)												
I	-27.25***	-25.50***	126.56***±0.32	2.88**±0.41	17.96***±0.547	1.04	0	0	0	0	0	-
II	28.01***	-17.49***	0	0	0	125.62***	130.75*** ±0.23	-20.63*** ± 0.55	30.83*** ±0.85	-24.93*** ±1.25	-60.67*** ±2.52	D
Number of tillers per Plant												
I	-10.37***	-1.13	19.88***±0.25	-2.19±0.20	0.88±1.21	3.63	0	0	0	0	0	-
II	-21.88***	14.38***	0	0	0	91.81***	24.37***±0.21	-5.43*** ± 0.14	12.08*** ± 0.69	-24.10*** ±0.68	48.33*** ± 1.99	C
Number of panicles per plant												
I	27.90***	15.40***	0	0	0	13.59***	29.88***± 0.21	-2.80*** ±0.13	1.33 ± 1.33	-11.21*** ±1.10	-16.66***± 3.07	D
II	-0.6	8.9**	0	0	0	0.08**	25.63*** ± 0.22	-2.80*** ± 0.18	6.67***± 1.89	-11.63*** ±1.46	12.67**± 4.18	C
Panicle Length (cm)												
I	-11.25***	-11.50***	21.80***±0.44	2.13***±0.13	3.33±0.66	0.01	0	0	0	0	0	_
II	1.5	-5.75***	22.52***±0.39	-1.88±0.24	2.64±0.54	8.8	0	0	0	0	0	_
Number of primary branches per panicle												
I	7.13***	-6.12***	0	0	0	21.76***	17.25***± 0.19	1.06*** ± 0.11	11.58***± 0.90	7.39*** ± 0.79	-17.67***± 2.26	D
II	-8.40***	-7.79***	6.88***±0.144	-0.38±0.22	2.96*±1.81	3.14	0	0	0	0	0	_
Number of secondary braches per panicle												
I	-8.13*	79.13***	0	0	0	308.58***	39.13***± 0.61	7.81*** ± 0.24	-15.41***± 1.77	-38.47*** ±1.93	116.3***± 6.06	D
II	-11.13*	-24.13***	27.47***±0.45	2.063*±0.27	10.66***±0.48	3.74	0	0	0	0	0	_
Number of grains per panicle												
I	4.88	7.88	95.17***±0.56	18.61***±0.59	15.23*±1.75	3.42	0	0	0	0	0	_
II	16***	-143***	0	0	0	1109.33***	34.87***±1.09	2.06*** ± 0.27	15.17*** ± 2.38	18.35*** ± 2.80	-17.33 ± 8.96	D
Number of filled grains per panicle												
I	-4.13	17.88**	61.17***±0.41	14.41***±0.43	26.76***±0.60	0.15	0	0	0	0	0	_
II	-4.88	-120										
.38												
***	0	0	0	496.34***	133.50*** ± 0.74	40.63*** ± 0.56		123.50***±1.78	179.25*** ± 2.14	-212***±6.36	D	
Fertility percent (%)												
I	9.52***	15.48***	66.62***±0.49	-0.89±0.45	-0.13±0.71	6.69	0	0	0	0	0	_
II	4.74***	-11.57***	0	0	0	99.06***	67.60***± 0.22	7.29***± 0.36	4.32*** ± 0.62	23.09*** ± 0.99	-21.75***±1.98	D
1000 Grain Weight (g)												
I	-6.97***	1.75	19.77***±0.23	-3.04±0.233	-7.89±1.54	1.28	0	0	0	0	0	_
II	-1.93	-0.27	18.74***±0.22	-1.52±0.28	-1.47±0.34	2.49	0	0	0	0	0	_

* indicate significant at 5% level, ** indicate significance at 1% level, **indicates significant at 0.01% level; Where D: Duplicate, C: Complementary effect of epistasis

I.Furthermore, additive-dominance model is adequate for days to 50 percent flowering, days to maturity, panicle length(cm), number of primary branches per panicle, number of secondary branches per panicle,1000 grain weight(g), grain length, grain breadth, grain L/B ratio, straw weight(g), harvest index (%) and grain yield per plant(g) in Cross II. In Cross I all gene eûects for days to maturity, number of primary branches per panicle and number of secondary branches per panicle were significant except dominance gene effect in days to 50 percent flowering and number of panicles per plant.Roy and Senapati (2011)also reported that the dominance effect was not significant for the days to 50% flowering. In the case of the adequacy of the Simple additive-dominance model, only additive gene eûects were significant in panicle length, grain L/B ratio, straw weight(g) and grain yield per plant(g). Similarly, Only dominance gene effect was significant in grain breadth(mm). In plant height(cm), number of grains per panicle, number of filled grains per panicle and harvest index (%) both additive and dominance gene eûects were significant. In Cross II all gene eûects for plant height, number of tillers per plant, number of panicles per plant, number of filled grains per panicle and fertility percentage were significant except dominance x dominance gene effect in number of grains per panicle. In the case of the adequacy of the simple additive dominance model, only additive gene effect was significant in grain breadth(mm), straw weight(g) and grain yield per plant(g). Similarly only dominance gene effect was significant in, days to maturity and number of primary branches per panicle.

CONCLUSION

From this experiment all the different types of interactions were observed for most of the traits in Cross I and Cross II. It is worth noting that the presence of an additive, dominance, additive × additive and dominance × dominance interaction effects were present along with either duplicate dominant epistasis or complementary recessive epistasis for most of its traits in cross I and cross II. Selection may be delayed to later segregating generations followed by recurrent selection. Selection procedures i.e, pureline selection, mass selection, progeny selection, hybridization and selection with pedigree breeding is sufficient to harness the additive gene action. Heterosis breeding and recombinant breeding with the postponement of selection at latter generations are effective in harnessing dominance gene action to the full extent. So, biparental mating design, reciprocal recurrent selection and diallel selective mating system might be profitable in exploiting both additive and non additive gene action to obtain desirable recombinants.

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CRISPR-CAS9 APPROACH FOR DEVELOPING DESIGNER BIOFORTIFIED RICE

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According to the World Health Organization (WHO) about 2 billion people in the world are suffering from vitamin and mineral deficiencies, alsoknown as “hidden hunger”. This is an important and considerable health issue that occurs when a person is exposed to low-quality food lacking micronutrients, vitamins, and minerals in the food. Therefore, to overcome the micronutrient deficiency problems, food plate with food diversity is advocated. It often is not possible because of economic or other factors. More than half of the global population depends solely on rice (*Oryza sativa*), as a staple food, which is their source of nutrients, contributing up to 70% of the daily calories. Hence in order to overcome the above-said problem it is high time to opt for the bio-fortification of staple crops like riceandwheat. This is one of the most acceptable options to solve this alarming problem.Different approaches were followed by the scientific community for biofortification in rice. Except for Zn, no major success was achieved in rice for other traits. Biofortification by genetic means is the most viable approach. Successful reports for biofortification of rice for provitamin A, carotenoids, zinc, and iron content in the rice grain are available following the transgenic approach. However, the transgenic crops face regulatory issues for their uses by farmers and commercialization. The discovery of sequencespecific-based nuclease technology including the CRISPR/Cas9 tool developed during the last decades becomes the methods of choice for their precision in editing the genome and development of transgenic crops with desirable traits. They were also expected to circumvent the limitations of transgenic plants developed through traditional methods.

DESIGNER RICE FOR NUTRITION

Clustered, regularly interspaced, short palindromic repeat (CRISPR) associated protein 9 (Cas9) or CRISPR-Cas9 has emerged as the most accessible, economical and efficient technology to undertake genome editing in rice and develop designer biofortified rice cultivars to overcome the problem of hidden hunger.Targeting gene knockout by *Agrobacterium*-mediated transformation of two rice branching enzyme (SBE) *SBEI and SBEIIb* through CRISPR/Cas9 genome editing technology has been effectively employed for the development of high amylose rice (Sun *et al*., 2017). The *sbeII*mutant plants showed an increase of amylose content (AC) and resistant starch (RS) content as high as 25 and 9.8 respectively. Recently Dong and his colleagues demonstrated targeted gene insertion of marker-free DNA in rice using CRISPR-Cas9 genome editing. They reported that this method provided a targeted insertion of a 5.2 kb carotenoid biosynthesis cassette at two genomic safe harbors in rice. The marker-free rice plants were obtained with high carotenoid content in the seeds with no detectable penalty in morphology or yield. Whole genome sequencing revealed the absence of off-target mutations by Cas9 in the engineered plants.These results demonstrated targeted gene insertion of marker-free DNA in rice using CRISPR-Cas9 genome editing and offer a promising strategy for genetic improvement of rice and other crops. Yang and his team knock out five rice carotenoid catabolic genes (OsCYP97A4, OsDSM2, OsCCD4a, OsCCD4b and OsCCD7) to increase the amount of â-carotene accumulation in rice endosperm by the

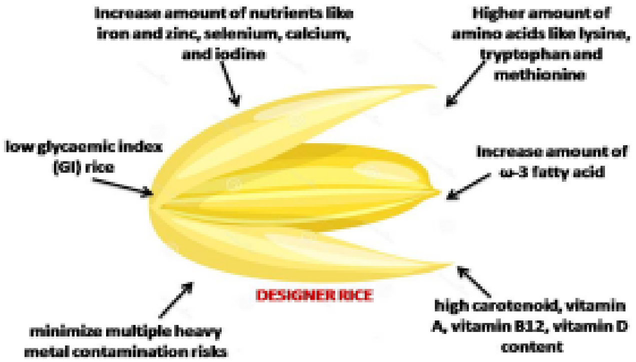

Figure 1. Designer Rice

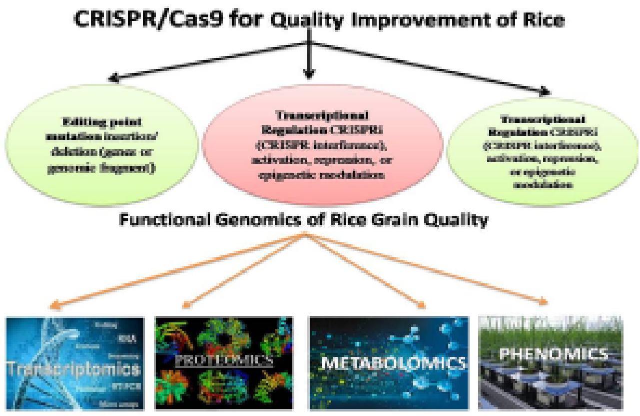

Figure 2. Molecular basis of quality assessment by Crispr/ cas9

CRISPR/Cas9 system. Knockdown of OsVIT2 by CRISPR-based approach has become an example of attaining the ample amount of grain Fe, similar to the published T-DNA insertion for silencing of this gene in different rice cultivars. Besides the improvement of nutritional value, genome editing systems are also used to modify rice genes resulting in non-toxic and healthier varieties with reduced amount of multiple heavy metal contamination risks in rice grains.

The use of CRISPR/Cas9 editing system got the success in knocking out the metal transporter gene *OsNramp5* and developed *indica* rice lines with low accumulation Cd. Field trials of the *OsNramp5* mutated *indica* rice lines showed that the concentration Cd was consistently less (0.05 mg/ kg) as compared to the wild-type *indica* rice (0.33 to 2.90 mg/kg) without affecting the plant yield. Recently a new strategy like multiplex genome editing in rice was reported which is an easy and well-understood system, especially for comparing and dissecting the functions and relationships of major genes/QTLs (Xu *et al.*, 2016). Multiplexing in rice can significantly edit 82% of the desired target sites representing deletion, insertion, substitution, and inversion events, thus exhibiting high efficiency of editing.In near future, this method is expected to be a very useful tool for the development of designer rice.

CONCLUSION

Genetic biofortification strategyis a viable approach for the development of highly nutritious food, particularly rice for the nutritional security of millions. CRISPR/Cas-based genome editing tool is a fast, sustainable and cost-effective approach for the improvement of rice grain quality. Recently multiplex editing through CRISPR/ Cas is found to be an easy and well-understood system, especially for comparing and dissecting the functions and relationships of major genes/QTLs and targeting insertion and deletion of more than two targeted traits. It can also be used for the development of a designer biofortified rice with a higher quantity of essential amino acids, fatty acids, vitamins (carotenoid, Vit B12, VitD) andminerals such as iron, zinc, selenium, calcium, iodine, low glycaemic index (GI) rice and reduce multiple heavy metal accumulation risks in the grains.

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RICE BIOFORTIFICATION

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After independence, a trending population boom occurred, but no substantial increase in food grain production to feed them resulted in food grain insufficiency. The introduction of high yielding varieties (HYV's) that are highly fertiliser sensitive during the Green Revolution period (1965-70) solved the problem of food grain insufficiency and food grain production has now increased to 257 mt in India (Jena et al., 2018). Poverty was the major issue during the pre-green revolution era, but it has now been transferred to micronutrient malnutrition, i.e. night blindness, xerophthalmia, iron deficiency anaemia, etc. In 50 percent of the world's agricultural soils, Zn is deficient and is regarded as the most important micronutrient deficiency in crops worldwide. Around 2 billion people worldwide are suffering from zinc deficiency and about 1.5 million children die from zinc malnutrition every year (Jena et al., 2018). Globally, approximately 0.8 million individuals and nearly 0.45 million children are at risk of dying from zinc deficiency each year. India has one of the highest rates of soil and human diet deficiencies in Zn. 50 percent of Indian soils are Zn deficient, if no management is performed, rising to 63 percent by 2025. In India, approximately 0.15 million children die each year because of Zn deficiency. Zinc deficiency leads to diarrhoea cases, with 25 percent of global diarrhoea deaths among children under 5 years of age. Around 48,000 Indian children per year could be saved by Zn fortification in staple foods (WHO, 2015). Night blindness and xerophthalmia, which is the absence of serum (plasma) retinol concentrations, are caused by vitamin-A deficiency (Hotz et al., 2007). It has been shown that periodic community delivery of vitamin A decreases the risks of xerophthalmia and mortality in young children (WHO, 2009).According to a survey, zinc deficiency was calculated highest in Asia, followed by Iron and Vitamin A (Amy Saltzman et al., 2017). Iron deficiency was found to be approximately similar for Asia and Africa followed by Latin America and the Caribbean and subsequently the Vitamin A deficiency was found to be highest in Asia, followed by Africa and Latin America and the Caribbean (Figure 1). As per the total kilocalories uptake in Asia, Africaand Latin America and the Caribbean, rice is the most consumed food crop followed by wheat, maize, potato and cassava.So the approaches to relieve Zinc, vitamin-A and Iron deficiency is change of diet, supplementation or Bio-fortification particularly in rice as it is the staple food.

BIOFORTIFIED RICE - ADVANTAGES AND LIMITATIONS

Biofortification is the production, without sacrificing agronomic efficiency and significant consumer preferred characteristics, of nutrient-dense staple food crops using the best traditional breeding practises and modern biotechnology. As plants expand, biofortification is based on making plant foods more nutritious. The foods are applied to traditional fortification nutrients when they are being processed (Nestel et al., 2006). For over a billion individuals, rice is a staple food crop. Rice endosperm is deficient in many nutrients, including vitamins, proteins, micronutrients, etc. (starchy and most edible component of rice seed). Nutrient reach is the Aleurone layer of dehusked rice grain but is lost during milling and polishing. Unprocessed rice, that is, smelly or nasty in taste, becomes rancid. Rice provides 30-50 percent of the daily consumption of calories. Rice farming is

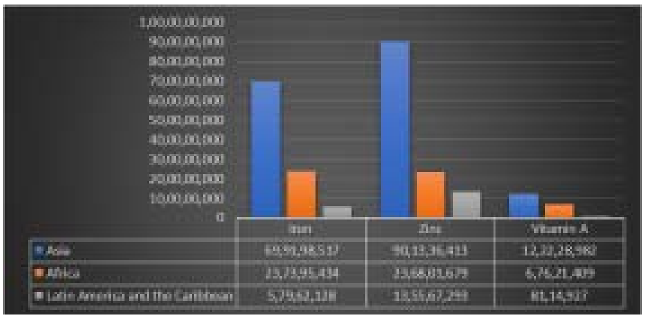

Figure 1. Population at risk for micronutrient deficiency

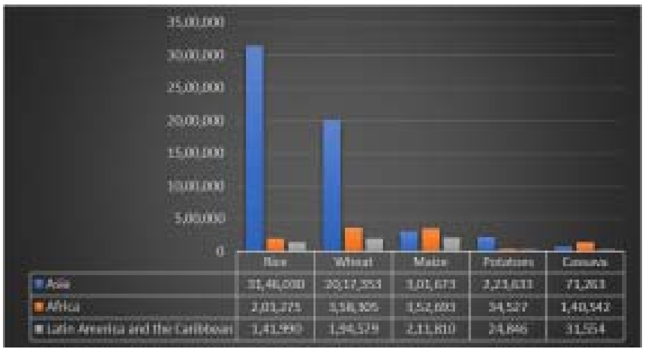

Figure 2. Total kilocalories per day (million) of top five staple crops

the primary source of jobs in India and globally, for the most part. Rice, due to its broader adaptability, plays an important role in food preservation. Rice endosperm, embryo, and bran contain 32%, 13%, and 55% respectively of iron, and they also contain 57%, 9%, and 34% respectively of zinc. Around 20.7 percent, 17.05 percent, and 36.61 percent Zn loss occurs during de-hulling, polishing and cooking. Rice is primarily grown in flooded soil where zinc is not very accessible to the crop because in reduced conditions it is bound to sulphur and carbonate.

It is a genetically modified enriched rice genome of provitaminA (â-carotene). All golden rice credits are awarded to the Rockefeller Foundation, the EU and the Swiss Federal Institute of Technology. Professor Ingo Potrycus and Dr. Peter Beyer were considered the creators of golden rice enriched with â-carotene. They used the soil bacterium (Agrobacterium tumifascience) crtl gene and the gene Daffodil gene for genetic makeup alteration. By breeding, golden rice cannot be achieved. Two grades of golden rice are available; golden rice1 (SGR1): promoter is modified here and contains 5-7ìg of â-carotene per gramme of rice and Golden rice2: replacement of Pys daffodil with maize gene and 31 ìg of â-carotene per gramme of rice. Some â - carotene enriched popular rice varieties are IR 64, IR 36 (mega varieties with broad Asian coverage), BRRI dhan 29 (the most popular boro rice variety in Bangladesh), PSB Rc 82 (the most popular Rice variety of Philippines), OS 6561 (most popular in Vietnam), Chehirang (leading variety in Indonesia), Swarna (important in India).

Biofortification of rice has many benefits, i.e. increased nutritional value, and decreased mortality caused by adult and child micronutrients, decreased diseases of dietary deficiency and a healthy population with good and rapid immune responses to infections. Biofortification of rice also has some drawbacks with these benefits, i.e. high cost of processing, i.e. machinery, technology, patenting, etc., potential negative interaction of biofortified rice on other plants / non-GM rice crops causing loss of wild type rice varieties, low significant equivalence, i.e. inability to provide high micronutrient and protein content compared to supplements.

CONCLUSION

The Green Revolution greatly increased production and achieved the food security dilemma of developing nations such as India, but it is far from developed nations in terms of dietary diversification. Approximately half of the world's population recorded Zn, Fe and vitamin A deficiencies leading to impaired immune function, iron deficiency anaemia, and xerophthalmia, respectively. People were advised to be careful about diversifying their daily diet to solve the problems of micronutrient deficiency, but most people do not afford to supplement their diet because of poor economic conditions. There was considerable potential for biofortification of staple crops such as rice and wheat to solve the problems of nutrient deficiencies. To relieve micronutrient malnutrition, awareness of dietary diversity must be controlled. Research and development of nutrient-enriched biofortified crops should be carried out to resolve this issue, as individuals from underdeveloped countries cannot afford supplemented and diversified foods. There are many elements of biofortification, but one is simpler. Therefore, the definition of food security can now be well defined as a sufficient amount of access to healthy foods.

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IRC/TM-1/PP-35

A PERFECT PCR BASED CO-DOMINANT MARKER OF OSABCC1 LIMITING SHOOT TO GRAIN TRANSLOCATION OF ARSENIC IN RICE

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Arsenic accumulation in rice grains is a serious public health concern affecting millions. Rice accumulates arsenic efficiently than any other cereals. Arsenic accumulation in the human body through drinking water and food results in various diseases including cancer. Rice is the primary route for dietary exposure of arsenic to humans (Signes-Pastor et al. 2008). Development of low arsenic-accumulating varieties for contaminated areas is considered an effective and sustainable solution for reducing the dietary exposure of arsenic to humans through consumption of rice.

Arsenic tolerance breeding in rice is associated with complex physiological and genetic challenges. Previously identified genes such as Lsi1 and Lsi2 could not be used in breeding due to lack of identification of suitable mutants. Arsenic phenotyping is also a difficult and laborious process. Moreover, molecular markers for easier selection of low arsenic accumulating genotypes are not available. Identification of novel alleles of important genes involved in arsenic accumulation from available germplasm and their molecular markers can therefore greatly accelerate arsenic tolerance breeding.

OsABCC1, a C type ABC protein gene in the rice genome, significantly limits shoot to grain translocation of arsenic by sequestering arsenic in the vacuoles of phloem companion cells in the first internode of rice (Song et al. 2014). Vacuolar sequestration of arsenic in the first internode by OsABCC1 is how rice saves its next generation of seeds from toxicity. OsABCC1 is therefore an important gene target for arsenic tolerance breeding in rice. The objectives of the present study were to

1. Identify a novel allele of OsABCC1 from native rice germplasm

2. Develop a PCR based co-dominant marker of OsABCC1 for selection

METHODOLOGY

100 genotypes along with 148 recombinant inbred lines (RILs) and near isogenic lines (NILs) from a cross between Gobindabhog and Shatabdi were cultivated in an arsenic contaminated field (22.92º N, 88.54º E), Nadia, India during wet seasons in 2017, 2018 and 2019 respectively for estimation of grain arsenic by FIAS-AAS(Perkin Elmer). The RIL population was developed by single seed descent method and NILs were derived by selfing heterozygous RILs. Relative quantification of OsABCC1 was done by Real Time PCR from the first internode of Gobindabhog and Shatabdi and their NILs during dough stage of grain filling. The whole gene was sequenced from Gobindabhog and Shatabdi by Sanger sequencing to identify single nucleotide polymorphism(SNP). One SNP in the 15th intron was used to develop a PCR based co-dominant marker. The marker was validated in the germplasm and RIL population.

RESULTS

In this study, grain-arsenic content in one hundred genotypes revealed a large variation ranging 0.053mg/kg to 0.49mg/kg. All aromatic genotypes accumulated significantly less arsenic in grains.

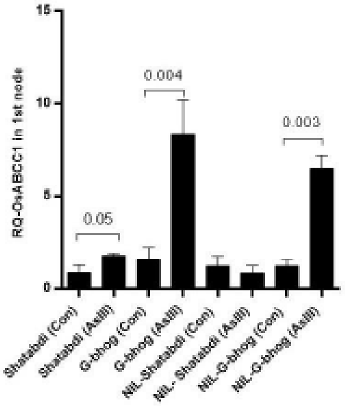

Figure 1. Relative abundance of OsABCC1 transcripts during dough stage in the first internode of Gobindabhog and Shatabdi and two NILs carrying Gobindabhog and Shatabdi alleles when grown in control (Con) and arsenic contaminated (AsIII) soils. Three biological replicated samples are indicated with SD. P value of Student's t test of parents and the two types of NILs are given on each pair.

Compared to high accumulating variety, Shatabdi, 6-8 times transcript upregulation of Arsenic sequestering gene, ABCC1, was observed in the first internode of low accumulating variety Gobindabhog when 5 mg/kg of arsenite was present in soil. Comparison of the genomic sequence of OsABCC1 identified 8 SNPs between the two genotypes; 5 in introns and 3 silent mutations in exons. We identified a PCR based co-dominant marker targeting a SNP (T/G) between the two genotypes which clearly distinguished 100 genotypes into low (mean 0.14mg/kg) and high (mean 0.35mg/kg) accumulating groups. All aromatic genotypes, either long or small grain, carry the Gobindabhog-type ABCC1 allele and are low accumulators of arsenic. Gobindabhog allele carrying 62 RILs and NILs showed almost 40-50% less As-accumulation in grains relative to 84 RILs and NILs carrying ABCC1-Shatabdi allele.

CONCLUSIONS

Identification of novel alleles of low arsenic accumulating genes and their molecular markers will greatly accelerate arsenic tolerance breeding in rice. In this study, we identified a novel allele of OsABCC1 from the local aromatic genotype Gobindabhog and developed a PCR based co-dominant marker for low arsenic accumulation genotyping in rice. The marker will be useful in introgression of low accumulating alleles of OsABCC1 into high yielding photoperiod insensitive varietal backgrounds more easily and accurately.

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IRC/TM-1/PP-36

YIELD ENHANCING ABILITY OF JAPONICA TYPE SPIKE1 GENE FROM AN AUS RICE AND ITS ALLELE SPECIFIC EASY-TO-USE MARKER

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Rice production needs to be enhanced 50% by 2050 to feed the predicted 9 billion world population without any chance of increased availability of cultivable land. Development of high yielding short and medium duration variety were achieved after introduction of Sd1 or green revolution gene. For further yield enhancement, breeders are targeting pyramiding of several yield enhancing QTLs and genes from diverse sources. SPIKE1 (Os04g0615000) gene on chromosome 4 is confirmed to be involved in yield enhancement by improving spikelet number per panicle but yield positive SPIKE1 allele is only reported in tropical and temperate japonica rice. Its yield enhancing ability in different indica background was explained by higher expression and dissimilarity in three amino acids relative to indica allele. Although aus and aromatic subpopulation is originated by different pathways as that of indica type but no report of allelic status of SPIKE1 gene in aus or aromatic subpopulation is observed. Multiple origin but single domestication theory showed the introgression of domestication related alleles from both japonica and indica into aus subpopulation. A few bp deletion causes a narrow leaf phenotype that Nal1 affects polar auxin transport as well as reduces the number of vascular bundles between two veins thus plays an important role in the control of lateral leaf growth and it is allelic to SPIKE1 (Fujino *et al*., 2008). It was also shown that GREEN FOR PHOTOSYNTHESIS (GPS) locus which improves carboxylation efficiency in rice, is also allelic to SPIKE1 (Takai *et al*., 2013). This GPS-allele increases mesophyll cell number between vascular bundles which leads to thickened leaves and pleiotropically enhances photosynthesis rate. Several allelic variants are reported to be involved in higher rate of net photosynthesis both in indica and japonica rice. Identification of yield positive allele of SPIKE1 in aus or aromatic subpopulation will be useful in rice breeding for their easier cross compatibility with indica-HYVs. The objectives of the present study were to

1. Identify a yield positive allele of SPIKE1 in aus or aromatic subpopulation
2. Develop a single PCR tube based co-dominant marker for marker assisted selection

METHODOLOGY

100 random genotypes of rice comprising local land races including some high yielding varieties were studied for important yield attributing parameters, flag leaf breadth and relative quantification of SPIKE1 was done by Real Time PCR. Based on contrasting phenotypic and real time data full gene sequences of some genotypes were compared. Besides a popular variety Shatabdi, Bhutmuri, an aus-type landrace of Bengal had the yield positive allele exactly similar to japonica allele. 165 recombinant inbred lines (RILs) and near isogenic lines (NILs) from a cross between Bhutmuri and IR64 were cultivated in a Jaguli field (22.92º N, 88.54º E), Nadia, India. The RIL population was developed by single seed decent method and NILs were derived by selfing heterozygous RILs. Relative quantification of SPIKE1 was done by Real Time PCR from the young panicles during 25 mm stage. The whole gene was sequenced from Bhutmuri, Vandana, IR64, Shatabdi etc by Sanger sequencing to identify single

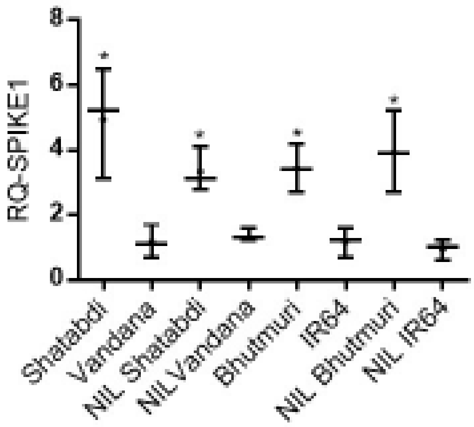

Figure 1.Relative abundance of SPIKE1 transcript in 25 mm stage of young panicle with three biological replications from the genotypes and NILs.

nucleotide polymorphism (SNP). One SNP in the 3'UTR was used to develop a PCR based co-dominant marker. The marker was validated in the RIL and NIL population.

RESULTS

In this study, one hundred genotypes revealed a large variation on yield attributing parameters and flag leaf breadth. Compared to Vandana and IR64, Shatabdi, Bhutmuri showed 4-5 times transcript upregulation of SPIKE1 gene. By comparing the genomic sequence of SPIKE1 among Bhutmuri, Shatabdi, IR64, Vandana, Dular etc we identified clearly two groups with 8 SNPs; 3 in introns, 3 mutations in exons and 2 in 3' UTR regions. Based on the A/G mutation at 9081 bp position at 3'UTR a single PCR tube based codominant marker has been developed and this marker has been validated in 165 RILs and NILs produced by a cross between Bhutmuri and IR64.

Comparison of yield (g)/sq m, filled grains/ panicle and panicles/plant among four genotypes and NILs carrying indica type parental SPIKE1 alleles [NIL-Van(S) and NIL-IR64 (S)] was done and another yield positive SPIKE1 [NIL-Shat(S) and NIL-Bhut(S)] allele and the means differ significantly at the probability $p<0.05$ and $p<0.01$ respectively by two way ANOVA analysis.

Comparison of the rate of photosynthesis (Pn), total conductance of CO2 (gtc) and vascular bundle number (VBN) between two major veins of the flag leaves, of Shatabdi, Vandana, Bhutmuri, IR64, SPIKE1-NIL Shatabdi, Vandana, Bhutmuri and IR64 (with five replication in each) was done. They show significant fifference at $p<0.05$ and $p<0.01$ respectively by Student's t test between the parents and between two groups of NILs.

CONCLUSIONS

Identification of single tube co-dominant marker for the yield positive SNP from aus type indica rice will be more useful in accurate selection of yield positive homozygous lines at the early segregating population and it will be easier for cross compatibility with indica-HYVs.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-37

GENOTYPE DEPENDENT LEAF AREA IMPROVEMENT OF RICE UNDER LOW LIGHT IS CORRELATED WITH HIGH PHOTOSYNTHESIS RATE PER DRY WEIGHT IN UNIT AREA AND YIELD ENHANCEMENT

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Preferred plant architecture of most of the short-stature, high yielding, N-responsive varieties with thick and erect leaves in rice breeding program considers no dearth of solar radiation. Thus, most of these rice varieties lack genotypic plasticity, particularly, for the areas where solar radiation drops below 500ìmol/m^2/sec. In the eastern states of India, rice plants receive less than 500ìmol/m^2/sec during wet seasons, i.e. during the months, July to October, consequently, rice suffers yield loss. It is also observable by the huge yield gap between wet and dry seasons in this zone (2.8 tone/ha vs 5.1 tone/ha). Although yield is complex traits depends both on source and sink but photosynthesis efficiency and high remobilization capacity play important roles in improving yield, particularly, if light is below optimal (Evans and Poorter, 2001; Fabre et.al., 2016). Rice also improves leaf area (LA) under low light but genotypic variation and their correlation with the yield improvement ability is not described. Therefore, variation of LA between semi-dwarf high yielding varieties and other local landraces adopted to semi-deep and deep water ecologies (usually receives low light intensity), if exists, may be useful in rice breeding program, particularly, if photosynthetic plasticity also presents in these genetic resources. Leaf size and shape controlled by many quantitative trait loci (QTLs) located on 12 chromosomes and a few of them were cloned also. Leaf size controlling genes or QTLs influence the rice yield also as photosynthetic products of top three leaves have the major contribution in grain filling and flag leaf alone contributes more than 50%.

We identified large variation in leaf area in rice and its positive correlation with shade tolerance index. Most of the semi-deep rice genotypes showed high yield by improving leaf area, chlorophyll b and photosynthesis rate in DW per unit area and a few of them also plastic. Relative abundance of NAL1 gene in flag leaf was high in most of the genotypes with high SLA index but the gene is not upregulated under LL.

METHODOLOGIES

We grew 30 genotypes both under open and shade following randomly block design with three replications. Shade-net (30% light-cut) was provided at the height of 3m keeping 1.5m open from the ground so that sufficient air can flow.Photosynthetically active radiation (PAR), temperature and relative humidity was measured daily at 9hrs, 13 hrs and 15:45 hrs during the period, transplanting to maturity, by portable automatic weather station. No significant difference in relative humidity and temperature was observed between open and shade during growth period.

The LAI was obtained by multiplying the leaf area per gram by the total dry matter of all green leaves from the sample area and dividing by the area occupied by the sample.Photosynthesis rate (Pn) of the flag leaf were measured with portable gas-exchange systems (LI-6800; LI-COR, USA) at the two days after heading. The ambient CO2 concentration in the leaf chamber of LI-6800 was kept at 380 molm^{-2}s^{-1}.

RNA was isolated from three plants of each line and the sample was pooled as described earlier.

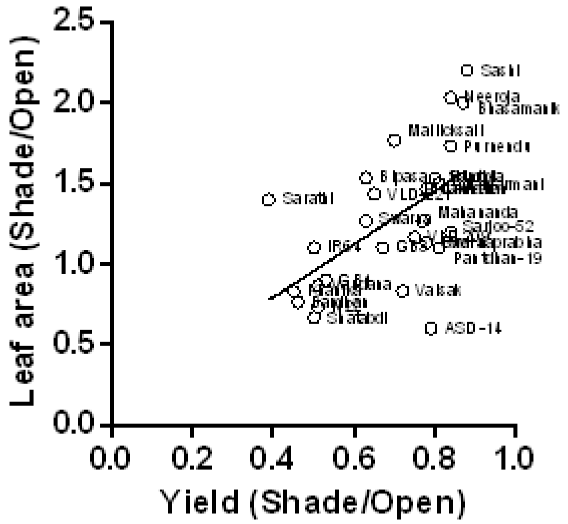
Quantitative real-time PCR analysis was performed on a StepOnePlus Real-Time PCR System (Applied Biosystems, USA) using a SYBR green PCR master mix(Applied Biosystems, USA) as described earlier Bhattacharyya et al 2002.

RESULTS

This study observed observed wide variation of leaf area among the genotypes ranging from 737 cm^2 to 2676 cm^2 under open and 555cm^2 to 4478cm^2 under shade with mean 1545cm^2 and 2088cm^2 respectively.Wide range of specific leaf areaalso observed with a range 8.9-30.6 under open and 11.2-57.4 under shade with mean 16.5 and 28.1 Thus, the consideration of leaf area index, LAI and specific leaf area index, SLAI (ratio of shade by open) reflects the genotypic specific acclimatization ability and plasticity under shade. Under shade 30% and 70% increase of LA and SLA was observed.

THRESHOLD LIGHT INTENSITY FOR IMPROVING LEAF AREA

To identify the threshold light intensity for leaf rea and specific leaf area expansion, we arranged another two shade-areas with two and three lairs of white-net, thereby, four different situations created including one open condition with ambient light intensity another with single layer of net. Both genotypes, Purnendu and IR64 started leaf-area expansion at 622 µmole/mt^2/sec PAR or below but Purnendu started improvement of SLA even above 622 µmole/mt^2/sec**.** Both leaf area and SLA declined sharply in between 351 and 160 µmole/mt^2/sec but leaf area at 160 µmole/mt^2/sec became less than those of ambient condition but SLA remain greater at the same low light intensity than those under ambient light (approx. 1000 µmole/mt^2/sec).Negligible expression observed at 30 DAT in all the genotypes except Laldhan. At PI stage, Bhasamanik, Laldhan, Pantdhan19 and Sashi showed high expression relative to remaining genotypes under shade. Less expression found in Purnendu although high SLAI (2.7) recorded.



CONCLUSION

Overall, rate of net photosynthesis rate reduced to half in shade as compared to open by most of the genotypes butimprovement of photosynthesis rate per DW in unit leaf area under shade was observed only in tolerant genotypes. High LAI with high photosynthesis rate per DW in unit leaf area can be targeted during shade-tolerance breeding program and contrasting parents will be useful for the mapping of the traits.

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IRC/TM-1/PP-38

IDENTIFICATION AND ANALYSIS OF LOW-LIGHT TOLERANT RICE GENOTYPES IN EASTERN INDIA

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In India and South Asia, rice is cultivated mainly in rainy season (*kharif rice*) when it receives significantly less irradiation (below 500 ìm/m-1/sec-1) due to overcast cloud throughout the growing season. Low irradiance reduces the photosynthesis vis-a-vis dry weight, as rice exhibits optimum net photosynthesis at the range of 800-1000 ìm/m-1/sec-1 (Murchie *et al* 2002; Kasajima *et al* 2011). Depending on the stage of rice, low light intensity can affect grain yield by 34-55% (Dutta *et al*, 2018; Janardhan *et al*, 1980; Nayak and Murty, 1980; and Voleti and Singh, 1996) and it is due to reduced tiller number, dry weight (Venkateswarlu 1977, Singh 2005), spikelet number (Adhya *et al* 2008), test weight (Voleti and Singh 1996, Jiao and Li, 2001). Several reports indicated that mechanism of high yielding ability under shade varies according to varieties (Janardan and Murty 1980, Nayak and Murty 1980). Tolerant varieties adjust the low irradiance by improving net photosynthesis rate with stronger antioxidant activities and higher amount of chlorophyll a and b better translocation efficiency from source organ to sink organs vis-à-vis prevents impaired sink size.

As variety specific tolerance mechanism is reported earlier so our objective was to screen a large set of genotypes in field for identification of tolerance genotypes with diverse mechanism of low light tolerance which will finally help in pyramiding of target traits.

METHODOLOGY

300 rice genotypes, predominantly landraces or its derived lines, collected from eastern and north eastern India were grown both under white shade net (30-35% light-cut) and open conditions in university experimental field (Latitude 22.87° and longitude 88.20) for the first year (2015) in augumented design. Based on high yielding ability under open field, 100 genotypes were selected and grown further for consecutive three *kharif* seasons (2016, 2017 and 2018)in randomized block design. Five randomly selected plants from each row were used for taking observations, like, no of panicles per plant (PN), dry weights (50 days after transplanting) (DW), days to 50% flowering (DFF) and grain yield per plant (YP).

The chlorophyll content was calculated following the equations proposed by Barnes *et al.*1992. Flag leaves were considered for the estimation of net photosynthesis rate (Pn) at the panicle initiation stage (within two days of emergence) using portable photosynthesis analyser Li6800 of LiCor, USA using various intensity of light ranging from 50 to 900 ìm photon m-2s-1. Mean value of consecutive three years' data as well as proportion of performance under low light and open expressed as index, considered for PCA, Pearson correlation and two-tailed t-test analysis using XLSTAT 2019. Two-way ANOVA was made using Graph Pad Prism 6. Stable genotypes were identified based on stability analysis (Eberhart and Russel Model, 1966) and as per model, stable genotypes were those where mean square deviation from regression line (Sdi2) not significantly (at 5% level) different from zero.

RESULTS

100 high yielding genotypes were selected for

growing consecutive three years for analysis of yield attributing and other parameters. Index is calculated as the ratio of performance under shade by open. The mean value of per-plant yield (PY) under low light intensity was 8.19gcompared with the open 16.81g with more than 50% reduction where as 38%, 34% and 22% reduction of panicle number (PN), grain number (GN) and test weight (TW) were observed in the same condition. Under shade, 39% and 19.7% of the total yield-variation is controlled by genotypes and years respectively where as 71% and 2% under open grown plants. Heritability (broad sense) of the yield under shade is low (58% vs 83%) relative to open. GN, TW and DW showed significant correlation between open and shade and no correlation observed for PY, PN and Chla/b. Purnendu showed best shade tolerance ability (STI, 0.79) but Pantdhan19 yielded highest, 15.8g. Purnendu, Sashi and Pantdhan19, showed less yield reduction by maintaining or even by increasing grain numbers under shade and test weight. On the other hand, maintenance of equivalent number of panicle under both situations was the key for the tolerance of Bhasamanik, Sasarang, Rudra and Swarnaprabha. Both open and shade grown plants showed wide range of variation both for chlorophyll a and b with mean increase of 12% Chla/b under shade. 34% reduced mean dry weight observed ranging from 32 to 90% although Sasarang, Rudra and Purnendu limited less than 20% reduction under shade. PCA identifies the mutual relationship between characters and help us deciding the important characters explaining maximum contribution towards variation and related genotypes for those contributing character. Three eigen-vectors with near one eigen value explain almost 70% of the total variation. First component explains 35% variability and STI and PNI, have the major contribution with their positive association. In second component explains around 19% variability, mainly contributed by GNI, TWI and DWI. GNI and SWI are negatively associated with DWI and PNI. The study identified stable genotypes considering three year's PY and PN of 20 contrasting genotypes following Eberhart and Russel model (1966).

CONCLUSION

Genotype dependent shade tolerance was manifested by either improving or maintaining equal amount panicle number or grain number or test weight. Thus, stable shade-tolerant rice lines Purnendu, Sashi, Pantdhan19 from a large set of genotypes with different adjustment ability to keep up 72% or more yield of open-grown plants can be used further for the yield improvement in *kharif* season as well as analysis at the physiological and molecular levels.

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IRC/TM-1/PP-39

AGRO-MORPHOLOGICAL AND QUALITY CHARACTERIZATION OF FINE AND SEMI-FINE GRAIN RICE (*ORYZA SATIVA* L.) FOR TEMPERATE AGRO-ECOSYSTEM

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Rice (*Oryza sativa* L.) plays a significant role in livelihood of people of Jammu and Kashmir State. Kashmir valley has a tradition of growing short to medium bold seeded rice varieties. But with change in life style and preferences, high demand for fine grained and aromatic rices is being observed in the market. This has resulted in a huge import of such rices from neighbouring states. Fine and semi-fine grain basmati rice is praised for its unique quality and gives pleasant flavour after cooking. The aromatic basmati and fine grain rice varieties offers high returns to farmers, enjoying a preferential treatment both in domestic and international markets generating three times more income, so farmers are more inclined to it.

The testing and evaluation of fine/semi-fine grain basmati types of rice is being continuously carried out at Khudwani centre of SKUAST-Kashmir, a unique temperate research centre of the country. The results have shown that grain size, grain texture and cooking quality traits are not as per the standard. The foremost reason is that these varieties are late maturing and as a result have to face lower temperatures particularly at flowering and grain filling stages. This influences grain chalkiness, head rice recovery and overall grain quality. In this connection an experiment was undertaken during 2017 at Khudwani centre of SKUAST-Kashmir (1690 m amsl) with the objective to characterize a number of fine and semi-fine grain rice genotypes and evaluate some promising ones for cooking quality and aroma.

METHODOLOGY

The experimental material consisted of 92 rice genotypes along with four check varieties. The materials were laid in augmented block design in the field and plot size given to each genotype was 15 m^2 with crop geometry of 20 cm x 15cm. Agro-morphological and cooking quality characters were recorded as per the descriptors for rice formulated by IBPGR-IRRI Advisory committee (IRRI, 1980).

RESULTS

The results have revealed a broad-spectrum variability for traits like days to 50% flowering (81.0-115 DAS), number of tillers/plant (10.2-24.4), number of spikelets/ panicle (50.2-207.1), panicle length (20.1-26.8 cm), panicle fertility (57.3-89.2%) and for grain yield (15.5-85.8 q/ha)[Table 1]. The most promising genotypes identified on the basis of agronomic features were AVT-FG V1, IRTON-25, AVT-FG-V2, AVT-I E(H)2511, IVT M(H) 2817, PVT-V1 and IVT-BT-3010 (Table 1). Cooking quality analysis of some promising varieties showed significant variations within different quality parameters. The longer kernel length, higher elongation after cooking, intermediate amylose content and strong aroma were found to be the distinctive features of the identified promising rice cultivars (Table 2). The testing of these promising varieties in multilocation trials representing different ecotones of the valley will help in identifying most stable

Table 1: Agro-morphological trait characterization of promising fine and semi-fine grain rice genotypes

Genotype	DF	PH	NT	PL	DM	NG	PF	GY
AVT-FG-V1	102	91.2	11.9	26.4	143	128.6	84.82	75.07
AVT-FG-V2	103	91.1	12	25.0	142	58.6	88.82	69.36
AVT-FG-V3 (SKUA-494)	110	90.9	13.8	25.4	143	124.7	88.01	67.28
AVT-FG-V4	106	87.6	13.3	26.1	144	145.3	85.12	60.05
AVT-FG-V5	106	91.1	13.0	25.4	143	175.6	89.22	85.83
AVT-FG-V6	105	90.0	11.9	26.8	143	110.6	83.66	82.97
AVT-FG-V7 (SKUA-420)	111	87.0	14.1	25.6	157	137.3	89.18	45.08
AVT-FG-V8	105	91.9	12.3	25.7	143	109.3	70.37	69.77
PUSA BASMATI-1509	115	94.7	13.8	27.4	153	50.2	62.98	15.58
PUSA SUGAND-3	115	88.7	13.8	23.0	143	162.9	81.98	19.87
IVT-BT-3024	100	88.1	11.5	24.3	141	188.9	88.76	20.27
IVT-BT- 3027	101	91.6	12.4	26.8	140	115.7	74.30	26.40
IVT-BT-3022	101	93.8	11.7	24.3	143	78.0	57.31	22.50
IVT-BT-3020	114	86.7	10.2	21.2	141	182.5	55.95	26.35
IVT-BT-3010	104	91.7	13.9	24.2	141	182.5	80.45	75.40
Genotype/ Ecotype	DF	PH	NT	PL	DM	NG	PF	GY
GS-390	81.0	104.8	11.5	25.0	133	207.1	70.41	22.00
GS-393	94.0	138.1	10.7	24.6	130	160.7	77.82	22.00
GS-407	95.0	138.2	10.8	25.7	130	119.2	75.39	24.20
PVT-V1	97.0	125.3	12.7	20.0	146	146.9	81.02	56.74
GSR-33	101	119.5	16.7	21.2	147	119.5	77.85	66.99
GSR-30	115	75.3	17.6	19.5	146	115.5	71.56	76.83
IRTON-23	103	66.7	24.4	21.1	146	119.8	72.08	75.00
IRTON-25	103	119.9	17.3	21.8	141	152.0	88.01	70.00
IURON-8	108	106.8	10.5	22.8	150	121.6	82.66	63.91
IURON-20	107	66.4	14.1	23.5	145	108.0	75.15	68.07
AVT-1-V3	97	96.4	12.7	25.0	146	162.5	72.38	49.61
AVT-IE(H)2511	93	108.8	13.7	21.7	143	150.3	81.06	71.95
IVT-IM(H)2817	98	103.6	12.3	23.7	143	119.1	81.46	57.44
IIRON-35	113	95.4	12.0	20.1	144	115.2	77.31	34.03
Range	81.0-115	75.3-138.2	10.2-24.4	20.1-26.8	130-157	50.2-207.1	57.3-89.2	15.5-85.8

DF= Days to 50 % flowering; PH=Plant height (cm); NT= No. of tillers/ plant; PL=Panicle length (cm); DM= Days to maturity; NG=No. of grains/panicle; PF=Panicle fertility (%); GY=Grain yield (q/ha)

Table 2: Cooking quality traits of promising fine and semi-fine grain rice genotypes

Genotype	KLAC	KBAC	Aroma	GC (mm)	ASV (1-7 scale)	AC (%)
AVT-FG-V1	8.4	1.7	4	46	2	25.4
AVT-FG-V5	10.36	2	3	44	3	23.6
AVT-FG-V6	13.88	2	4	45	4	27.0
IVT-BT-3010	8.44	1.72	4	40	7	24.3
AVT-IE(H)2511	9.1	2.1	4	37	1	20.5
IVT-M(H)2817	10.1	2.3	3	20	2	26.5
IRTON-23	9.8	2.2	3	44	1	23.4

KLAC=Kernal length after cooking: KBAC=kernel breadth after cooking: ASV=Alkali spread value

and farmer preferred variety for wide cultivation across the state.

CONCLUSION

Agro-morphological traits evaluation of 92 fine/ semi-fine rice genotypes showed much variation. Some of the promising rice varieties on the basis of various agronomic traits also exhibited good cooking quality. Hence, these genotypes are suggested for wider testing in order to find the most stable cultivars for general cultivation across the valley.

IRC/TM-1/PP-40

IDENTIFICATION OF SUPERIOR ALLELES FOR HIGH YIELD-POTENTIAL UNDER DROUGHT AND THEIR FUNCTIONAL MARKERS FOLLOWING CANDIDATE GENE APPROACH IN RICE

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Drought reduces yield by 15–50 per cent depending on the stress intensity and crop growth period at which the stress occurs in rice. Drought stress occurs at any stage of rice growth and the magnitude of loss depends on growth stages; among these, drought stress at the flower initiation stage may cut yield much as plants do not get any scope to decrease the loss by physiological and phenological adjustments. Drought stress at the reproductive stage (panicle development to anthesis) reduces yield severely because it hampers the spikelet primordia development and promotes floral sterility. Efforts initiated for the development of variety which simultaneously yield both under water stress as well as under non-stress environment.

Several genes have been identified already which influence the performance of rice yield under drought. Among them, it has been observed that overexpression of candidate genes in root, viz, OsNAC10 (NAC domain containing gene, AK069257), OsAP37 (Apetalous 37, AK061380), significantly improve rice yield (Jeong*et al*., 2010; Oh *et al*., 2009).Overexpression was made by transgenic approach using strong root-specific promoter. There is no information regarding the status of these genes in landraces of rice or available drought tolerant varieties/ genotypes. So efforts will be initiated to identify the status of these genes in drought tolerant genotypes. Ultimately, it will lead to identification of superior alleles and their functional markers which will be useful in rice breeding program for developing drought tolerant lines. So, the objectives of this study are

i. Identification varieties/landraces with high yield potential under water deficit condition.

ii. Identification of superior alleles for the drought tolerant candidate genes using relative quantification of transcript.

iii. Development of functional candidate gene based marker.

METHODOLOGY

Thirty rice genotypes comprising of landraces collected from upland ecology, known drought tolerant genotypesand high yielding cultivars evaluated for their reproductive drought tolerance ability both under soil cylinder experiment (15-20% moisture w/w) at the rainout shelter as well as under rainfed low land field. Drought stress was imposed by withdrawing water by two weeks in a set of cylinders at the panicle initiation stage keeping another set well irrigated.

RESULTS

Drought stress in soil-cylinder experiment reduced plant yield (PY) on water sufficient condition, as expected, from an average of 14.92g-10.95g under drought i.e. almost 23% mean reduction. Mean difference between WS and WD grown plants for most of the parameters likeflag-leaf temperature (^{0}C) mean (33.2 ± 1.16 vs 35.8 ± 1.2), CG/panicle (22± 9 vs 46± 8.1), root fresh wt (57.1 ± 31.5 vs 22.9± 11.9), root dry wt(g) (24.6± 14.1 vs 8.6± 4.4). Mean filled grain reduced to 62.0 from 85. A strong and positive relationship between filled grain and PY both under WD (r= 0.686) and WS (r=0.542) was observed but chaffy grain showed a negative correlation with yield under drought stress but not under WS. High net photosynthesis rate showed also positive correlation (0.308) with yield under drought but the correlation was insignificant under WS. Bi-plot analysis using two major components of PCA analysis identified Chotogora, Kariagora, Rasi as the tolerant high yielding genotypes along with known tolerant lines N22 and Dular. Yield and its attributing parametersof all 30 genotypes compared in regional research substation at Sekhampur following RBD both under well-watered and water deficit (irrigation withdrawn at the 45 days after transplanting) conditions. Mean yield reduction was 1.71 kg/10m^2 which was about 40% ranging from 19% to 58%. Chotagora, N22 and Bhutmuri produced 4.32 t/ha, 3.84 t/ha and 3.79 t/ha with drought tolerance index (ratio of yield in Water deficient by sufficient) 0.81, 0.80 and 0.67 respectively. When yield potentiality of newly identified two lines, Chotogora and Bhutmuri was compared with N22, no significant differences noticed among these three genotypes under WD but Chotogora produced better yield under WS condition. Thus, reproductive drought tolerance ability of Kariagora, Chotogora was almost similar to Dular and N22, if not better and Chotogora and Bhutmuri can be considered as high yielding donor parent for improving yield under drought-prone areas in addition to N22 and Dular. Like soil cylinder experiment, yield under WD was positively correlated with filled grains/panicle.

Over-expression of two genes, OsAP37 in leaves and OsNAC10 transcription factors in roots improves yield during terminal drought stress. Sequencing of the full length genomic DNA OsAP37 and NAC10 was done among eight genotypes. Multi-allignment identified SNP based alleles for both genes: Chotogora and N22 carry the same AP37 allele as reference Nipponbere (Japonica) whereas Chotogora, Kariagora and N22 possess same NAC10 allele like Nipponbere and remaining genotypes are the same as that of IR64 (Indica). Relative abundance of AP37 and NAC10 transcripts was compared in stress grown five genotypes, Satabdi, Chotogora, Kariagora, N22 and IR64. Transcript abundance of AP37 was 10-12 times higher in three rice genotypes with higher drought tolerance index, Kariagora, Chotogora and N22. Similarly, expression of NAC10 transcript was also 5-6 folds greater in Kariagora and Chotogora on Satabdi. This study also developed SNP derived PCR based markers for both genes. Kariagora NAC10 allele when validated in F$_8$ population, it showed yield advantage over N22 allele under reproductive stress.

CONCLUSIONS

Overall this study identified reproductive drought tolerance aus type landrace, Chototogora, Kariagora and Bhutmuri, and among these, Chotogora and Bhutmuri capable of producing high yield both under WS and WD. They are suggested for cultivation in the vast drought-prone rainfed low land areas of red and lateritic soil and use in the hybridization program also. Other than high filled-grain/panicle, narrow gap of the flag-leaf temperature between WS and WD and high potential yield no specific physiological and morphological characters seem to contribute directly to higher yield. However, instead of the selection parameters available during drought stress, better recovery capacity as reflected by high grain yield should be the criteria for the final selection of reproductive drought tolerance lines. SNP derived PCR based markers from the OsAP37 and OsNAC10 allele of Chotogora and Kariagora can be useful after further validation for the improvement of yield when drought develop during panicle initiation to flowering stage.

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IRC/TM-1/PP-41

DEVELOPMENT OF AN ALLELE SPECIFIC MARKER OF YIELD ENHANCING NOG1 GENE IN RICE

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Rice (*Oryza sativa)* is the staple food for one third of the world's population and one fifth of the total land area occupied by cereals, is under rice production. FAO had raised its forecast of world paddy production in 2017 by 2.9 million tonnes to 759.6 million tonnes (503.9 million tonnes, milled basis). The average yield of rice is 3.5-5 t\ha. In present scenario to fulfill the increasing demand of rice the average yield must be increased. Some rice genotypes like Satabdi (8t\ha), Ajay (7.5t\ha), Khitish and Rajlaxmi (7t/ha) lead to the stagnation of yield in rice. Our challenge is to break this yield plateau. For this both source and sink must be improved. Recently, rice breeders are aiming towards developing rice varieties which not only perform better under favorable condition but also perform well in different agro ecological condition. Such a variety is really missing across the globe Deb. Genetic diversity as contained in folk varieties (also called landraces) of rice and its wild relatives provides the bedrock of evolution for cultivated rice (Oryza sativa) and its differentiation into various cultivars to adapt to different environments. Additionally, most of the landraces of rice varieties do not fetch better market price or acceptable due to lower yield and poor grain quality. So, efforts are really required for identification of new high yielding candidate genes resources with good grain quality as well as possessing other criteria in normal situation. There is no information regarding the status of these genes in landraces of rice or available in high yielding acceptable varieties/genotypes. So, efforts will be initiated to identify the status of these genes in high/low yielding varieties and landraces. Ultimately, it will lead to identification of superior alleles and their functional markers which will be useful in rice breeding program for developing high yielding lines. Recently, several yield enhancing genes of rice are identified following map based cloning. *NOG1* is such a gene which improves grain/panicle without a negative effect on the panicles per plant, test weight and heading date. Introduction of favorable *NOG1* allele increases the grain yield by 25.8% in the rice genotypes carrying *NOG1*-unfavourable allele. Even over expression of *NOG1* can further increase the grain yield by 19.5% in the *NOG1*-containing variety.A 12 bp light sensitive Cis-sequence repeat is identified on the 5'-upstream regulatory element of favourable *NOG1* alleles.hence,our hypothsis was the rice genotype with higher expression NOG1 gene with 12 bp repeat element can be targeted for the improvement of rice yield.

OBJECTIVES

Identification of superior allele for NOG1 gene and validation of allele specific markers associated with increased grain yield of landraces under West Bengal condition.

MATERIALS AND METHODS

Allele specific primer pairs were designed from the promoter region (position - Forward primer 1189bp and Reverse primer 1353bp) – expected band size: 164 bp and 152 bp of NOG1 to identify the 12bp IN/DEL variation.200 genotypes were screened based on PCR based markers followed by field-phenotyping for the consecutive three years. RNA extraction was done from flag leaves during panicle initiation stage using thermo scientific GeneJET Plant RNA Purification Mini

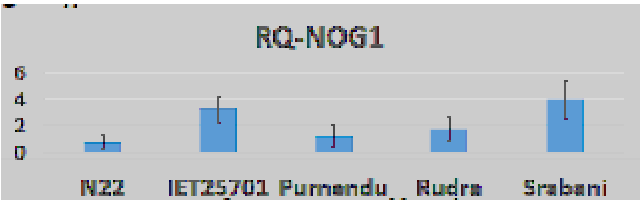

Fig. 1. Relative expression of NOG 1 gene in flag leaf of different genotypes

Kit. Crossing were done between N22 (NOG-), IET25701 (NOG+) & Rudra (NOG+), Purnendu (NOG-) parental pairs and were utilized for validation. Selection was done on the basis of Real time PCR and Yield related parameters i.e. Total grain number per panicle, primary branch number, grain number of primary branches, the secondary branch number and grain number of secondary branches.

RESULT

In this study, two hundred genotypes revealed a large variation on yield attributing parameters i.e.grain number per panicle. Compared to N22 and Purnendu , Rudra, IET25701 showed 4-5 times transcript upregulation of NOG1 gene. Hence, these two contrasting genotypes are used as parents to develop RILs and hetrozygyte derived NILs lines. A PCR based In/Del marker has been developed and this marker has been validated in 130 RILs and hetrozygyte derived NIL lines produced by a cross between N22and IET25701 and Rudra and Purnendu. Comparision of Number of grains per panicle were done in both RILs and NILs with single point analysis shows significantly differencein the means at the probability $p<0.05$ and $p<0.01$ respectively.

CONCLUSION

In-Del based marker, developed from the Up-stream regulatory elements of NOG1 is useful for the identification of yield enhancing alleles from a large number of genotypes very easily. NOG1 allele of IET25701 is useful for the enhancement of yield in rice.

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IRC/TM-1/PP-42

ASSOCIATION MAPPING FOR AGRONOMIC AND GRAIN QUALITY TRAITS IN RICE (*Oryza sativa* L.)

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Rice is staple food for more than half of the world's population. It also serves as a model monocot plant for genetic and genomic study. India has the largest area under rice with about 44 million hectares and second in production with 110.15 million tons in world during 2017-18 (Neerja et al. 2019). The estimated Indian population by 2050 is 1.63 billion and a per capita demand about 250 g/day, the productivity needs to be increased from the present 2.05 t ha^{-1} to 3.3-4.05 t ha^{-1} to meet the requirement of about 150 million tons of rice (Neerja et al. 2019). Since the current yield trends are not sufficient to feed the projected population by 2050. Developing high yielding varieties is priority to feed the projected population by 2050. To meet the food needs of the growing population, plant breeders select for agronomically important traits like yield. Determining the genetic basis of quantitatively inherited traits is a major goal in plant breeding. Identification of QTLs or genes associated to particular trait accelerated the crop improvement either by introgressing the identified QTLs/genes in desired genotype by marker assisted breeding or by transgenic technology. Over the last two decades, conventional linkage mapping has facilitated the identification of individual quantitative trait loci (QTLs) associated with yield factors, biotic and abiotic stress tolerance and other quality traits in rice. However, it has relatively low resolution and is time-consuming as it requires generation of large size mapping population from biparental crossing. In contrast, the association mapping is a powerful approach to identify associations between traits of interest and genetic markers using diverse genotypes.Association mapping provides broader allele coverage as a high-resolution gene mapping method as compared to the biparental mapping method.Many QTLs can be mapped simultaneously and reported QTLs can also be validated. Several useful QTLs and genes reported for agronomic, yield and nutritional traits in various biparental and natural mapping populations in rice.However, there is a need to continuously search for novel alleles to cater to the diverse needs of breeding programs to mitigate the adverse effects of climate change and to meet the food and nutritional demands of farmers and consumers (Descalsota-Empleo et al. 2019).The present study was conducted to characterize the rice germplasm and identify molecular markers associated with agronomic and grain quality traits that could be useful for breeding programs.

METHODOLOGY

Forty-eight germplasm of rice was grown in the experimental field of Rice research farm, Bihar Agricultural University, Sabour, Bhagalpur. The seedlings were transplanted in a Randomized Complete Block Design in two replications with spacing of 20 cm row to row and 20 cm plant to plant. All the recommended agronomic packages of practices were adopted during the entire crop period. In each replication, five random plants from middle portion of the rows were chosen and the observations were recorded on days to 50% flowering,plant height, panicle length, flag leaf length, flag leaf width, effective tillers per plant, number of grains per panicle, test weight, grain yield per plant, grain length, grain breadth and grain length/ breadth ratio. DNA was extracted from the forty-eight germplasm of rice by using modified Dellaporta protocol. The DNA extracted was used for PCR amplifications with 56 SSR markers.The PCR products were resolved by agarose gel electrophoresis. The amplicons were visualized by UV light and documented in gel documentation system. The mean phenotypic data of two replications were subjected to analysis of variance (ANOVA) for all traits. The correlation coefficients were computed between all the traits under study. The genotypic data generated from 38 polymorphic SSR markers were used assesspolymorphism information content,similarity coefficients, population structure and kinship coefficients. Association between SSR markers and phenotypic performance (twelve traits) of the rice germplasm was calculated using software TASSEL Standalone Version 4.0. The two statistical models i) general linear model (GLM) and ii) mixed linear model (MLM) were used for the analysis.

RESULTS

SSR markers produced 110 polymorphic loci out of 38 polymorphic markers. Polymorphism information content value ranged between 0.10 and 0.37. The marker RM8085, RM475 and RM235 was highly informative. The Cluster analysis based on UPGMA method separated the 48 germplasm into five major clusters. The population structure analysis grouped the 48 rice germplasm into two subpopulations, one with 7 genotypes and the other with 41 genotypes. Kinship analysis indicated a total of 91.62% of the germplasm having their kinship estimates between 0.50 and 1.50. The association analysis identified 125 and 84 marker-trait association by GLM and MLM approaches, respectively at P values <0.05. The phenotypic variations demonstrated by the associated loci ranged from 8.11 to 38.66% and 6.71 to 27.24% for GLM and MLM, respectively. In GLM, marker RM430 located on chromosome 5 showed highly significant association with test weight. While in MLM, marker RM6324 located on chromosome 1, RM320 located on chromosome 7 and RM552 located on chromosome 11 showed highly significant association with grain breadth and RM6324 located on chromosome 1 showed highly significant association with test weight. The significant marker-trait association was lower in MLM compared to those in GLM. MLM method was proven to be useful in controlling false associations.

CONCLUSION

The markers identified in this study which needs to be further validated and would be very useful in marker assisted selection programs.

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IRC/TM-1/PP-43

RICE GENETIC RESOURCES: COLLECTION, CONSERVATION AND UTILIZATION

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The plant genetic resources (PGR) is the basic raw material for any crop improvement programme. It may consist of seed or vegetative propagules (tuber, rhizome, sucker, buds, cutting, seedling etc.) of crop plants, which contains the functional units of heredity. They are generally known as germplasm or genetic resource material. Sir Otto Frankel coined the word 'Genetic Resources'. Rice (*Oryza sativa L.*) is one of the most important cereal food crops for more than 50% of the world population and provides 50–80% of daily calorie intake. Rice is grown in more than 115 countries. In India, it is cultivated under a wide range of growing conditions. Below sea level farming in Kuttanad in Kerala and high altitude farming in the Himalayas. Because of its adaptation to such variable agro-ecosystems. The increased demand for rice will have to be met from less land, less water, less labour and fewer chemicals under changing climate. Can we meet the challenges to rice productivity, stability and nutritional quality improvement by strategic use of the available PGR? Can India, having more than 106,000 germplasm in the National Gene Bank (NGB) effectively use of these resources? Past experience suggests that germplasm still holds the key to our food and nutritional security of future generation. It is well known that the traditional rice varieties and their wild relatives constitute an invaluable gene pool in terms of resistance/tolerance to biotic and abiotic stresses, which can be exploited for developing modern new generation rice varieties having enough resilience to sustain the adverse climatic changes.

IRC/TM-1/PP-44

STUDY OF GENETIC PARAMETERS FOR YIELD AND NUTRITIONAL TRAITS IN RICE (*ORYZA SATIVA* L.)

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Rice is the world's most important food crop and a primary food source for more than one third of world's population. It is the crucial dietary and food security source for people of many Asian countries. The essence of plant breeding lies in the creation of genetic variation which is a prerequisite for any crop improvement programme.A thorough knowledge on nature and magnitude in the genetic variability and association of characters of a species is a pre-requisite for an effective breeding programme. Increased health consciousness among the rice consumers has resulted in greater attention to the genotypes containing higher levels of bioactive compounds, such as antioxidants and phenols. In this context, the present study was takenup to assess the genetic parameters for the yield and nutritional content of traditional coloured as well as white rice genotypes collected from the farmers of different districts of Telangana.

METHODOLOGY

The 30 genotypes (comprising of red and white pericarp) used in the present study were collected from farmers of different districts of Telangana.All the 30 genotypes were grown at Agricultural College Farm, Bapatla during *Kharif*2018 on separate raised nursery beds. Thirty days old seedlings were transplanted in the main field laid out in Randomized Block Design (RBD) with three replications.Observations were recorded on 17 different yield and nutritional traits *viz.*,plant height (cm), days to 50% flowering**,** number of productive tillers plant^{-1}**,** panicle length (cm), spikelet fertility (%), yield plot^{-1} (Kg), 100 grain weight (g), kernal length/breadth ratio, protein content (%), Zn content (ìgg^{-1}), Fe content (ìgg^{-1})**,** total starch content (%)**,** amylose content (%)**,** total antioxidant activity (mg AAE 100g^{-1})**,** total soluble phenol content (mg 100g^{-1}), glycemic index and phytate content (mg 100g^{-1}).Phenotypic and genotypic coefficients of variation (GCV and PCV) were computed according to Burton and Devane (1953). Heritability in broad sense was estimated as per Allard (1960) and genetic advance was estimated as per the formula proposed by Johnson *et al.* (1955).

RESULTS

Analysis of variance revealed significant differences among the genotypes for all the characters indicating presence of sufficient variability among the genotypes, thus, the possibility genetic improvement through selection is highly promising.Estimates from

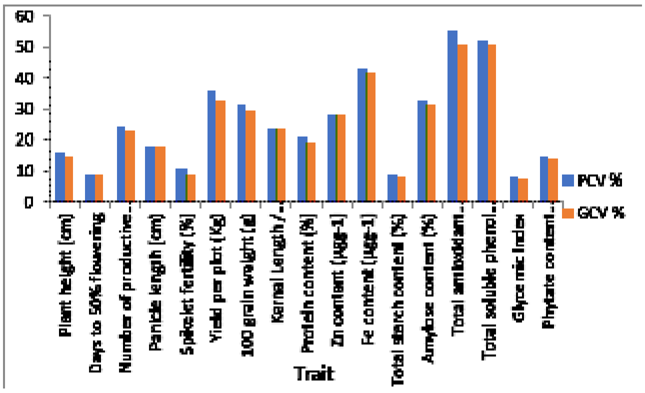

Fig 1. Graphical representation of trait wise GCV and PCV

GCV and PCV (figure 1) revealed, highest phenotypic and genotypic coefficient of variation was observed for total antioxidant activity (55.25 and 50.83 respectively), while glycemic index manifested the least values (7.83 and 7.72 respectively). The estimates of heritability ranged from 68.00 (spikelet fertility) to 99.40 (Days to 50% flowering). The maximum value for genetic advance as percent of mean was observed for Iron content (83.28) followed by yield per plot (72.75), amylose content (66.55) and 100 grain weight (64.42). The coefficient of variability studies indicated that the estimates of PCV were slightly higher than the corresponding GCV for all the characters, indicating that these characters were less influenced by the environment.Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.Similar estimates of slightly higher PCV than GCV were reported earlier by Sudeepthi*et al.* (2020).High heritability combined with high genetic advance as per cent of mean (figure 2) was observed for plant height, number of productive tillers plant^{-1}, panicle length, yield plot^{-1}, 100 grain weight, kernel length / breadth ratio, protein content, Zn content, Fe content, amylose content, total antioxidant activity, total soluble phenol content, phytate content. Thus, these traits are mainly under the control of additive gene action and hence these characters may be improved by following simple selection.High heritability with moderate genetic advance was recorded for days to 50% flowering, spikelet fertility, total starch content and glycemic index appear to be under the control of non-additive gene actions.Hence, instead of simple selection, other methods like heterosis breeding or recurrent selection could be better alternative methods for improvement of these traits. Similar results were also reported byUmesh*et al.* (2015).

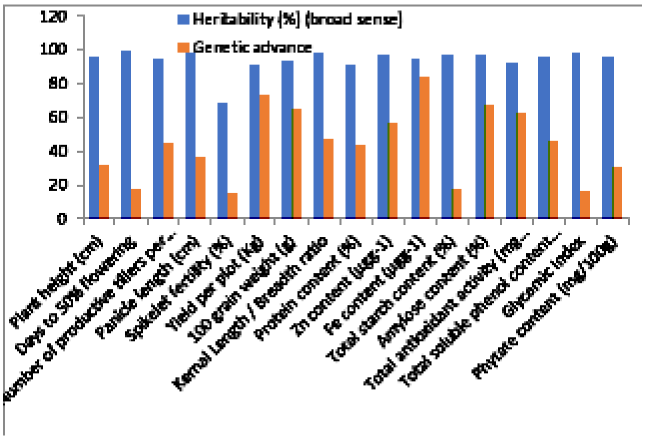

Fig 2. Graphical representation of trait wise Heritability and Genetic advance

CONCLUSION

High GCV and PCV coupled with high heritability and high genetic advance as percent of mean were observed for number of productive tillersplant^{-1}, yield plot^{-1}, 100 grain weight, kernel length/breadth ratio, zinc content, iron content, amylose content, total antioxidant activity and total soluble phenol content suggesting an additive type of gene action. Hence, good response to selection can be attained for improvement of these traits.

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IRC/TM-1/PP-45

STUDIES ON COMBINING ABILITY AND HETEROSIS FOR DEVELOPING HYBRIDS IN RICE (*ORYZA SATIVA* L.)

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Rice is one of the foremost cereal crops feeding over more than half of world's population. It is grown in more than a hundred countries and about 90% of the rice in the world is grown in Asia. Exploitation of heterosis (hybrid vigor) is one of the most important applications of genetics in agriculture particularly rice. It is not only contributing to food security, but also beneficial for environment, soil and water resources. Magnitude of heterosis is determined by the combining ability of the parents and crosses in hybrids and also influence by environmental factors.

METHODOLOGY:

To study combining ability and heterosis for developing hybrids in rice (*Oryza sativa* L.)" was conducted at Research Farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur Chhattisgarh during *Rabi* 2009-10 and *Kharif* 2010 to evaluate the variability, to estimate the GCA of parents and SCA of hybrids, to assess the magnitude of heterosis for various yield and related traits and to identify the maintainers and restorers for different CMS lines under study. The experimental material included three CMS lines *viz.*, APMS 6A, CRMS 31A and IR 79156A and seven testers *viz.*, NPT 2-2-694-1, NPT 9, NPT 80-1, ET 1-12, ET 1-13, TOX 981-11-2-3 and R 1244-1246-1-605-1 and their twenty one F1s were generated in line x tester pattern for the estimation of various genetic parameters, combining ability and heterosis. These hybrids and parents were raised in Randomized Complete Block Design (RCBD) with two replications. The data obtained was subjected to line x tester analysis Kempthorne (1957).

RESULTS:

Combining ability and heterosis was worked out for characters *viz.*, days to 50% flowering, pollen fertility (%), flag leaf length, flag leaf width, flag leaf area, plant height, productive tillers per plant, panicle length, fertile spikelets per panicle, sterile spikelets per panicle, number of spikelets per panicle, number of spikelets per plant, spikelet fertility (%), thousand grain weight, grain yield per plant and head rice recovery (%). The analysis of variance revealed the predominance of non-additive gene action for the all characters under study, indicating the possibility of exploitation of heterosis Virmani, (1994). Among the CMS lines studied, it was revealed that the CMS line IR 79156A was found to be the good general combiner and among testers NPT 80-1, TOX 694-11-2-3 and R 1244-1246-1-605-1 were found to be good general combiners for grain yield per plant, pollen fertility (%), fertile spikelets per panicle and spikelets per panicle.

CONCLUSION:

The hybrids APMS 6A/TOX 694-11-2-3, CRMS 31A/ET 1-12, IR 79156A/NPT 80-1 and IR 79156A/ET 1-13 were identified as a good combinations on the basis of SCA effects, *per se* performance for grain yield per plant and its attributes *viz.*, head rice recovery (%), pollen fertility (%), spikelets per panicle, 1000 seed weight and days to 50 % flowering.

Crosses APMS 6A/ET 1-13, CRMS 31A/NPT 80-1, CRMS 31A/ET 1-12, IR 79156A/NPT 80-1 and IR 79156A/ET 1-13 were identified as good heterotic hybrids for grain yield per plant, pollen fertility (%), spikelets fertility (%) and spikelets fertility (%).

Based on the pollen fertility percent and spikelet fertility percent, six genotypes were identified as potential restorer *viz.*, ET 1-12, NPT 2-2-694-1, NPT 9, NPT 80-1, TOX 981-11-2-3 and R 1244-1246-1-605-1. Testers *viz.*, TOX 981-11-2-3, ET 1-12 for APMS 6A; NPT 9, NPT 80-1, TOX 981-11-2-3, ET 1-12; R 1244-1246-1-605-1 for CRMS 31A; NPT 2-2-694-1, TOX 981-11-2-3; NPT 80-1 for IR 79156A identified were as potential restorers. Three genotypes in different combinations, were identified as potential maintainers *viz.*, ET 1-13 and NPT 2-2-694-1 for APMS 6A; NPT 2-2-694-1 for CRMS 31A and NPT 9 for IR 79156A. Molecular exploration may be used for further for more insight in quantitative understanding and the molecular understanding with respect to broad sense and narrow sense heritability with respect to additive and non additive gene action, combining ability and heritability or heterosis.

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IRC/TM-1/PP-46

STUDIES ON COMBINING ABILITY AND HETEROSIS FOR GRAIN YIELD AND QUALITY IN HYBRID RICE (*ORYZA SATIVA* L.)

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Rice is the most important food crop in the world and it feeds nearly half of the world's population. India is the second largest producer of rice in the world after china. In India it is grown in an area of 44.15 mha with a production of 116.47 mtand the productivity of 2638kg per ha (INDIASTAT, 2018-19). Plateauing trend in the yield of HYV's, declining and degrading natural resources necessitates looking for some innovative technologies to boost up rice production in the country. Hybrid rice is the best practically feasible and readily acceptable options available to increase the production. In India, Telangana State is only the hybrid rice seed hub around 90% of the hybrid seed is being produced in Karimnagar, Warangal and Nizamabad districts. The increased yield of rice hybrids alone does not endure profitability to farmers if their quality is not acceptable and don't fetch high premium in the market. Keeping in view of the present problems in hybrid rice, this study was undertaken to develop the high yielding rice hybrids with acceptable grain quality.

METHODOLOGY

In the present study five CMS lines were crossed with twelve restorers in line x tester design. The resultant 60 hybrids along with their parents and four checkswere evaluated in randomized block design with three replications during kharif, 2014 at Seed Research and Technology Centre, PJTSAU, Rajendranagar, Hyderabad for grain yield and its components. Data was recorded for days to 50% flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), number of filled grains per panicle, 1000 grain weight (g), spikelet fertility (%) and grain yield per plant (g). After harvest of the crop grain quality traits*viz.*, hulling (%), milling (%), head rice recovery (%), kernel length (mm), kernel breadth (mm) and kernel L/B ratio, kernel length after cooking (mm) and elongation ratio were recorded during *rabi*, 2014-15. Mean data was subjected to statistical analysis as per the line x tester designby using the software Windostat Version 9.1.

RESULTS

Analysis of variance for grain yield and its components revealed that, SCA variances were higher than GCA variances for the characters studied except for days to 50% flowering indicating the predominance of non-additive gene action. Among the lines studied, IR-58025A was found to be good general combiner for number of productive tillers per plant, panicle length, 1000 grain weight and grain yield per plant. The line, IR-79156A exhibited desirable *gca* effect for plant height, number of filled grains per panicle and spikelet fertility percentage. Out of twelve testers studied, RNR-2781 and RNR-15038 recorded significant positive *gca* effects for grain yield per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle, spikelet fertility (%) and 1000 grain weight and these were considered as best general combiners.

Based on *per se* performance, *sca* effects and the corresponding g*ca* status of parents, six crosses *viz*., IR-58025A x RNR-15038, IR-79156A x NWGR-3132, IR-58025A x RNR-2781, IR-79156A x RNR-2781, APMS-6A x RNR-15038 and APMS-6A x RNR-2781were identified as best specific cross combinations for grain yield per plant, number of productive tillers per plant, panicle length, number of filled grains per panicle and 1000 grain weight.

Heterosis for grain yield per plant is mainly because of simultaneous manifestation of heterosis for yield component traits. The hybrid, IR-58025A x RNR-15038 which expressed highly significant positive heterosis for grain yield over standard checks (MTU-1010 and KRH-2) also proved its performance in productive tillers per plant, panicle length, number of filled grains per panicle and grain yield per plant. Similar case with IR-79156A x NWGR-2781, IR-58025A x RNR-2781, IR-79156A x RNR-2781, APMS-6A x RNR-15038, APMS-6A x RNR-2781, IR-58025A x RNR-15028, IR-79156A x RNR-15038 and IR-68897A x RNR-2781 in respect to grain yield and most of its contributing traits. These hybrids could be utilized for exploitation of hybrid vigour in rice. Shivam and Harish (2013) observed that the crosses involving lines with IR-79156A, IR-58025A and APMS-6A found to be superior for grain yield.

Studies on grain quality analysis revealed that the line IR-79156A and the testers WGL-3962 and RNR-2781 were found to be superior for milling (%), head rice recovery (%), kernel length, kernel breadth, kernel L/B ratio and kernel length after cooking. In addition, the lines, IR-68897A and APMS-6A and the testers such as NWGR-3132, RNR-15038 and RNR-2456 showed good performance for some of the grain quality traits. Among the 60 hybrids studied, the hybrids APMS-6A x NWGR-3132 exhibited high mean, significant *sca* effect and standard heterosis for hulling (%), milling (%), head rice recovery (%), kernel length after cooking and kernel elongation ratio with intermediate alkali spreading value and intermediate amylose content. The hybrids, IR-68897A x RNR-2456, APMS-6A x RNR-15038, IR-58025A x RNR-2781, APMS-6A x RNR-2458 and IR-58025A x RNR-15038 were found to be good for some of the grain quality traits.

CONCLUSION

Based on overall study, it was concluded that the lines, IR-79156A, IR-58025A, APMS-6A and testers, RNR-15038, RNR-2781 and NWGR-3132 were found to be good general combiners for grain yield and its components. It can be emphasized that the hybrids *viz*., IR-58025A x RNR-15038, IR-79156A x NWGR-3132, IR-58025A x RNR-2781, IR-79156A x RNR-2781, APMS-6A x RNR-15038, APMS-6A x RNR-2781 were top ranking hybrids, in view of high *per se* performance, desirable *sca* effects and heterosis for grain yield and its component traits. Whereas, hybrids, APMS-6A x NWGR-3132, IR-68897A x RNR-2456, APMS-6A x RNR-15038, IR-58025A x RNR-2781, APMS-6A x RNR-2458 and IR-58025A x RNR-15038were better with respect to grain quality. The cross combinations such as IR-58025A x RNR-15038, IR-58025A x RNR-2781 and APMS-6A x RNR-15038 were found to promising for grain yield and grain quality.These hybrids could befurther tested in different agro-climatic zones over seasons for their superiority and stability.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-47

MARKER ASSISTED INTROGRESSION OF THE MAJOR QTL ASSOCIATED WITH TOLERANCE TO LOW SOIL P, *PUP1*, INTO THE POPULAR RICE VARIETY, WARANGAL SANNALU (WGL-32100)

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Phosphorus (P) is a vital nutrient required for growth and development of rice plant. Phosphorus (P) is one of the six essential macronutrients (N, P, K, Ca, Mg, and S) required by plants. Phosphorus deficiency is one of the most important abiotic stress factors that limit rice yields in India. Warangal Sannalu **(**WGL-32100) is a high yielding, medium-slender (MS) grain type rice variety with 135 days of duration, but is highly susceptible to low soil P. In the present investigation, we attempted to improve WGL-32100 for tolerance to low soil P by introgressing a recently cloned and characterised major QTL associated with low P tolerance, Pup1QTL (Wissuwa et al. 1998) through marker assisted selection.

METHODOLOGY:

Marker-assisted backcross breeding (MABB) coupled with phenotype-based selection was adopted for introgression of *Pup1* QTL into WGL-32100. Swarna (MTU 7029), a high yielding variety possessing *Pup1* was used as the donor and was crossed to WGL-32100 to generate F_1s. Two functional markers, K46-1 and K46-2 (Chin et al. 2011) specific for *Pup1* was used for foreground selection in F_1, BC_1F_1 and BC_2F_1 generations, while background selection was carried out based on physically observable phenotypic traits and parental polymorphic markers in each backcross generation. Backcrossing was done till BC_2 generation, after which the plants were advanced through pedigree method.

RESULTS:

The F_1s generated from the cross, WGL-32100/Swarna were screened for presence of the target trait *Pup1* QTL using the two QTL linked molecular markers i.e. K46-1 and K46-2 to identify the 'true' F_1s showing heterozygous amplification pattern. A total of 12 'positive' F_1s were identified and then backcrossed to WGL-32100 with the F_1s being used as the male parent to generate BC_1F_1 plants. Out of 263 BC_1F_1 plants, a total of 144 plants were identified to be positive for K46-1, 129 plants were positive for K46-2 and 18 were identified to be double positive for *Pup1* QTL. The 18 double positive BC_1F_1 plants were then subjected for background selection using 133 parental polymorphic SSR markers and a single 'positive' BC_1F_1 plant # WS 49 possessing maximum recovery of recurrent parent genome (73%) was selected and then backcrossed with WGL-32100 to generate BC_2F_1 plants. A similar marker-assisted selection procedure was followed for selection of BC_2F_1 plants and a single 'positive' BC_2F_1 plant # WS 49-29 possessing maximum recovery of recurrent parent genome (88%) was selected and selfed to generate BC_2F_2, BC_2F_3, BC_2F_4 and BC_2F_5 plants. At BC_2F_5, five backcross derived lines *viz.*, WGL-1593, WGL-1590, WGL-1588, WGL-1596 and WGL-1602 possessing tolerant allele for *Pup1* QTL, high yield, medium slender grain type similar to WGL-32100 and recurrent parent genome recovery ranging from

88.8 % to 98.6 % were selected and advanced for further evaluation.

CONCLUSION:

Improved rice lines can be helpful to resource poor farmers who grow these varieties in soils with low P availability. Breeding lines of WGL-32100 possessing Pup1 QTL can serve as good donors for targeted transfer of the major QTL to other elite rice varieties and can be helpful to reduce the amount spent on subsidy of phosphatic fertilizers in India.

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IRC/TM-1/PP-48

DERIVING GENETIC COEFFICIENTS OF POPULAR RICE (*ORYZA SATIVA* L.) VARIETIES OF SCARCE RAINFALL ZONE OF ANDHRA PRADESH

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Agriculture is facing the challenge of adapting to the consequences of climate change, a phenomenon affecting crop productive stability by reducing water availability for growth. Yield estimation is one of the primary challenges for successful implementation of Pradhan Mantri Fasal Bhima Yojana (PMFBY) Programme. Conventional methods of crop yield estimation are more time consuming, laborious, expensive and limited to short window of data collection. Using these methods assessing yield losses is quite complicated and challenging. A comprehensive scientific approach which can assess/estimate yield losses of individual farm units is the need of the hour for successful implementation of insurance in agriculture. Crop modeling and system analysis have also been viewed as potential tool to quantify the effects of climate, seasonal weather condition, soil environment, management and genotype as well as their interaction on crop growth, yield, resource-use efficiency and environmental impacts (Shamim *et al*. 2012).Yao FengMei *et al*. (2005) derived genetic coefficients of different cultivars used for validating the model by repeatedly adjusting the model until a close match between the simulated and the observed phenology and yield was obtained. Crop simulation models are the better ways to understand the interactions between the different factors of the productive process and allow defining new scenarios to introduce changes in their variables. To bridge the gap, RICE-YES programme of IRRI is being implementing in Andhra Pradesh. Genetic coefficients of popular rice cultivars grown in different agro-ecological zones is highly essential to increase the yield estimation accuracy. Hence this experiment is proposed to derive genetic coefficients for popular rice varieties of the scarce rainfall zone to increase the yield estimation accuracy.

METHODOLOGY

A field experiment was undertaken at Regional Agriculture Research Station, Acharya N.G. Ranga Agricultural University, Nandyal, Andhra Pradesh during 2019-20 on vertisols under irrigated condition to derive genetic coefficients for popular rice varieties of the scarce rainfall zone to increase the yield estimation accuracy. The treatments consisted of seven rice varieties (BPT 5204, NDLR 7, NDLR 8, NLR 3041, NLR 34449 and BPT 2270) in randomized block design and replicated thrice. Recommended dose of fertilizers of 240 N, 80 P_2O_5 + 80 K_2O kg ha^{-1} was applied with nitrogen in three splits, phosphorus as basal and potassium in two splits. Data on days to reach different phenophases, biomass partitioning and leaf area index at monthly intervals upto harvest, plant height, productive tillers per square metre, panicle length, seeds per panicle, test weight, grain yield and harvest index at harvest was recorded. The data gathered in each observation were statistically evaluated for critical difference at 5% level of probability to assess the significance of treatment means using analysis of variance technique

RESULTS

Higher Leaf Area Index (LAI) of 2.00 and 6.82 was observed in NDLR 7 at 30 Days After Planting

(DAP) and 60 DAP respectively whereas higher LAI of 6.28 and 6.08 was observed in BPT 2270 at 90 DAP and harvest respectively. Lower LAI in NLR 33358 (1.46 and 3.38) at 30 DAP and 60 DAP, NDLR 7 (3.86) at 90 DAP and NLR 34449 (3.42) at harvest was recorded. Among varieties higher root dry weight per square metre was observed in NLR 3041 at 30 DAP, 60 DAP, 90 DAP and harvest (70.4 g, 251.7 g, 413.7 g and 447.4 g respectively). Significantly lower root dry weight per square metre was observed in BPT 2270 (46.9 g) at 30 DAP, BPT 5204 (142.9 g) at 60 DAP, NDLR 7 (171.7 g and 238.3 g) at 90 DAP at harvest respectively. Shoot dry weight per square metre differ among varieties at different stages. Higher shoot dry weight at 30 DAP, NDLR 8 (157.9 g), NLR 33358 (778.5 g), BPT 2270 (1326.3 g and 1812.1 g) was recorded. Significantly lower shoot dry weight per square metre was observed in NLR 34449 (127.1 g) at 30 DAP, BPT 2270 (505.8 g) at 60 DAP, BPT 5204 (1024.3 g) at 90 DAP and NLR 33358 (1375.6 g) at harvest respectively. Among the varieties tested NLR 33358 was short duration (106 days) and BPT 2270 was long duration (164 days). Plant height and panicle length was non significant whereas higher productive tillers per square metre (400.4) and harvest index (47.4) was observed in NLR 33358. Higher seeds per panicle (250.7) was observed in NDLR 7. Lower seeds per panicle (196.9) was observed in BPT 5204. Higher test weight (16.37 g) and grain yield (7907 kg ha^{-1}) was observed in BPT 2270. Lower test weight (12.82 g) and grain yield (6320 kg ha^{-1}) was observed in NLR 33358. Lower harvest index (41.8) was observed in NDLR 7.

CONCLUSION

Studies on different parameters of popular rice varieties of scarce rainfall zone showed differential response to various growth and yield parameters. Long duration rice varieties with higher grain yield would not fit in the climatic situation where supply of irrigation water is for shorter period. The short duration varieties with optimum grain yield would be better choice for scarce rainfall zone and data collected was utilized for yield estimation accuracy.

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IRC/TM-1/PP-49

ASSOCIATION MAPPING REVEAL SOURCE, SINK AND THEIR RELATIONSHIP OF HIGH-YIELDING SHORT-DURATION RICE

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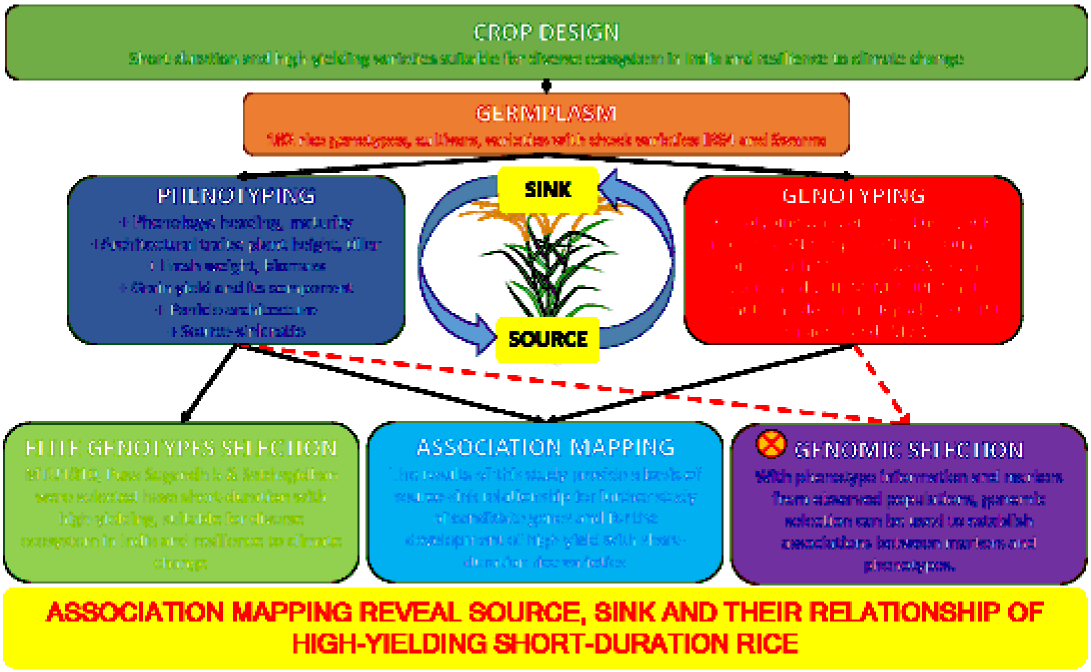
Breeding high-yieldingshort-duration rice varieties resilience to climate change is a novel strategy for food security, sustainable development, feeding 9 billion people by 2050. Short-duration varieties have less risk of damage caused by flooding, drought, and saltwater intrusion. High-yielding rice varieties will provide better income for farmer and grain yield in rice is mainly depend on source-sink relationship. Understanding the mechanism of source, sink and their relationship will contribute in improving grain yield potential and quality (Fernie et al., 2020).The objective of this study is to ***i***,grouping diverse genotypes based on source and sink traits for rice breeding program resilience to climate change; ***ii***,selecting the elite short growth duration high yielding genotypes, suitable for diverse ecosystem in India and ***iii***,dissecting quantitative trait controls sources, sink and their relationship in rice by association mapping method.

METHODOLOGY

Field experiment with 182 rice genotypes were laid out in RCBD with three replications in Kharif season 2020, ICAR-Indian Agricultural Research Institute, New Delhi. Two or three seedlings were transplanted per hill at a plant density 15x20 cm (33 plant per m^2). Genotyping was performed using 50K rice genic SNP



chip 'OsSNPnks'. A subset of 27,835 SNPs with a minor allele frequency (MAF) > 5% and a missing data ratio < 0.1 was used for association analyses. GWAS was performed with MLM, SUPER and FarmCPU models using R package GAPIT version 3 and rMVP.The Gramene QTL database and QTL annotation rice online database (QTARO) were searched to identify the physical locations of the previously reported QTLs. The candidate genes were determined using the genome browser of the Rice Annotation Project Database. All statistical tests and graphs were performed using R v.4.0.2 (R Core Team, 2020).

RESULTS

Population structure was analyzed using SNP markers and combined with previous study of Tiwari et al. (2015) and McCouch et al. (2016) showed that the 04 genotypes groups were identified (indica, basmati, aus and japonica). Hierarchical clustering analysis of 07 phenotypic traits of 182 diverse genotypes were classified into 05 groups.Traditional varieties and improved varieties were clustered in different groups. Genotypes with higher tiller numbers tend to have shorter plant height. Three elite genotypes were selected MTU1010, Pusa Sugandh 5 and Sabhagidhan. These genotypes have short-duration from 76 to 81 days that is 5-7 days shorter than IR64 and have significant higher.Association mapping of source traits, sink traits and source-sink ratio showed that, QTL/genes associated with sources traits located in chromosomes 2, 6. QTL/genes associated with sources traits and sink traits located in chromosomes 2, 6 and 9. QTL/genes associated with source-sink ratio located in chromosome 1, 7 and 11.

CONCLUSION

Three elite genotypes MTU1010, Pusa Sugandh 5 and Sabhagidhan were selectedas short-durationand high-yielding genotypes, suitable for diverse ecosystemof India and resilience to climate change.There is a trade-off between plant height and tiller number.QTL/genes associated with source-sink ratio located independently with QTL/genes associated sources and sink traits. The results of this study will provide a basis of source-sink relationship for further study of candidate genes and for the development of high-yielding short-duration rice varieties.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-50

DEVELOPMENT AND EVALUATION OF SHORT DURATION EXTRA LONG SLENDER EXPORT ORIENTED RICE CULTURE MTU 1341

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Rice is the major staple food crop in India. Among the global rice exporting countries, India is one of the leading country with total exports worth of 6350 million USD including basmati and non-basmati. Approximately a quantity of 4.45 million tonnes of basmati rice and 5.04 million tonnes of non-basmati rice is being exported during 2019-20.(www.airea.net). India exports basmati rice majorly to Iran, Saudi Arabia, UAE, Iraq, USA, UK and other countries and non-basmati rice to Nepal, Benin, Somalia, Guinea, Togo and other countries. In recent past the non-basmati rice exports (53%) are gaining more importance and development of rice varieties having export potential is the need of the hour to meet the domestic and export demand.

OBJECTIVE

To develop rice varieties with high yielding, extra long slender grain type and good cooking quality with export potential.

METHODOLOGY

MTU 1341, an extra long slender rice culture developed by crossing MTU 1010 as female parent and KMP 149 as male parent. The segregating population were advanced by pedigree breeding method and the line MTU 2261-11-3-1-2 (MTU 1341) was identified with high yield and extra long slender grain. The rice culture was tested in station trials viz., OYT, PYT and AYT at RARS, Maruteru, followed by multi location testing during Kharif, 2016 and 2017. The data was summarized and the rice culture MTU 1341 is having superior yield over check and the quality data was analyzed and found to be suitable for rice exports in non-basmati segment.

RESULTS AND CONCLUSIONS

The rice culture MTU 1341, recorded an average yield of 7461 kg/ha in station trials in comparison with best check MTU 1010 (6089 kg/ha) with 22.5 percent increase over the check. In multi location trials conducted during Kharif, 2016 and Kharif, 2017 the rice culture MTU 1341 recorded an average yield of 6824 kg/ha in comparison with check variety MTU 1010 (5184 kg/ha) with an yield advantage of 31.6 percent. Owing to the superior performance of the culture it was decided to test the

Table 1: Evaluation of MTU 1341 rice culture in station trials and multi location trials

Name of the Trial	Year of testing	Grain yield (kg/ha)		Percentage increase over check
		Entry(MTU 1341)	Check(MTU 1010)	
OYT-Early	Rabi 2014-15	8264	6975	18.48
PYT-Early	Kharif 2015	6810	5030	35.39
AYT-Early	Rabi 2015-16	7310	6262	16.74
Average over Station Trials		7461	6089	22.5
MLT-Early I Year (pooled)	Kharif 2016	6664	4661	42.97
MLT-Early II Year (pooled)	Kharif 2017	6984	5707	22.38
Average in MLTs		6824	5184	31.6

culture MTU 1341 in farmers fields during Rabi, 2020-21. (Table 1)

MTU 1341 has kernel length of 7.01 mm and kernel breadth of 1.99 mm with L/B ratio of 3.52. It also has 68% milling percentage and 60% of head rice recovery. With an average yield of more than 25 percent over the rice variety MTU 1010 along with good grain quality, the rice culture MTU 1341 can be a good rice culture for the state of Andhra Pradesh with export potential in non-basmati segment.

Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-51

EVALUATION OF HIGH YIELDING, MID-EARLY RICE VARIETY WITH BETTER GRAIN QUALITY

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The research work was carried out breeding a superior high yielding, mid-early, medium slender variety of rice with better cooking and milling qualities at Main Rice Research Station, Nawagam and paddy Research station, Dabhoi of Anand Agricultural University and two paddy stations *viz.* Navsari and Vyara of Navasari Agricultural University, Navasari. The grain yield of NWGR 15022 was recorded 5137 kg/ha which is 26.8, 14.1 and 4.3 *per cent* higher over the state check *viz*., GR 4 (4136 kg/ha), GR 12 (4541 kg/ha) and Mahisagar (5205 kg/ha), respectively. It possesses good grain quality traits *viz.*, high head rice recovery (62.51%), medium amylose content (25.42%) and Length and breadth ratio (3.41) and medium slender grains having milled grains (5.46 mm), high cooked kernel length up to 9.2 mm, volume expansion ratio is 4.63.

Key Words: *NWGR 15022, high yielding, Cooking and milling qualities*

Rice occupies about five *per cent* of the gross cropped area and cultivation is about 7.5 to 8.0 lac hectares in the state. In the Gujarat, farmers are growing early and fine grain varieties *viz*., GR 4 and GR 12 are most popular among farmers as well as consumers and were released in the year of 1981 and 2005, respectively, whereas, Mahisagar in 2016. The productivity of GR 4 and GR 12 varieties going to decreasing; hence an urgent need to develop a quality variety of medium slender grain group. Hence, systematic efforts were made to evolve a superior early, medium slender kernel type rice variety with better cooking and milling qualities.

METHODOLOGY

The NWGR 15022 was developed through cross of GR-11 x IR-60 by pedigree selection method, than it was evaluated for yield with promising entries including check varieties, GR 4,GR 12 and Mahisagar in different trials *viz.*, PET-E, SSVT-E and LSVT-E-

Table 1. Evaluation of high yielding, mid-early rice variety with better grain quality along with checks

Year	Expt.	Locations	Grain yield (kg/ha)				C.D. at 5%	C.V.C.V%
			NWGR 15022	GR 4 (a)	GR12(c)	MahiSagar(d)		
2017	PET-E	NWG	4977	-	3935	4977	1112	13.2
		DAB	3885	-	4042	4343	754	8.7
2018	SSVT-E	NWG	5750^{d}	-	-	4857	569	7.7
		DAB	5512^{d}	-	-	4405	671	9.1
2019	LSVT-E-F	NWG	5954^{a}	4457	5265	5613	907	10.5
		DAB	6014^{a}	4667	5333	5513	915	11.0
		NVS	5701^{ac}	3328	3866	5420	1033	11.7
		VYA	3301	4091	3700	4274	979	14.5
Overall Mean	5137	-	-	4925	-	-		
% increase over check	-	26.8	14.1	4.3	-	-		

Note:1.*a=GR-4 c=GR-12, d =Mahisagar indicates Significant at 5% level than respective check.*
2. NWG= Nawagam, DAB= Dabhoi, NVS= Navsari, VYA= Vyara locations.

Characters	NWGR 15022	GR 4	GR 12	Mahisagar
DFF (days)	97 (86-107)	87 (79-92)	95 (84-103)	91(78-97)
Days to Maturity	127(116-137)	117(109-122)	125(114-133)	121(108-128)
Plant height (cm)	121(110-126)	109(108-112)	119(115-126)	111(105-120)
Panicle length (cm)	22.0(19.5-23.9)	20.0(16.8-22.2)	23.0(22.5-23.8)	24.0(21.8-25.8)
Number of productive tillers/ plant	10(8.0-12.0)	10(8.0-11.0)	9(8.0-11.4)	9(7.0-10.7)
1000 grain wt. (g)	14.6(12.9-15.1)	13.5(12.9-14.2)	14.6(12.7-15.6)	15.8(14.0-17.5)
Mill (%)	69.44	67.58	68.28	73.86
HRR (%)	62.51	57.00	61.85	64.59
KL (mm)	5.46	5.34	5.48	5.45
KB (mm)	1.60	1.50	1.54	1.62
ASV	5.00	4.00	5.00	5.00
KLAC(mm)	9.2	8.5	8.8	9.2
AC (%)	25.42	25.53	25.31	25.10

Mill: Milling (%): HRR: Head Rice Recovery (%); KL: Kernel Length (mm); KB: Kernel Breadth (mm); KLAC: Kernel Length after cooking; ASV: Alkali Spreading Value; AC: Amylose Content (%). These cooking grain quality parameters derived during 2019.

F during *Kharif* season of 2017, 2018 and 2019, respectively. The experiment was framed in a Randomized Block Design with three replications. The Genotypes were grown in 4.95 meters apart with two meters width by maintaining 20 cm ×15 cm plant spacing of individual genotype. The agronomic characteristics were measured as per Table 1. The grain and biochemical properties of NWGR 15022 were mentioned in Table 1. The data pertaining to various characters were analyzed as per the procedure of randomized block design given by Panse and Sukhatme (1978) for individual environments.

RESULTS

The grain yield of NWGR-15022 was recorded 5137 kg/ha which is higher over the check *viz*., GR 4, GR 12 and Mahisagar. The yield potential of this variety is 6014 kg/ha. The NWGR-15022 was found mid early maturity (116 to 137 days) with medium slender kernel type. The yield attributing traits of NWGR-15022 *viz*, length of panicle (19.5-23.9 cm), higher number of productive tillers/plant (8.0-12.0) were found superior over the checks (Table 1); these results are in agreement with those obtained by Sedeek *et* al. (2009). The NWGR-15022 culture is mid tall in plant stature (110-126 cm) and possesses 12.9-15.1 g test weight, 5.46 mm grain length with breadth 1.60 mm, having Kernel length/breadth (mm) ratio of 3.40 which is enough categorised in fine grain group of medium slender (Table 2). The Grain quality characteristics of the NWGR-15022 were mentioned in Table 3. The amylose content of NWGR-15022 (25.53%) found *at par* with check. The milling qualities are better means 69.44 % with head rice recovery 62.51 %.

CONCLUSION

The average yield of variety is 5137 kg/ha along with 6014 kg/ha yield potential. Considering its salient merits of NWGR 15022 *viz.*, medium slender grain type, compact panicle, good tillering ability, mid-early maturity, good cooking and grain qualities may suit for commercial release of variety.

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IRC/TM-1/PP-52

INDUCED MUTATION IN AROMATIC RICE-FREQUENCY AND SPECTRUM OF VIABLE MUTATIONS OF ECONOMIC VALUES

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Keeping a view to search viable mutations of economic importance in seven aromatic rice varieties are included and their dry seeds were treated by applying two light radiation doses of gamma rays i.e. 300 and 500 KGy. with control (2000 seeds per treatment) and grown during *Kharif* 2018 in large plot. Both frequency and spectrum of viable mutants were found and characterizations of economic importance varied with the treatment as well as varieties. During 2019, the 62 and 37 treatment variation\mutant plants were found in seven varieties in M_2 of 300 KGy and in M_2 of 500 KGy, respectively. In Pankhali 203 the most desirable and effective viable mutants are found under 300 KGy. treatment; There is a rising pressure in our country for production of high grain quality, aromatic rice that fulfilling demand and export market. Unfortunately, these traditional cultivars are known certain pockets with poor yield and lodging susceptibility and tall plant (>170cm). Hence, there is need to improve the yield potential of such cultivars by reducing the plant height without losing aroma and other quality characters of parental variety.

Key Words: *viable mutations, gamma-rays, aromatic rice**,** M_2 generation*

OBJECTIVES

Well adopted aromatic rice varieties along with traditional aromatic rice with object to develop early maturing, high yielding aromatic rice mutant and short/ medium stature mutant.

METHODOLOGY

Many traditional aromatic rice cultivars are famous *viz.*,Krishana Kamod, Improved Kali Kamod, Indrayini, Pankhali-203, Rajbangaliyu, Ambemohar and GR-101 release variety in western zone of India due to their excellent grain quality and aroma. Two thousands pure, healthy and dry seeds (moisture 12%) were irradiated by applying two light doses of gamma rays *i.e.* 300 and 500 KGy. doses of ^{60}Co. gamma rays at Anand Agricultural University, Anand, Gujarat. and grown during *Kharif* 2019 with 1000 of each un-irradiated seed lots of each variety Different types of viable mutations and their frequency were scored and selected in each treatment starting from germination to maturity. The mutant plants (affecting growth habit) are harvested separately; those showing more features are listed in details in Table1.

RESULTS

From M_2 generation 109 mutant individual plant selections were identified from seven varieties during 2019. The varieties *viz;* Pankhali 203 record more sensitive than GR-101 with regard to the frequency of viable mutants. With regards to spectrum of viable mutations, a total of 27 types of macro-mutations were observed; 21 types in each of GR-101 and Krishna Kamod. The frequency of different mutants over cultivars were found *viz.*, 27 early/mid late maturing, 8 extra early maturing, 33 long panicle, 30 increased tillering, 29 bushy and dwarf plant, 22 broad leaf and non-lodging, 32 pigmented grain, 13 short slender grain, 38 straw colour grain, 11change in grain size and 29 high yielding plants.

CONCLUSION

Isolation of few semi-dwarf mutant coupled with earliness have assumed great significance for improving traditional aromatic rice, similarly, several workers reported that dwarf and semi-dwarf plants

Table: 1 Frequency and spectrum of induced viable mutations of Gamma-ray in M2 generation in rice varieties

Particulars	Gamma-ray		Total Mutant trait wise	Gamma-ray		Total Mutant trait wise	Gamma-ray		Total Mutant trait wise	Gamma-ray		Total Mutant trait wise
Variety name\dose	Krishana Kamod			Improved Kali Kamod			Pankhali -203			GR-101		
	0.3	0.5		0.3	0.5		0.3	0.5		0.3	0.5	
Total M_2 plants studied	1200	900		850	1000		1350	1250		950	770	
Spectrum of mutations				Frequency of mutations								
Early / midlate maturing	5	1	6	0	3	3	5	1	6	3	2	5
Medium \Semi-dwarf	5	2	7	2	3	5	5	0	5	3	4	7
Increase tillering	3	1	4	1	1	2	10	4	14	3	2	5
Bushy\dwarf plant	2	2	4	1	1	2	7	2	9	1	3	4
Non Lodging or broad leaf	1	5	6	1	1	2	1	1	2	1	1	2
Grains variation	3	8	11	2	1	3	11	3	14	1	0	1
Straw colour(black & others)	5	5	10	2	3	5	2	1	3	2	3	5
Long panicle/awns	-	3	3	2	2	4	9	4	13	1	1	2
Change in grain\ pigmentation	3	4	7	2	1	3	4	1	5	1	2	5
High yielding	4	3	7	2	2	4	4	1	5	3	2	5
Total No. of beneficial mutants	**14**	**7**	**21**	**5**	**6**	**11**	**19**	**8**	**27**	**07**	**06**	**21**
Frequency/100 M2 plants	1.17	0.78	1.94	0.59	0.60	1.19	1.41	0.64	2.05	0.74	0.78	1.52
Complete spikelet sterility (%)	20	30	25	15	25	20	18	22	20	28	32	30

contd.....

Particulars	Gamma-ray		Total Mutant trait wise	Gamma-ray		Total Mutant trait wise	Gamma-ray		Total Mutant trait wise
Variety name\dose	Indrayini			Rajbangaliyu			Ambemohar		
	0.3	0.5		0.3	0.5		0.3	0.5	
Total M2 plants studied	958	1010		975	1078		877	600	958
Spectrum of mutations	Frequency of mutations								
Extra Early maturing	2	3	5	0	3	3	2	0	3
Medium \Semi-dwarf	3	2	5	4	1	5	1	0	1
Increase tillering	2	1	3	2	2	4	1	0	1
Bushy\dwarf plant	3	2	5	2	2	4	1	0	1
Non Lodging or broad leaf	1	1	2	1	2	3	1	0	1
Long panicle/awns	4	1	5	3	2	5	1	0	1
Change in grain\ pigmentation	3	1	4	2	3	5	3	0	3
Total No. of beneficial mutants	7	4	11	5	8	13	05	0	5
Frequency/100 M2 plants	0.73	0.40	1.13	0.51	0.74	1.25	0.57	0.00	57.00
Complete spikelet sterility (%)	35	38	36.5	32	28	30	25	30	27.5

found in rice after mutagenic treatments. The 29 high yielding, mutants were found; this is in accordance to findings of Shadakshari *et al.*, 2001 that high yielding mutants showing 15-20 % more grain yield than normal are observed in both genotypes; Several workers also reported such mutants in rice after mutagenic treatments (Domingo *et al.*, 2007).

A total of 33 plants out of 13468 M_2 plants for increased tillering (more than 14 compared to 5-10 tillers/plant in normal) were observed in seven varieties.

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IRC/TM-1/PP-53

STUDY OF BIOCHEMICAL ATTRIBUTES DURING LONG TERM STORAGE OF RICE

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Rice is a staple food for about 65% of global population majorly in underdeveloped countries where food security is a national concern. In most of the places it has been consumed in the form of cooked rice. Surprisingly, old rice or stored rice are more preferred over newly harvested rice because of better cooking and eating quality. The changes in grain quality due to the effect of aging are irreversible and mostly beneficial. Aged rice has better commercial value, owing particularly to improved milling yield, higher consumer preferences in terms of cooked rice texture, flavor and associated parameters. Natural ageing through conventional processes requires undesirably long storage duration, in addition to associated higher operational and maintenance costs. Alternatively, artificial ageing of rice has been investigated by researchers to achieve similar results in lesser time and lower cost.

Therefore, post harvest storage of rice becomes an important step to enhance the flavor and simultaneously it provides a simple solution of food security for any nation. Although the mechanism of rice aging is not fully understood, understanding the biochemical changes during storage is important in the evaluation of cooking and eating quality. Hence the study was performed with an aim to know the mechanism of rice aging through biochemical aspect during long term storage of rice.

METHODOLOGY

Fifteen rice varieties including colored rice, non-colored rice (white rice) and non-colored scented rice has been used in the experiment. The biochemical parameters were estimated at the interval of three months till 24 months of storage.

Lipid peroxidation estimation through Malondialdehyde (MDA): Properly powdered brown rice samples were use to estimate MDA content by using the colorimetric method as described by Hunter et al. 1963.

Free Fatty Acids (FFA) estimation was done by using the protocol mentioned by Cox et al. 1962 with slight modification. 10 gm of finely ground grain sample was used to estimate the acid number followed by estimation of FFA which was expressed in percentage (With respect to Oleic acid).

RESULTS

The estimation of Malondialdebyde (MDA) and Free Fatty Acid (FFA) content was done in aged rice at the interval of 3 months till 24 months old rice grain in 12 samples of different rice varieties varying in seed color. The level of FFA and MDA content almost become static, after 15 months of aging. Observation shows that in all the 12 varieties FFA production increases till 9 months of aging then slightly decrease and after 15 months it remains constant. FFA value ranges from 0.247% to 0.412% in pigmented varieties and 0.416% to 0.639% in non-pigmented varieties after 24 months of ageing. Level of FFA production was found to be less (15-20%) in pigmented varieties as compared to non-pigmented varieties. Similarly the MDA content also increases till 12 months of aging and then become constant in all the selected varieties. The value of MDA varies from 0.889 to 1.97 µM/10g in pigmented varieties, 1.356 to 2.971 µM/10g in non

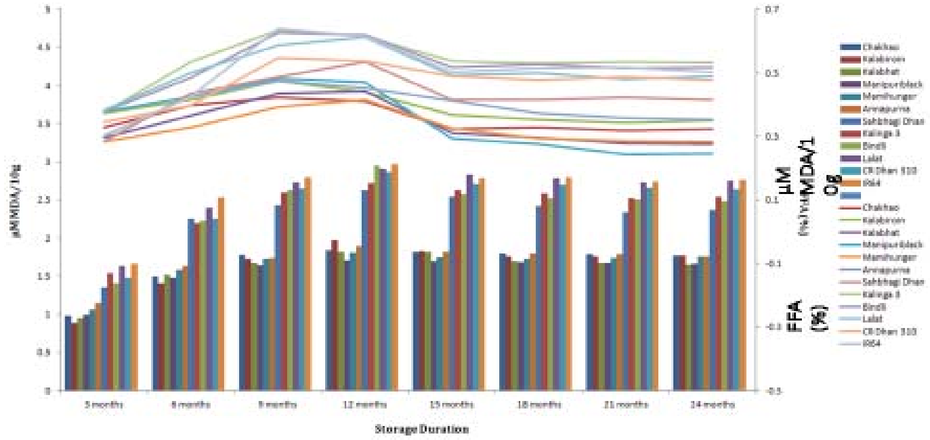

Figure. Variation in Malondialdehyde (MDA) and FFA concentration in pigmented and non pigmented rice varieties during 24 months of storage. MDA content is expressen in µM per 10 gram of sample and FFA is expressed in percentage.

pigmented varieties and 1.282 to 2.518 µM/10g in scented varieties. Like FFA, the decreased (20-25 %) generation of MDA was also observed in pigmented rice as compared to non pigmented and scented rice. The cooking and eating quality also become stable after 15 months of storage. The antioxidant activity was also estimated but no significant difference has been noticed in the studied rice varieties though the level of antioxidant was recorded more in pigmented varieties as compare to non pigmented and scented rice varieties.

CONCLUSION:

During storage many biochemical changes takes place in the rice grain which is reflected through the change in cooking and eating quality. Texture, pasting and thermal properties of rice are important attributes that are the signature of aged rice. Textural properties include attributes of cohesiveness, hardness, tooth pull, roughness, particle size, tooth pack and looseness of rice grains. These properties are influenced majorly by storage duration. Generally aging is done for 6 to 8 months whereas for some rice it requires at least 2 years to attain the appropriate aged attributes. Ageing improves pasting property of rice that is an indicator for suitability of rice flour for baking purpose. Moreover, ageing improves milling properties. Ageing also enhances volume expansion and water absorption of rice upon cooking, resulting in a product with firmer texture and less stickiness, compared with the cooked counterparts from freshly harvest paddy. Though the dynamic procedure of lipid peroxidation occurs during early storage but become constant after 8-12 months of storage could be the reason of stabilizing the others factors too which directly affect the grain quality. Hence minimum 12 to 15 months of aging could be preferred to attain the best quality of aged rice.

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IRC/TM-1/PP-54

PROTEOMICS APPROACHES OF DIFFERENTIAL GRAIN FILLING IN DIFFERENT SPATIAL LOCATIONS OF PANICLE IN RICE CULTIVARS EXHIBITING VARIATIONS IN THEIR PANICLE COMPACTNESS

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Rice production needs to be increased to at least 800 million tons to feed the World's expected population of approximately 9.6 billion by 2050 (Das et.al,2016). In order to achieve such a higher grain yield, rice breeders have increased the grain numbers within the panicle with no much increase in panicle length which caused more panicle compactness. However, increase in grain number due to more panicle compactness did not improve grain yield proportionately because of poor filling of spikelets which are specifically located in the basal part of the panicle.Grain filling in rice is basically a function of the translocation of photosynthetic assimilates like sucrose from the source leaves to developing endosperm where it is converted to starch by many starch synthesizing enzymes. Our previous work analysed the activities of different starch synthesizing enzymes (Panda et.al,2015) and expression of ethylene receptor and their signal transducer genes (Sekharet.al., 2015) associated with grain filling of rice. Decreased activity of enzymes involved in starch biosynthesis have been found associated withpoor grain filling especially in the grains located in the basal part of the panicle and in compact panicle cultivars. Many researchers also studied the involvement of plant hormones like ethylene with inhibitory effect and ABA and Auxin with stimulatory effect on grain filling (Kuanar et.al, 2010) during post anthesis stages of grain development. Similarly, transcriptome analysis revealed differential expression of 623 genes in rice caryopses after 15 days post-flowering in near isogenic lines (NILs) of rice genotypes exhibiting variation in grain chalkiness (Liu et.al., 2010). In this context, a proteomic approach based on 2-D electrophoresis and mass spectrometric analysis may be an effective tool in analysing differential grain filling in rice and the present work intend to exploit the usefulness of proteomics to unravel the possible reasons for spatial differences in grain filling of lax- and compact-panicle rice cultivars.In the present work, attempt has been made to understand the reasons for differential grain filling in different spatial locations of the panicle by analysing the comparative proteomics in compact-panicle cultivar Mahalaxmi and lax-panicle cultivar Upahar having poor and good grain filling properties respectively.

MATERIALS AND METHODS

Two rice cultivars namely Mahalaxmi (compact-panicled) and Upahar (lax-panicled) were used in the present experiment. All recommended agronomic practices were followed during the cultivation of the plants in the field. Dry weight, soluble carbohydrate concentrations and ethylene production of apical and basal grains of both the cultivars were measured during post-anthesis period. Proteins from the developing spikelets were also extracted and their differential expression patterns were studied using two-dimensional electrophoresis followed by mass spectrometry. Further, primers were designed to study the spatio-temporal expression of the genes encoding some important proteins that exhibited either higher or lower expression in the basal spikeletscompared to the apical ones in Mahlaxmi over Upahar by RT-PCR analysis.

RESULTS

The results revealed a significant difference in the panicle morphology between the compact panicled rice cultivar Mahalaxmi and lax cultivar Upahar. Though the length of panicle was greater (27.7cm) in Upahar compared to Mahalaxmi (25.0cm), panicle weight, total grain number and percentage of unfilled grains was quite higher in Mahalaxmi. Production of ethylene was also higher in the basal grains than the apical ones and also in the corresponding spikelets of Mahalaxmi compared to Upahar.Comparative proteomic analysis showed expression of 391 protein spots in the gel images of the protein extracts from the apical and basal spikelets of Mahalaxmi. Out of these total protein spots, 45 were differentially expressed in the apical and basal spikelets; 34 proteins were more strongly expressed in the apical spikelets compared to basal whereas 11 were more prominently expressed in the basal compared to apical spikelets. On the other hand, 21 proteins were differentially expressed in the apical and basal spikelets of Upahar. Although many proteins were differentially expressed in the 2-DE gel images from the protein extracts of apical and basal spikelets in the compact- and lax-panicledrice cultivars, the most prominent proteins were S-adenosylmethionine synthase, enolase and cell division control protein 48 (CDC48). RT-PCR studies also confirmed greater expression of the gene transcript level of S-adenosylmethionine in the basal spikelets of Mahalaxmi compared to apical spikelets whereas no such difference was observed in lax-panicle cultivar Upahar.

DISCUSSION AND CONCLUSION

Although several proteins were up- and down-regulated in the basal spikelets compared to the apical ones of Mahalaxmi, greater expression of the proteins like S-adenosylmethionine synthase and lower expression of CDC48 in the basal spikelets seems more crucial for grain development in rice. S-adenosylmethionine synthase could inhibit grain filling by stimulating more ethylene synthesis in the basal spikelets which in turn is responsible for inhibition of endosperm cell division (Panda et.al., 2009) mediated through lower expression of CDC48 leading to poor grain filling in the basal spikelets of Mahalaxmi. Higher expression of ethylene synthesis precursor gene like S-adenosylmethionine in the basal spikelets of Mahalaxmi also supports greater ethylene production and hence more inhibition in grain filling.However, only two of these proteins were differentially expressed between the apical and basal spikelets in Upahar indicating more differential metabolic activities in the apical and basal spikelets of Mahalaxmi than that of Upahar. Hence, differential expression of proteins accompanied by variation in ethylene production in the apical and basal grains is the principal factors responsible for variation in grain filling of rice cultivars that contrast for panicle compactness.

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IRC/TM-1/PP-55

DYNAMICS OF NON-STRUCTURAL CARBOHYDRATES UNDER HEAT STRESS

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Carbon acquired during the process of photosynthesis is majorly used as a substrate for metabolism, a fraction of it though is retained in the form of non structural carbohydrates (NSC). The concentration of NSC, including starch and soluble sugars, is often used as a measure of storage. While numerous functions of NSC have been recognized, the source- sink dynamics model relies on the concept that the stored NSC pool while functioning as a carbon reservoir alters its concentrations to meet the plants demand for respiration and growth.

Despite the critical role played by NSC in the plant carbon balance, the understanding of the dynamics, role and regulation of NSC under environmental stresses remains limited. Nonstructural carbohydrate (NSC) content is crucial for plants for surviving under different abiotic stress conditions. High and stable grain yield of rice under changing environments is significant for meeting the increasing global food demand. The process of grain filling in rice requires carbon both from photosynthesis as well as from the translocation of prestored NSC from mature leaves and leaf sheaths plus culms to panicles. Attempts have been made to explore the potential of remobilized stem reserves in supporting grain filling under heat-stress conditions, a major abiotic stress associated with climate change.

The present experiment was designed to understand the ability of different rice genotypes to remobilize stored non-structural carbohydrates (NSC) under heat-stress conditions to support grain filling,

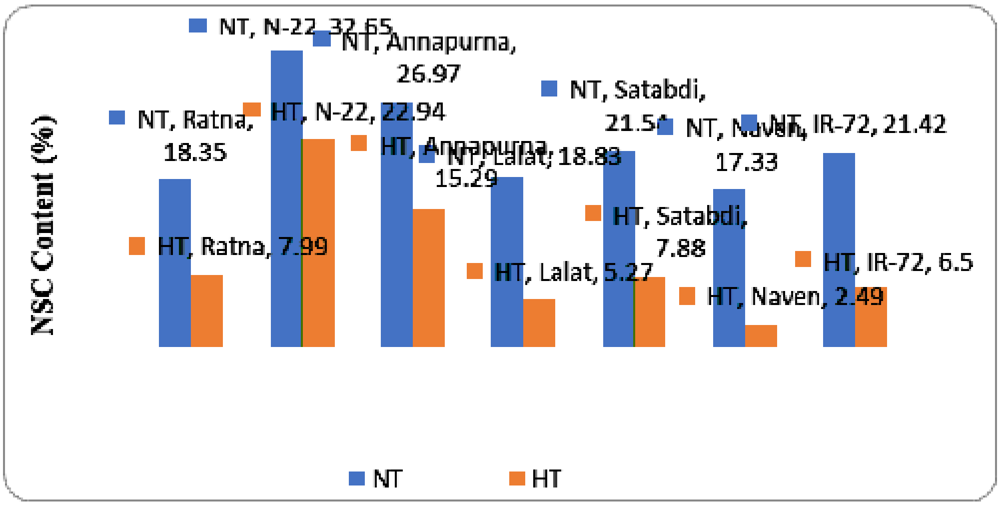
METHODOLOGY:

Seven rice genotypes including heat-tolerant, Nagina22 (N22) and heat-sensitive, IR72, Naveen based on our previous trials, were evaluated in this study. The plants were grown under staggered sowing to expose them to different temperature regimes; the maximum and minimum temperatures during grain filling stage at first planting were 30-36.5^{O}C and 22.5-27.3^{O}C respectively (control temperature) while for the second planting were 34.8-39.5^{O}C and 24.8-27.5^{O}C respectively (high temperature).

Sampling from both the temperature regimes was done to quantify the Non Structural Carbohydrate (NSC) content (expressed as aggregate of total soluble sugar and starch in glucose). Three plants from each variety were sampled for biochemical analyses; the plants were separated into leaves, stem and panicle and immediately dried and stored. Thereafter, the samples were grounded; the extraction was carried out in 80%ethanol. Total soluble sugar (TSS) determination was carried out using the supernatant by anthrone method while the starch was quantified in the residue remaining after soluble sugars via the perchloric acid method.

RESULT:

Non- structural carbohydrate (total sugar and starch) content was estimated from flowering till maturity stage in both source and sink tissues in the seven genotypes grown under two different temperature conditions. The ability to accumulate total sugar and starch was found to be different among the seven genotypes studied. Naveen, IR72, Lalat accumulated significantly lower amount of NSC in the stem while N22 accumulated significantly higher amount of NSC than all other genotypes, followed by Annapurna. The remobilization efficiency was found to be genotype-dependent. Differences were found between the



genotypes with regard to remobilization of NSC from under diverse temperature conditions. Under heat-stress conditions, the mean NSC remobilized from source to sink was 463.7mg/g dry weight while it was 367.3 mg/g under normal condition.

While analyzing the tendency of the genotypes under diverse temperature conditions it was observed that under elevated temperature conditions, the TSS content decreased for the heat sensitive genotypes like Naveen, IR72, Lalat while it increased for heat tolerant genotypes like N22 and Annapurna. Similar pattern was observed in case of starch also. Values shown by heat tolerant genotypes remained unaltered across treatments. The studies were in line with that reported by Moura *et al*, 2017. The results indicate that higher remobilization of preanthesis-stored NSC from the stem occurs under heat-stress conditions, as there might be a reduction in NSC accumulation in the source due to impaired enzyme activities (Tahir and Nakata, 2005).

Our study showed that N-22 (32.65% in source to 22.94% in sink tissues) and Annapurna (26.97% in source to 15.29% in sink tissues) showed higher translocation ability of NSC and can be concluded to have better partitioning efficiency than the other genotypes (Fig).

CONCLUSION:

The result of this study indicated genotypic variation in reaction to heat stress in terms of the ability to accumulate NSC and later to remobilize them during grain filling under heat-stress conditions.

These results also suggest that higher translocation capacity shown by N22 and Annapurna can contribute to their lower spikelet sterility rate and higher 1000-grain weight stability therefore indicating that selection of genotypes with higher capacity of stem NSC translocation at elevated temperatures could lead to more grain yield stability.

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IRC/TM-1/PP-56

ADAPTABILITY AND YIELD STABILITY OF MID-EARLY RICE GENOTYPES

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Multi-location yield trials of 11 mid-early (110-125 days) rice genotypes were conducted at Bhubaneswar, Chiplima, Jeypore and Ranital over 3 years. The genotypes included 8 pre-release varieties and three released varieties (Konark, Lalat and Bhoi). All trials were laid out in randomized block design with 3 replications. In each trial, the plot size was 2 m × 3 m and 25-30 days old seedlings were transplanted with 20 cm × 15 cm spacing and 2 seedlings per hill. Fertilizers were applied @ 80 kg N, 40 kg P2O5 and 40 kg K2O per hectare. Normal cultural practices and plant protection measures were followed in each trial. In all trials, data were recorded on net plot grain yield. Grain yield data of the 12 environments was analyzed to assess GxE interaction and adaptability. Stability parameters of genotypes were estimated using the Linear Regression model of Eberhart and Russell (1966). Stability of yield performance of genotypes was also estimated using other parameters like coefficient of variation CV (Francis and Kannenberg, 1978), stability factor SF (Lewis, 1954), R1 and R2 (Langer et al., 1979), Wricke's ecovalence W (Wricke, 1962) and AMMI stability value ASV (Purchase, 1997). The year component of the environment variable was eliminated by averaging over years and G×L interaction was analyzed by AMMI model (Zobel et al., 1988) to identify genotypes adapted to specific locations. ANOVA of yield data of the 12 environments revealed highly significant differences among genotypes and environments and significant GxE interaction indicated differential performance of genotypes over environments. Considering mean, and the Linear Regression parameters b and S^{2}d values jointly, 3 of the 6 genotypes giving above average yield showed stability of performance of which Lalat showed adaptability to all environments, while OR 2200-5 and Konark showed specific adaptation to rich environment. Stability assessment on the basis of parameters like CV, SF, R1, R2, W and ASV revealed that the genotypes OR 1929-4, Lalat, OR 1739-47 and Bhoi showed stability of yield performance according to 6 or 5 parameters. AMMI (Additive Main and Multiplicative Interaction) analysis showed differential performance of the genotypes in the 4 locations and of the 6 higher yielding genotypes, Lalat, OR 2200-5 and OR 1976-11 had low GxL interaction, while OR 2006-12, OR 2172-7 and Konark had high GxL interaction. AMMI-predicted yield showed that Lalat and OR 2006-12 were high yielder and possessed broad adaptation to most locations. Genotypes showing good adaptation to specific locations were OR 2200-5 for Ranital, OR 2172-7 and OR 1916-19 for Bhubaneswar, OR 1976-11 for Chiplima and Konark for Ranital.

Key words: Rice, GxE interaction, LR model, AMMI model, Adaptability, Stability

IRC/TM-1/PP-57

GERMPLASM INNOVATION OF HIGH TEMPERATURE TOLERANCE FROM TRADITIONAL RICE LAND RACES USING GENETIC VARIABILITY, GENETIC ADVANCE AND PRINCIPAL COMPONENET ANALYSIS

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Rice is a major staple crop in the world and demand for rice is increasing every year (Ray et al., 2013). Landraces are genetically dynamic and display equilibrium with both the environment and abiotic stresses. During the green revolution era, many potential landraces of rice are being replaced by high yielding varieties to meet the food requirements. Despite being less productive they are known to have a high genetic variance for several biotic and abiotic stresses (Hanamaratti et al., 2008), so they can be explored for rice improvement programmes. Kerala is, known to have highly diverse rice germplasm and the landraces belonging to this region are expected to have high genetic variability for many biotic and abiotic stresses. Many rice landraces of Kerala were not yet characterized and utilized effectively. Genetic diversity among the populations and their genetic relationships aids in conservation and parental selection in the improvement programme. With this background an experiment was performed to detect the genetic diversity and heat tolerance behavior of ninety traditional rice land races of Kerala.

METHODOLOGY:

The experiment was conducted at Regional Agricultural Research Station, Pattambi, Kerala Agricultural University, India (10°48’41.1"N 76°11’24.9"E), oldest rice research station in Kerala. The experimental material was collected from germplasm collection from Regional Agricultural Research Station, Pattambi, Kerala Agricultural University (Table 1). This experimental site is rice target environment and severely prone to heat and drought stresses. The selected diverse panel of landraces were grown in pots during wet season; Mundakan (August –December) of 2012-2013 and dry season; Puncha (January –May), 2013-2014. In both seasons, 30g seeds of each landrace were planted in pots filled with soil, sand and cowdung with equal v/v ratio. Twenty-one days old seedlings were transplanted to pots filled with soil, sand and cowdung with equal v/v ratio @ 2 seedlings/ pot. After 8 days of transplanting, gap filling was done and one healthy seedling was maintained per pot. The experiment was laid out in completely randomized design with two treatment levels i.e. control and high temperature stress (38+/-2^{o}C) with three replications each. At the time of panicle initiation, a set of 90 landraces with three replicates were transferred to temperature controlled green house for heat stress induction. The high temperature stress was induced from panicle initiation to maturity stage by keeping the pots in a temperature controlled green house. Average maximum temperature during this period was 39.5^{o}C and average minimum temperature was 25.4^{o}C and maximum and minimum RH of 90.6% and 59.2% respectively. The daily temperatures including maximum and minimum temperatures were recorded under control as well as heat stress conditions using digital thermo-hygrometer throughout the experiment. Management practices were followed as per package of practices recommendation of Kerala Agricultural

University. Fertilizer dose of N:P:K in the ratio of 90:45:45 Kg/ha in three split doses @ 1/3 dose of each fertilizer at basal, tillering and at panicle initiation stages. Six replications were maintained for a single landrace until the panicle initiation stage. Five plants per each replication were maintained. Data were recorded on plant height, days to 50% flowering, tiller number, productive tiller number, canopy temperature, spikelet tissue temperature, grain yield per plant, straw yield per plant and spikelet fertility percentage for control and stress induced plants.

RESULT:

The results related to genetic parameters *viz.*, phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as percent of mean for all the 10 characters. Phenotypic coefficient of variance was found higher than genotypic coefficient of variance for all the traits except the days to 50% flowering disclose the environmental impact on the expression of such characteristics. In this study, all the ten traits recorded high heritability, which indicates they were least influenced by environmental impacts. Even then, choosing of these characters may not have been helpful because broad sense heritability is based on overall genetic variance, including additive, dominant and epistatic variations. So, the heritability values along with genetic advance will be useful for the selection criteria. Among the traits, the highest heritability was observed for days to 50% flowering (1%) followed by number of filled grains per panicle (0.978%) and number of unfilled grains/panicle (0.922%). The principal component analysis under high temperature condition indicated that among 10 PCs initial 4 PCs contributed upto 60% variation with eigen value more than one (Figure 1). The PC1 contributed 19.34% variation and the variation was due to the traits productive tiller number (0.674) and tiller number (0.626) with higher positive factor loading values. The trait grain weight (-0.096) with lower negative factor loading value also contributed to the variability of PC1. The second principal component was holds for 15.86% variation and the trait filled grains/panicle (0.708) with positive factor loading value and canopy temperature (-0.016) with lower negative factor loading value contributed to the variability of this component. The third and fourth components were responsible for 14.27% and 10.35% variation respectively. Under third principal component the traits canopy temperature (0.670) and plant height (0.514) with higher positive factor loading values and the trait filled grains/panicle (0.049) with lower negative factor loading values are contributed to the variability of this component. The parameter grain weight (0.707) with higher positive loading value and days to 50% flowering (-0.045) with lower negative factor loading value were contributed to the variability of fourth principal component. Biplot diagram depicted the distribution of genotypes based on the traits. Quadrant one included genotypes with higher filled grains/panicle and grain weight, second quadrant included genotypes more tillers, productive tillers and plant height. Genotypes with higher canopy temperature, spikelet tissue temperature, straw weight and unfilled grains/panicles are distributed over third quadrant and fourth quadrant possess genotypes with more days to 50% flowering.

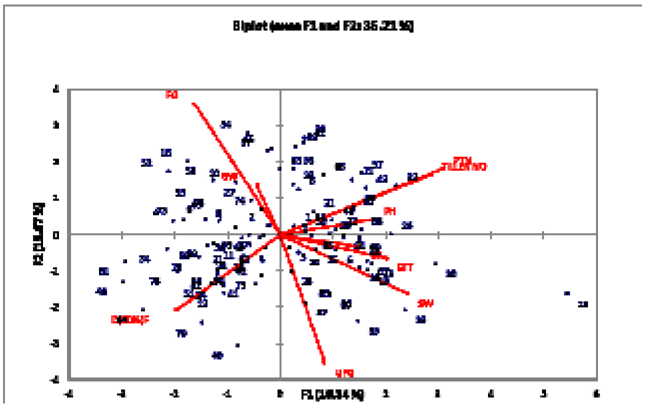

Figure 1: Biplot between PC1 and PC2 under high temperature condition

CONCLUSION:

Under high temperature conditions, spikelet sterility is the major limitation for reproductive success and better yield. Genetic analysis revealed that landraces were containing marked phenotypic variability. High values of GCV, PCV, heritability and genetic advance were found for the traits number of unfilled grains/ panicle and number of filled grains/panicle, indicating the pre-ponderance of additive gene action and therefore scope for improvement of the trait through selection. Four principle components were depicted having Eigen value >1 and cumulative variation of 59.84% in which the contribution of individual PCs was; PC1 (19.34 %), PC2 (15.86 %), PC3 (14.27 %) and PC4 (10.35%). Based on the performances of various physio-morphogical traits under control and heat stress conditions, we were able to identify Karuthacheera, LN-9956-Vellakaravala (Pavumba) and Pokkali white were recorded the highest number of fertile grains under high temperature.

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IRC/TM-1/PP-58

TEST CROSS NURSERY FOR IDENTIFICATION AND DEVELOPMENT OF PARENTAL GENOTYPES AND HYBRIDS IN RICE

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A Test Cross Nursery (TCN) was conducted during Kharif 2015-16 in order to indentify suitable parental material and hybrids in rice, especially of early and medium maturity duration. The material used for crossing were involving exotic as well as indigenous rice lines.

METHODOLOGY

Total 181 F_1 crosses were made during Kharif 2014-15 involving selected exotic and indigenous rice lines used as male and an established CMS (Cytoplasmic Male Sterile) line Pusa 6A used as female. All of these crosses were evaluated in a trial in augmented design along with the four checks during Kharif 2015-16. F_1s were planted along with their male parents.

RESULTS

Out of total 181 genotypes, 32 were found to be working as restorers for Wild Abortive (WA)-CMS cytoplasm whereas 18 genotypes were found to be working as maintainer for the cytoplasm. Out of 32 F_1 hybrids which were having more than 75% of the spikelet fertile, 7 hybrids were found to be having significantly superior yield over the hybrid as well as varietal checks of medium maturity group whereas 5 hybrids of early maturity group was found to be having significantly superior yield over the respective hybrid and varietal checks of their groups. The 18 F_1s which had shown desirable pollen and spikelet sterility were back-crossed with their respective male parents.

CONCLUSION

Through the TCN conducted in the present study, good parental genotypes were identified for further use in the hybrid rice breeding programme. Using genotypes identified as maintainers, the diversification of the available CMS lines can be undertaken.

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IRC/TM-1/PP-59

PARENTALPOLYMORPHISM AND PHENOTYPIC CHARECTERIZATION FOR GRAIN NUMBER TRAITS IN RICE

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Rice is the major food crop for more than half of the global population. Demand of rice productivityis assessed to be around 600 million tons up to 2030 against the current production of around 503 million tons which leaves a gap of around 97 million tons rice. Enhancement of grain yield is the only way to avoid today's upsurge in food demand. Evaluation of grain yielddepends on the grain number per panicles and its component traits like number of tillers, and the numberof spikes present per panicle.Important phenotypic traits could be helpful in choosing rice genotypes for breeding(Soumya Mohanty et al., 2018). Molecular marker innovation can fundamentally improve the productivity and exactness of reproducing measure.PCR based markers mostly microsatellites have revealed a great potential in the analysis of genetic diversity, gene tagging and genome mapping studies because they are very informative, technically simple, require less time, and need small amounts of DNA(S Mohanty et al., 2017). DNA profiling is the key to identify the target gene which was done by parental polymorphism to know genetic diversity along with phenotypic variation.

OBJECTIVE:

I. Identification of molecular markers differentiating low grain number (Heera) and high grain number (PDK Sriram) parental genotypesthrough parental polymorphism survey.

II.Phenotyping of recombinant inbred line (RIL) mapping population

METHODOLOGY:

The experimental material of the present study consists of two rice cultivars, namely PDKV Shriram(high grain number), Heera (low grain number) and 188 F9 recombinant inbred lines developed from the cross between them. The F2 plants were advanced to F9 recombinant inbred lines (RILs) following single seed descent methodduring 2018-2019 (FIG.2). Using miniprep (Dellaporta) method DNA was isolated from both the parents along with 188 RILs. A set of 1152 microsatellite markers uniformly distributed over 12 rice chromosomes were used to assess polymorphism between two rice cultivars.The PCR amplification was carried out in a 20ìl reaction mixture volume containing 40ng of genomic DNA and reaction mixture.

The amplified products were separated on 3% agarose gels using 1X TBE buffer and stained with ethidiumbromide (0.5ìg/ml). The gels were visualized under UV radiation and photographed using a gel documentation system to detect polymorphisim. The size of the amplified bands was determined based on the migration relative to molecular weight size markers (50 bp DNA ladder).

The percentage of polymorphism was calculated using the formula:

%of polymorphism= (No. of polymorphic loci/ Total No. loci used)X 100

The RILmapping population alongwith parents, were evaluated for grain number and its component traits at experimental field conditions ofNational Rice Research Institute (NRRI), Cuttack during *Kharif*, 2018 following Alpha Lattice design. For phenotypic data the standard agronomic practices were adopted for normal crop growth. Five plants were selected frommiddle of the row for data collection. The data on 10 traits recorded were days to 50%flowering (DFF), plantheight (PH), number of tillers/ plant (TN), number ofpanicles/ plant (PN), panicle length (PL), number offertile grains per panicle (GN), number of chaff perpanicle (CN), number of spikelets per panicle (SN),spikelet fertility percentage (SFP) and 1000-grain weight (GW).

Considering important traits mean values of five randomly selected plants from each of the three replications of RILs and parents were carried out and analyzed statistically for their variance following simple lattice design. Analysis of variance, phenotypic correlation and Principal component analysis were estimated by using PAST3.0 statistical package.

RESULT:

Parental polymorphism survey was done using 1152 random microsatellite markers from all the 12 chromosomes throughout the genome. Out of which only 118 markers revealed polymorphism among parents (9.64%) (Fig 1, Table 1). Among 12 chromosomes analyzed chromosome 3 shows highest polymorphism (20.45%) followed by chromosome 5(14.15%) and 4 (12.93%). Similarly chromosome 10 showed lowest percentage of polymorphism (1.53%).

All the ten phenotypical traits were evaluatedfor RILs along with their parents (Fig. 2). Mean and range values were calculated for RILs and individual parent (Table 2).

The analysis of variance revealed highly significant difference among the RILs for all the 10 yield traits indicating a large amount of genetic variability is present in RIL population for effective selection and QTL mapping(table 3). Phenotypic correlation coefficientrevealed grain number (GN) is highly and positively significant with spikelet number (SN) (0.00), spikelet fertility percentage (SFP) (0.00), thousand grain weight (TGW) (0.00001);similarly plant height(PH) is highly significant with panicle length(PL), grain number(GN) and spikelet number(SN); tiller number (TN) is highly significant with panicle number(PN); panicle length(PL) is highly significant with grain number(GN) and spikelet number(SN); chaff number is highly significant with spikelet number(SN) and spikelet fertility percentage (SFP): spikelet number(SN) highly significant with spikelet fertility percentage (SFP) and thousand grain weight (TGW) whereas days to 50% flowering (DFF) is moderately significant with all the traits except tiller number(TN) and spikelet fertility(SFP) (Table 4).Principal component analysis revealed the patterns and inter-relationship between RILs with grain number component traits.The first four principal components explained a total of 74.58% variability in the all qualitative traits (Table 5). The analysis of eigenvectors gave the information of qualitative traits for percentage of variation to the first four principal components, which were 29.04%, 19.83%, 15.90% and 9.81% respectively and inter related components PC1 and PC2 (Fig.3).

CONCLUSION:

PDKV Shriram and Heera are high grain and low grain indica rice varieties, respectively and showed comparatively lower percentage (9.64%) of polymorphism because of the same genetic background. ANOVA revealed highly significant variation among all the traits which confirms the RIL mapping population is suitable for further QTL mapping. The correlation study showed the strong and positive significant association of grain number and spikelet number with the other associated traits. The association studied indicating grain number of rice can be improved by selecting lines having higher performances for these traits. Further PCA biplot confirmed the positive association of grain number related traits with RILs. Finally correlation study and PCA were complementing each other, Therefore,selections ofsegregating lines with desirable traits are to be effective in accumulation of favourable genes for bringing together into the common genetic background of cultivated indica rice (Oryza sativa L.)

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IRC/TM-1/PP-60

IDENTIFICATION OF NEW QUANTITATIVE TRAIT LOCI FOR RESISTANCE TO BROWN PLANTHOPPER IN RICE LANDRACE SINNASIVAPPU

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Hopper-burn caused by brown planthopper (*Nilaparvata lugens* stal) is the most devastating insect damage in rice causing severe yield reduction worldwide. It directly damages rice crop by sucking sap from leaves and leaf sheaths causing drying and death of crop under severe infestation. It causes indirect damage by transmitting rice ragged stunt and grassy stunt virus. Breeding for host plant resistance is the most promising and economic means for managing brown planthopper (BPH) infestation.

Several genomic sources of cultivated and wild relatives of rice were identified and characterized for resistance against BPH. Inheritance of resistance was reported to be both qualitative and quantitative. To date 40 genes (*Bph 1* to *bph 40*) were identified using classical genetics and molecular approaches (Du et al., 2020). Fourteen BPH resistance genes (*Bph 1, bph 2, Bph 3, Bph 6, bph 7, bph 9, Bph 10, Bph 14, Bph 15, Bph 18, Bph 21, Bph 26, Bph 29* and *Bph 32)* have been cloned and mechanisms underlying resistance were reported. However success has been very limited in breeding for BPH resistance. Differential reaction of resistance genes/QTLs across the countries wherein different biotypes are prevalent is found to be the primary constraint.

We found a Sri Lankan local land race, Sinansivappu (AC No.15444) as a potential genetic source for BPH resistance across the locations and years against biotype 4 in India. It was also reported earlier to exhibit wide spectrum of resistance to all 4 biotypes across the countries in the world (Heinrichs *et al.*, 1985). But the potential of BPH resistance genes/QTLs present in Sinnasivappu remained unexplored until now. Hence the aim of the current study is to identify novel resistance gene/QTLs in the landrace Sinnasivappu using Genotyping by sequencing (GBS) (Elshire et al. 2011) and develop closely linked SNPs for MAS in rice breeding programs.

METHODOLOGY

The mapping population comprising of Recombinant Inbred Lines (**$F_{10:11}$**) was developed from a cross made between Swarna, a popularly grown mega rice variety but highly susceptible and Sinnasivappu, a resistant check used in BPH screening experiments. A total of 140 RILs were phenotyped along with parents; and checks in glass house during seedling stage against Biotype 4 following standard seed box screening test. GBS was performed in RIL population for SNP discovery. Construction of linkage map and QTL analysis was done using QTL IciMapping version 4.1 (Meng *et al.*, 2015) utilizing the high resolution SNP marker data obtained in GBS method and phenotypic data on damage scores

RESULTS

The damage score recorded for resistant parent Sinnasivappu (2.8) was found to be significantly different from that of susceptible parent Swarna (8.6) using *t* test ($P < 0.01$). The frequency distribution of data on damage scores in RIL population showed a continuous distribution ranging from 0.29 to 9 revealing quantitative inheritance pattern controlled by poly genes. The Shapiro-Wilk (W) normality test indicated the near normal distribution (W> 0.90) of the data of the RIL population suggesting involvement of multiple genes.

Table 1: QTLs for resistance to BPH identifed in Swarna/Sinna sivappu RIL population

Trait	QTL name	Chr#	Left Marker flanking QTL	Right Marker flanking QTL	LOD	QTL Position (Mb)	Phenotypic variance explained (%)	Additive effect	Source of resistance alleles
Damage score	qDS_3	3	C3_7457660	C3_6332631	7.95	6.33 to 7.45	13.1	1.27	Sinasivappu
	qDS_5	5	C5_13157270	C5_13157287	4.17	13.157270 to 13.157287	6.0	0.84	Sinasivappu

SNP genotyping using GBS revealed 15580 polymorphic homozygous SNPs from which 3620 were physically aligned to the *Nipponbare* reference genome after filtering SNP markers with missing data and segregation distortion. A high density genetic linkage map was constructed using 3620 SNPs distributed on 12 linkage groups covering 21237.51 cM with an average marker interval of 5.86 cM. The lengths of linkage groups ranged from 1124.31 (Chr #01) to 3443.50 cM (Chr #1) while the marker loci in each linkage group ranged from 153 (chr 9) to 739 (chr 1)..

QTL analysis detected two QTLs designated as *qDS 3* and *qDS 5* for seedling resistance (Table 1**)**. The genomic region of *qDS3* was mapped in 1.12 Mb region flanked by SNP markers C3_7457660 and C3_6332631 between 6.33 Mb to7.45 Mb region on the Nipponbare reference genome. It explained 13.1% of phenotypic variation for damage score with a LOD score of 7.95. The resistant alleles were contributed by the donor. A minor QTL *qDS5* was also detected on chromosome 5 in the marker interval between two SNP markers *i.e* C5_13157270 and C5_13157287 at 13.15Mb position in reference genome. Both SNPs were separated by only 17 bp. It accounted for 5.9% of total phenotypic variance for resistance with a LOD score of 4.17. The donor alleles govern resistance at this QTL region.

The genomic region of major QTL *qDS3* was found to be different from the previously reported resistance loci namely *bph 11*, *Bph 13*, *Bph14*, *Bph 19* and *Bph31* on chr #3 (Hirabayashi *et al*., 1998; Renganayaki *et al*.,2002; Du *et al*.,2009; Chen *et al*.,2006 and Prahlada *et al*., 2017). But *qDS3* showed overlapping genomic region (6.33 Mb to 7.45 Mb) with that of earlier reported *Bph 19* gene (7.18 to 7.24 Mb. And *qDS5* is novel in the sense that none of the reported resistant genes/ QTLs were present on chr # 5. Further based on the profiles of the cloned resistant genes, 2 LRR genes were found which might be the likely candidate genes underlying the major QTL *qDS3* region.

CONCLUSION

This study provided an insight into the quantitative resistance to BPH in Sinnasivappu, a potential local land race of rice exhibiting broad spectrum and stable resistance. By construction of a SNP-based genetic map a new major QTL, *qDS3* was mapped to 1.12 Mb region using RILs derived from the cross Swarna/Sinnasivappu.The genomic region of QTL *qDS3* is found to be different as compared to the previously identified resistance loci on chr #3. It showed overlapping genomic region (6.33 Mbp to 7.45 Mb) with earlier reported *Bph 19* gene (7.18 to 7.24 Mbp) but not coinciding with the reported region. Fine mapping and validation of *qDS3* is in progress for identifying candidate resistance gene(s) which could be of benefit for breeders for incorporation into other elite rice germplasm.

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IRC/TM-1/PP-61

MARKER ASSISTED INTROGRESSION OF SEEDLING AND REPRODUCTIVE STAGE SALINTIY TOLERANCE INTO MEGA RICE VARIETY MTU1010

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Rice is the staple food for more than half of the world's population and is considered as life for Asians. Salinity is the second most important abiotic stress in rice growing countries next to drought and is a serious constraint hampering the rice production worldwide. Breeding rice varieties with tolerance to salinity (seedling and reproductive) offers an economically viable and sustainable option to improve rice productivity in saline areas. '*Saltol*', a major QTL for seedling stage salinity tolerance and *qSSISFH8.1* a QTL for reproducitve stage salinity tolerance with linked molecular markers created opportunity for the breeders to transfer the QTLs into widely grown rice varieties through marker-assisted backcross breeding (MABB).

OBJECTIVE

To introgress *Saltol* and *qSSISFH8.1* into mega rice variety MTU1010 through marker assisted back cross breeding.

METHODOLOGY

For introgression of '*Saltol*' into mega variety MTU 1010, crossing was taken with FL 478, a donor developed at IRRI for seedling stage salinity tolerance at Regional Agricultural Research Station, Maruteru. Three cycles of back crosses of MTU1010/ FL 478 was generated for introgression of salinity tolerance using fore ground (RM 10694) and recombinant markers (RM 10793, AP 3206) on chromosome 1 and BC_3F_1 was selfed to generate BC_3F_2. Phenotyping and genotyping was done in BC_3F_2 and plants that survived were further advanced to generate fourteen introgression lines (ILs). Based on the background genome recovery two ILs MST36 and MST40 were further crossed to CSR27 a donor having QTL *qSSISFH8.1* for reproducitve stage salinity tolerance and two cycles of back cross of MST36/CSR27 and MST40/CSR27 were generated using HvSSR08-25 and RM3395 as foreground markers and RM3215 and RM1384 as recombinant markers. All the genotyping work is performed as per Girija Rani *et al* 2019 and electrophoresis was carried out using 3% high resolution metaphor Agarose.

RESULTS & DISCUSSION

For Saltol introgression, a total of 5,400 plants of 30 families of BC_2F_2 were evaluated. A total of 1800 plants were selected based on phenotypic similarity with MTU1010 and were genotyped. In foreground selection using RM 10694, out of 1800 plants 363 plants were having *Saltol*, a major QTL for seedling stage salinity tolerance. In recombinant selection, AP 3206 at proximal end and RM 10793 at distal end were used and 142 plants out of 363 were double recombinants which were further studied for salinity tolerance in hydroponics. When these 142 plants were screened under hydroponics, a total of 83 lines were survived. Thirty lines were tolerant with a mean score of 3 as per SES of visual salt injury at seedling stage while 53 lines were moderately tolerant with a mean score of 5. These 83 lines were further evaluated and based on phenotyping and genotyping (foreground and recombinant selection) 37 introgressed lines with seedling stage salinity tolerance were identified which were further promoted to yield evaluation trials at station followed by multilocation testing under saline environment and fourteen best ILs with increased seedling survival better than MTU1010 were selected. Among these fourteen lines, eight introgression lines

Table1 : Back Ground Genome Recovery in *Saltol* Introgression lines of MTU1010

Chr wise per cent similarity	Marker_number	DST-3-94-10	DST-5-61-3	DST-6-64-8	DST-6-89-13	DST-6-96-16	DST-8-162-4	DST-9-64-5	DST-9-157-13
% similarity considering all loci		97.55	94.57	97.01	91.15	96.93	98.11	97.86	98.01
1	9838	96.71	90.93	94.75	91.36	95.89	94.43	97.57	94.19
2	15785	99.23	97.19	96.24	88.00	93.51	99.73	99.54	99.73
3	22670	98.28	97.38	98.48	90.76	96.68	99.02	98.70	99.58
4	26389	96.93	95.69	97.27	91.46	97.25	99.84	99.70	99.92
5	30593	99.13	92.43	99.78	92.62	99.79	96.32	99.40	96.35
6	35980	98.28	95.89	99.70	93.44	99.83	98.95	90.04	99.49
7	38285	96.92	93.61	97.03	85.71	94.94	99.13	98.86	95.38
8	40812	97.60	89.21	95.62	91.73	99.76	99.52	98.01	98.49
9	43210	98.98	95.92	99.54	93.12	99.54	99.79	99.54	99.75
10	44460	91.28	96.56	90.38	93.16	99.52	99.60	99.35	99.60
11	47067	98.24	95.99	99.54	94.69	99.50	99.19	99.30	99.65
12	49019	91.88	97.22	91.04	88.28	89.26	99.43	99.48	99.64

had 91 to 98% genome recovery of MTU1010 when genotypic backgorund selection was done on advanced lines developed by phenotypic selection for closeness to receipient parentsusing 50K SNP chip at National Institute for Plant Biotechnology, New Delhi.

Based on the background genome recovery and phenotpyic similarity with MTU1010 two lines were further crossed to CSR27 for introgression of *qSSISFH8.1* during kharif 2018 and F_1s were evaluated during Rabi 2018-19 and based on foreground and recombinant selection BC_1 were generated and BC_1F_1s were evaluated during Kharif 2019 and BC_2 were generated and were positive plants were further backcrossed to generate BC_3 in Rabi 2019-2020 and during kharif 2020 BC_2F_2 plants were phenotyped for seedling stage salinity tolerance and were simultaneously genotyped to select positive plants which will be further advanced to next generation.

CONCLUSION

The present study was undertaken to introgress *Saltol* and *qSSISFH8.1* in to mega variety MTU 1010 for seedling and reproductive stage salinity tolerance. A total of 14 ILs of MTU1010 with *Saltol* were devloped and introgression of *qSSISFH8.1* is under progress.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-62

EFFECT OF ZINC AND SULPHUR FORTIFIED BRIQUETTES ON YIELD AND QUALITY OF RICE IN MEDIUM BLACK SOIL OF KONKAN REGION

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Rice (*Oryza sativa L.*) is one of the three major food crops worldwide. Approximately 50% of the world's population uses rice as a staple food. Rice production in India accounts for 17.95% of the world's total production. Fertilizer is the key input in increasing agricultural production and productivity of the land. The efficient management of fertilizer through briquettes containing nitrogen and phosphorus further enhanced the efficiency of fertilizers in lowland transplanted rice (Bulbule *et al.*, 2008). Reduction in yield of rice is often blamed to zinc and sulphur deficiency. Rehman *et al.* (2008) reported that Zn deficiency is considered to be the most important nutritional stresses limiting rice production in Asia. Zinc (Zn) plays a major role in the growth and development of rice (Chaudhary *et al.*, 2007). The seventeen essential nutrient elements, Zn is the fourth most deficient nutrient element in Indian soils (Shukla and Behera, 2011). Zinc is one of the vital nutrients which is required for various biochemical and metabolic process in rice such as synthesis of cytochromes and nucleotides, auxin metabolism, production of chlorophyll, activation of several enzymes. The sulphur plays key roles in protein production, chlorophyll formation and oil synthesis. Sulphur improves growth, crop yield, seed formation and oil percentage in oil seed plant, protein, cereal quality for milling and baking (A.O.A.C. 1970). The aim of the study was to assess the effects of different types of zinc and sulphur fortified briquettes on rice yield and grain quality characteristics.

Rice quality comprises milling, appearance, cooking and eating and nutritional quality, etc. With the continuous improvement of economic life, people's requirements for rice quality, especially flavor, taste and nutritional quality, are becoming stricter (Cai *et al.*, 2011). The application of fertilizer plays a crucial role in improving rice yield and is also a key factor affecting rice quality (Liu *et al.*, 2019). Studies have shown that different fertilizer types, as well as fertilization modes and rates directly affect rice yield and quality (Tang *et al.*, 2019).

METHODOLOGY

The field experiment is conducted by using 11 treatments and 3 replication with Randomized Block Design in *kharif* 2016-2019. The Karjat-3 rice variety is used for experiment. Among treatments one treatment of RDF and absolute control, three different types of briquettes (UB-Suphala, UB-DAP and UB-KAB) with 5kg, 10kg and 15 kg zinc fortified (in the form of $ZnSO_4$) briquettes were applied.

According to the treatment 250 g of paddy samples were collected from the field. The samples were aged for three months for getting the better grain quality results. Milling quality was based on standard to determine the brown, milled, and head rice rates. The chalky kernel rate and chalkiness were measured by appearance of milled rice. The cooking time was determined by pressing the cooked rice grains in a hand and determining when there was no hard heart in the middle, and the time was recorded. The gel consistency and alkali spreading value is determined by using the protocol developed by Cagampang (1973) and Bhattacharya and Sowbhagya (1972). Biochemical quality: amylose level was conducted according to Standard Evaluation Systems for Rice (IRRI, 1996).

RESULT

The treatment T_8 gave highest grain (52.16 qha^{-1}) and straw (61.90 qha^{-1}) yield of paddy. The grain yield was increased 26.10% as compared to RDF (100:50:50 NPK kg ha^{-1}). The Zinc and Sulphur content in rice grain is increased in treatment T_8 i.e. 12.0 mg kg^{-1} and 0.56 mg kg^{-1} respectively. The milling percentage of rice was found increased by 3.52 % percent in the treatment T_8 as compared with treatment T_2 i.e. RDF (100:50:50 NPK kg ha^{-1}). The application of UB-KAB+10 kg $ZnSO_4$ briquettes (T_8) gave acceptable range of cooking and biochemical characteristics i.e. amylose content, gel consistency, alkali spreading value and gelatinization temperature was found 23.97%, 77, 4.0 and intermediate (70-74 ^{O}C). The same result was noticed by Dou *et al.*, 2017 zinc and sulphur fortified fertilizer application is responsible for improvement of rice grain quality.

CONCLUSION

The grain yield, zinc-sulphur content in the grain, milling and cooking quality of the grain was improved in the treatment UB-KAB+10 kg $ZnSO_4$ briquettes as compared with recommended dose of fertilizer.

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IRC/TM-1/PP-63

HIGH DEFINITION GENOME LANDSCAPE OF MEGA RICE VARIETY RANJIT FOR RICE IMPROVEMENT PROGRAM

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Assam is one of the major rice growing states in the country where, rice is the most important crop and covers 2.54 million (M) ha of the total 3.3M ha cropped area. Traditionally, rice is grown in three overlapping seasons Ahu, Sali and Boro in the state as a consequence of agro-climatic conditions and is dependent on rainfall. Ranjit and Bahadur (semi-tall stature) are the most popular varieties of Assam and they cover about 65 per cent of rice growing areas in the state. Around 0.38M hectares and 0.5M hectares rice growing areas are chronically affected by drought and flood respectively. The mega rice variety Ranjit, predominantly grown in Assam during kharif season is susceptible to both flood and drought stress as well as other biotic and abiotic stress. A traditional drought tolerant cultivar ‘Banglami’ has been used for crossing with Ranjit to prepare drought tolerant Ranjit variety. Whereas Ranjit-Sub1 variety has been released to overcome the flood challenge. It has been reported that the Ranjit-Sub1 helped in increase in the overall rice yield by up to 66% in flood affected condition. The present study of preparation of high quality genomic landscape of mega rice variety Ranjit will help in rice breeding program towards development of Ranjit based biotic and abiotic stress tolerant variety.

METHODOLOGY

Seeds of rice variety Ranjit (IC-575203) were germinated in petri dishes and transplanted into pots after 7 days in the ratio of one seedling per pot. Genomic DNA was extracted from 80-100mg of young rice leaves (powdered) using Qiagen DNAeasy Plant Mini kit. The quantification and quality of the genomic DNA were assessed using Nanodrop2000, Qubit and agarose gel electrophoresis, respectively. 500ng of Qubit quantified DNA was sheared using Covaris S220 sonicator to generate specific fragments with size range of 200-350 bp. Resultant fragments were amplified for 2 cycles of PCR using Illumina-compatible primers provided in the NEXTflex Rapid DNA sequencing Bundle. The libraries were sequenced on Illumina HiSeq X Ten (Illumina, San Diego, USA) for 150 bp paired-end chemistry following manufacturer’s procedure.

For Oxford Nanopore sequencing, a total of 2 ìg of genomic DNA was taken and cleaned up using Zymoclean Large Fragment DNA Recovery kit (Zymo Research, USA). The purified DNA was then taken as an input for library preparation. Sequencing was performed on GridION X5 (Oxford Nanopore Technologies, Oxford, UK) using SpotON flow cell R9.4 (FLO-MIN106) in 48 hrs sequencing protocol on MinKNOW 2.1 v18.08.3.

The Illumina raw reads were trimmed based on quality score 30 using Trim Galore v0.4.0 and nanopore raw reads were trimmed for adapter removal using Porechop v0.2.4. The genome size estimation was performed with jellyfish v2 with Illumina PE data. Hybrid assembly was carried out by Flye assembler using trimmed Nanopore reads. Assembled genomes were aligned with Illumina PE data with BWA-MEM v0.7.1 followed by two round of polishing with Pilon v1.23.

The assembly were subjected to reference guided pseudo molecule preparation with RAGOO v1.11. The gap between scaffold was maintained at 100 N s. The gold standard reference Indica genome has been used for pseudo molecule preparation. This final pseudo molecule has been subjected to completeness analysis based on BUSCO and further used for downstream analysis.

The library of repetitive and different transposable elements of both the genome were identified with RepeatScout v1.0.5 and Tandem Repeat Finder v4.09 separately. Both of this repeat library and rice repeat reference of RepBase v25.06 has been used to hard mask the respective genome with RepeatMasker v4.1.0.

Gene model was predicted through *ab initio* and evidence based prediction method. In case of evidence based method gene annotation information was generated using transcriptome data. Previously sequenced transcriptome of Ranjit and Banglami from drought related experiment has been used in this study. The transcriptome has been mapped to respective genome using HISAT2 followed by gene identification was performed with Cufflink v2.2.1. For *ab initio* based gene prediction, hard masked genome, as well as transcriptome mapped genome were used in AUGUSTUS taking rice as model reference.

The total predicted genes were annotated using BLASTX taking NCBI - non redundant (NR) database as reference and InterProScan was also performed using EBI database as reference. The pathway analysis has also been performed with Kyoto Encyclopedia of Genes and Genomes (KEGG) database. The annotation has been performed with the help of Omicsbox v1.3.11.

RESULTS

A total of 56.7Gb data of Illumina and 35.8Gb & 17.8Gb Nanopore data has been generated comprising of 49,162 and 26,346 million bases respectively. The estimated genome size of Ranjit is 422Mb and the overall depth of sequencing id ~178X. The hybrid assembly of the genome has been performed with hredfi. assembler followed by two round of polishing with Pilon. This results in the assembled genome comprising of 972 scaffolds with a total coverage of 402 Mb (95.26%) genome having N50 value of 2.003 Mb. A total number of 968 scaffolds were anchored on Indica Rice reference genome. The BUSCO analysis shows that the completeness of the assembly is of 87.2%.

The genome contain 51.81 % repetitive region with a total of 208Mb. Among which 76.12% were identified as simple repeat. A total number of 2,576 retro transposons and 57,648 SSR's were were identified.

Gene prediction has been performed with help of transcriptome data, where 80 million high quality reads were mapped on the genome with HISAT2, followed by Cufflink based gene analysis that helped in identification of 96 thousands transcripts. These transcripts were subjected to Augustus based gene prediction that identified 28,348 genes. Out of which 25,565 genes were finally annotated with NCBI non-redundant and InterPro database.

CONCLUSION

The near chromosome level gold standard de novo annotated assembly of the mega rice variety Ranjit genome containing positional information about transcripts and Simple Sequence Repeats will be a useful resource for development of different stress tolerant rice variety.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-64

INTROGRESSION OF *Pi54* AND *Pi1* BLAST RESISTANCE GENES AND *qDTY*$_{12.1}$ FOR YIELD ENHANCEMENT UNDER DROUGHT STRESS

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Drought stress is the major constraint to rice production and yield stability in rainfed ecosystems. Though many QTLs were identified for drought stress tolerance, a large effect QTL, *qDTY*$_{12.1}$ offers significantly to the yield under reproductive stage drought stress and its effect on yield was also evident in the irrigated conditions. In addition to the drought, incidence of blast disease caused by *Magnaporthe grisea* is another production constraint commonly observed in the rainfed ecosystem. The continuous occurrence of these two stresses increases the yield loss to the tune of 65%. Till date, more than 100 rice blast resistance genes and 350 QTLs were identified for conferring resistance to the blast diseases. Among them, two major blast resistance genes *viz.*, *Pi54* and *Pi1* were known to confer broad-spectrum resistance against predominant races of the pathogen in India. The marker-assisted selection offers a choice of options for targeted pyramiding of abiotic stress resistance gene/ QTL along with major genes of blast resistance in the genetic background of rice varieties. Several studies were aimed these stresses independently but the present study aims at integrated strategy of improving the grain yield under drought stress through *qDTY*$_{12.1}$ coupled with incorporating two major blast resistance genes (*Pi1* and *Pi54)* in the genetic background of elite rice variety i.e., Varalu, through marker-assisted gene pyramding can be significantly help to tackle the problem of rainfed rice ecosystem.

METHODOLOGY:

Donor genotypes:

Drought tolerance: NILs of Vandana possessing *qDTY*$_{12.1}$, a high yielding, early maturing and popular *indica* rice lines suitable for the upland area.

Blast resistance: An elite breeding line possessing *Pi1* and *Pi54* genes in the genetic background of Samba Mahsuri called BPT-LT.

Recipient genotype: Varalu (WGL 14377) is an elite early maturing (90-95 days) upland rice variety, which is developed from the cross WGL-20471 X CR-544-1-2 released in 2002, was used as a recurrent parent.

Crossing scheme:

Simultaneous step wise back cross transfer approach coupled with phenotypic selection was adopted for the targeted transfer of *Pi1*, *Pi54* and *qDTY*$_{12.1}$ into the genetic background of elite cultivar Varalu. Two independent crosses were made i.e., Varalu X Vandana NIL (for introgression of *qDTY*$_{12.1}$ (cross-I)) and Varalu X BPT-LT (for introgression of *Pi54* and *Pi1* (cross-II)) followed by intercrossing at BC_2F_2 for pyramiding two traits. The F_1 progeny obtained from the independent crosses were screened with markers linked to the target traits. The true hybrids were independently backcrossed with the recurrent parent (RP) to produce BC_1F_1 hybrids. The plants with the target genes and maximum recurrent parent genome (RPG) recovery were again backcrossed to get BC_2F_1 generation. The best plants showing desired heterozygous alleles were selfed to produce the BC_2F_2 population among which the homozygous plants for respective target genes were intercrossed to develop ICF_1 progeny and further selfed to generate ICF_2 population. The selected lines possessing $qDTY_{12.1}+Pi54+Pi1$ were advanced through the pedigree method from ICF_3 to F_5 for field evaluation of agronomical traits against blast and reproductive stage drought stress.

Foreground and Background selection:

Foreground selection was done using peak marker as well as linked markers RM511, RM28099 (for $qDTY_{12.1}$ A), RM28130 and RM28163 (for $qDTY_{12.1}$ B) while RM206 for *Pi54*, RM224 for *Pi1*. For background selection a set of approximately 635 SSR markers representing ~53 markers per chromosome covering every 2-5Mb interval were selected from the high-density microsatellite map of rice.

Phenotyping:

The blast screening was carried out by using the procedure of Umakanth et al. (2017). The phenotyping of reproductive drought stress was done by using the procedure of Venuprasad et al. (2007).

RESULTS:

Ø Crosses were made between Vandana NIL/ Varalu and BPT-LT/ Varalu and true F_1s were screened for $qDTY_{12.1}$, *Pi1* and *Pi54* using tightly linked markers. True independent F_1s were backcrossed twice with recurrent parent to obtain BC_2 populations for both traits.

Ø The 422 BC_2F_2 plants (derived from two positive BC_2F_1 plants) were assessed for grain yield under reproductive drought stress and the presence of $qDTY_{12.1}$ (A and B) with linked markers and identified 26 plants having homozygous $qDTY_{12.1}$ genomic region. Among them, one plant (VVN-117-34-26) with maximum RPG of ~85% was used for inter crossing.

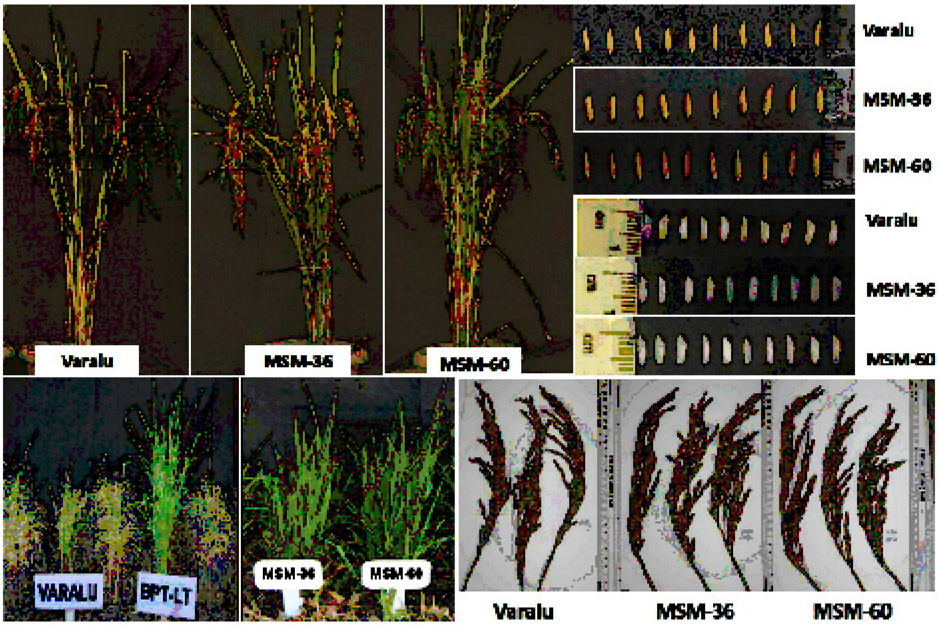

Figure 1: Performance of pyramided lines of Varalu having $qDTY_{12.1}+Pi54+Pi1$

Ø Upon screening of 500 BC_2F_2 plants (derived from two positive BC_2F_1 plants), identified 34 plants having *Pi1* and *Pi54* in homozygous condition. Two BC_2F_2 plants (VLT-175-13-10 and VLT-183-98-31) having both the genes in homozygous condition with maximum RPG of ~90% were forwarded for intercrossing.

Ø Twenty ICF_2 plants homozygous for all the three genes were identified and assessed for blast resistance, grain yield under reproductive stage drought stress. Identified six best lines (MSM-36, MSM-49, MSM-53, MSM-57, MSM-60 and MSM-63) having two blast resistance genes and $qDTY_{12.1}$ in homozygous condition with recurrent parent genome of 95-96.5% having minimal linkage drag of ~0.1 to 0.7Mb. These lines showed yield advantage under drought stress as well as under irrigated conditions (Figure 1).

Ø MSM-36 showed better performance in the national coordinated trials conducted across India, which indicates that improved lines of Varalu.

CONCLUSION:

In the present study a major QTL ($qDTY_{12.1}$) and two major blast resistance genes (*Pi54* and *Pi1*) were introgressed into the genetic background of upland rice variety, Varalu. Developed two best improved lines of Varalu i.e., MSM-36 and MSM-60 possessing high yield under drought stress and blast resistance along with >96% recurrent parent genome recovery. Improved lines do not showed any yield penalty under irrigated condition. These lines can be effectively disseminated for cultivation by rice farmers in drought-prone environments of India. The MAS derived improved versions of Varalu expected to replace Varalu, to combat the yield loss due to reproductive stage drought and blast, so as to sustain the rice production

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IRC/TM-1/PP-65

INDUCED MUTAGENESIS, A SOURCE FOR VARIATIONS TO CREATE A NOVEL GENETIC RESOURCES FOR RICE IMPROVEMENT

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Rice (*Oryza sativa*) is one of the most important crops in the world. Mutations can be used as a tool to create genetic variability and for gene functional studies. Induced mutations are one of the best available options to create variation among the well adapted mega varieties. Samba Mahsuri (BPT 5204) is a popular, high yielding, rice variety possessing medium slender grain with acceptable cooking quality. Unfortunately it is highly susceptible to various biotic and abiotic stresses. To overcome the constraints of this variety the genetic variability enhancement of Samba Mashuri would be useful. Furthermore the excellent combining ability of this variety will help in transferring such traits into other varietal backgrounds. Considering the merits, Samba Mashuri was used to develop a comprehensive mutant population. In the present study from the huge EMS mutangenized population identifed the novel genetic sources for major biotic stresses (Yellow stem borer, Sheath blight and Bacterial leaf blight) and for key agro-morphological traits, physiological traits, complete panicle exsertion and yield. Some of these mutants were characterized and identified the mutated loci. The objective of the present work is to increase the extent of variation in the gene pool of rice and to identify the novel variants which can be used as donors in rice improvement programme.

METHODOLOGY:

A total of 10,500 Samba Mahsuri grains were mutagenized with chemical mutagen, EMS (Ethyl Methane Sulfonate) using 0.8% and 1.2% concentration. The mutagenized seeds were grown to raise the M_1 generation. The M_1 plants were protected from out crossing and individual M_1 plants were harvested to obtain the M_1 seeds.

Screening of 10,500 lines of M_2 was done for Sheath blight, Bacterial leaf blight and yellow stem borer in batch wise and for key agro-morphological traits, physiological traits and yield attributing traits.

Sheath blight artificial inoculation of the isolate was done in colonized typha stem bits and observations were recorded after 20 days of inoculation and scored as per IRRI-SES scale (Standard Evaluation System) (IRRI, 1996) (Bhaktavatsalam et al. 1978).

The mutagenized population was evaluated for bacterial blight (BB) under artificial conditions following the clip-inoculation method; the lesion length was recorded after 15 days of infection and scored according to SES scale, IRRI (2014).

Screening for Yellow Stem Borer (YSB) tolerance was done in a phased manner at both vegetative and reproductive phases by augmenting the natural pest infestation through artificial releases (Devasena et al. 2018).

Further M_2 lines were phenotyped for various morphological (Plant height, Pink apicules, Albino, Xantha and Coloration), agronomical (panicle types, complete panicle emergence, early flowering, grain types and high yield with high grain number), physiological (strong culm, different types of flag leaf, sterile plant, stay green and shattering) and better panicle exserion studies.

Genomic similarity of mutant in comparison with wildtype (BPT 5204) was carried out among the promising mutants with Samba Mahsuri using whole genome re-sequencing.

Mutated loci were identified by following the Mutmap technique (NGS based approach) using the F_2 population derived from the mutant X wildtype. QTLs were also identified by using population derived from the mutant X diverse parent.

RESULTS:

Upon screening for YSB tolerance a total of 170 M_2 mutants showed tolerance. Re-testing of these lines showed nine (M_7) stable tolerant mutants. The primary screening of sheath blight tolerance revealed 482 tolerant plants. Rescreening of these mutants was continued up to M_7 and identified thirteen sheath blight tolerance mutants. The screening of bacterial leaf blight showed 801 resistance plants in M_2 generation. Upon repetitive screening till M_7 showed thirteen resistant mutants for bacterial leaf blight (Figure 1).

Variations in various morphological traits were observed in total population. Among them, 43 mutants having tallness and 36 dwarf mutants were observed. Of the total population, 191 mutants showed variations in the physiological traits. Among them, 26 mutants strong culm were identified, 73 early maturing (108-136 days) mutants were observed. Interestingly, four stay green mutants in the M_2 generation were identified.

We also observed sterile plants in M_2 generation. Complete panicle emergence (CPE) and Elongated Upper Internode (EUI) are two major traits that were studied under the category of panicle emergence. In this category we identified 155 (M_2) CPE mutants and 27 EUI mutants. In the M_2 generation, a total of 532 mutants having yield attributing traits were also identified. Among these traits, 484 mutants are having more number of productive tillers and better grain filling (Figure 1).

Genomic similarity of 49 mutants was done using whole genome re-sequencing which revealed a similarity range of 99.91 to 99.99% in comparison to the wild type.

Mutmap analysis of complete panicle emergence mutant (CPE109) indicated the mutated region on chromosome 11 at 20.14 Mb - 20.19 Mb regions which was also matched with the QTL analysis.

To determine the mutated genomic region(s) for sheath blight tolerance in ShB-1, Mutmap analysis was performed and found mutated loci on chromosome 1 (40.1 Mb to 41.0 Mb). 33 SNPs were identified, of which only three were in exonic region.

To identify mutated loci for conferring the culm strength, MutMap analysis was performed in strong

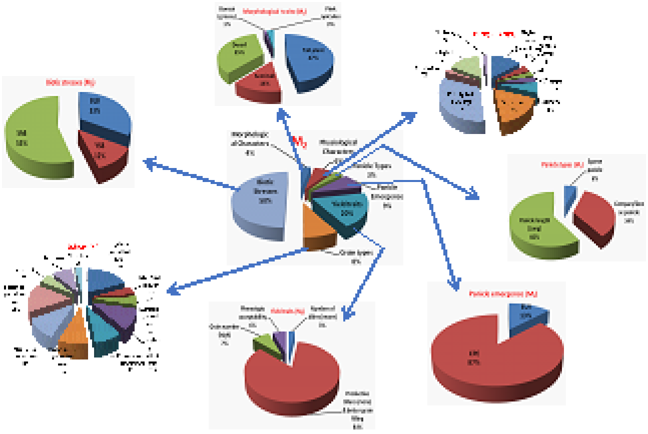

Figure 1: Distribution of mutants for various traits in M_2 generation

culm mutant (SC-11) and identified two peak regions on chromosome 5 (27.7Mb-29.2Mb) & chromosome 6 (6.2Mb-10.8Mb), the peak at chromosome 6 matched with the QTLs (qSC-2 & qSC3) identified using F_2 mapping population derived from SC-11 X TN1 (diverse parent).

CONCLUSION:

The lines showing enhanced tolerance to the challenging biotic stresses (YSB, ShB and BLB) as well as several economically important traits are unique genetic resources which can be utilized for the identification of novel genes/alleles for different traits. The mutant lines which have better agronomic features can be used as pre-breeding lines. The SNPs that are linked to the phenotype can be readily used in introgression programmes. Such studies will generate new knowledge and also have the potential for application in the crop improvement.

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IRC/TM-1/PP-66

PLANT GROWTH PROMOTION POTENTIAL OF ENDOPHYTIC ISOLATES ASSOCIATED WITH ETHNOMEDICINAL PLANTS OF MANIPUR FOR RICE GROWTH UNDER NETWORK CONDITIONS

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Agriculture in the 21st century warrants eco-friendly, sound and sustainable production of agricultural crops especially rice. Massive use of fertilizers, fungicides and other synthetic agrochemicals have resulted in increased fungicide resistance, environmental pollution, detrimental effects on beneficial non-target organisms and human beings. So, the use of bacterial inoculants as agricultural biofertilizers & biostimulants and biocontrol agents for major agricultural crops are increasingly preferred as better alternatives to anthropogenic agrochemicals. As Manipur falls in the **Indo-Burma Biodiversity Hotspot**, there is a great potential for exploring microbial biodiversity in her unique and underexplored biotopes.

MATERIALS AND METHODS

Sampling and Isolation of endophytic bacteria

Healthy rhizomes, stems, roots and leaves of the plants were collected and subjected to a five step surface sterilization procedure (Qin *et al.* 2009).

Biocontrol (antagonistic) assays of endophytic bacteria

The endophytic isolates were subjected to the Biocontrol Assays against indicator rice fungal pathogens namely *Curvularia oryzae*, *Rhizoctonia solani* , *Aspergillus niger, Bipolaris oryzae*, *Fusarium oxysporium* and *Pyricularia oryzae* (Dual culture method) (Hamdali *et al.* 2008*).*

in vitro tests for Plant Growth Promoting (PGP) traits

The bioactive endophytic isolates were further screened for plant growth promoting activities such as IAA production (Bano and Musarrat, 2003), Siderophore production (You et al., 2005, with some modifications), Ammonia production (Cappuccino and Sherman, 1992) and Phosphate solubilisation (Mehta and Nautiyal, 2001).

In vitro seed germination test

The bioactive strains which showed positive results in all the PGP traits tested were shortlisted for *in vitro* seed germination test (Vigor Index) on rice (Variety: ***Jatra***) seeds. The number of germinated seeds, root lengths and shoot lengths were noted and compared with the controls. 4 (four) replications were done per treatment and the experiments were repeated twice. Vigor index was calculated using the Baki and Anderson (1973) formula.

Growth promotion under net conditions

For the bioinoculant treated pots, 15 ml of the culture broth was spread by removing the upper layer of the soils (approx. 3 cm) surrounding the seeds. The pots were then covered with the same soils. 4 pots were kept for each treatment in a **randomized block design**. Parameters such as root and shoot lengths, fresh root and shoot weights, and dry root and shoot weights were measured (Tamreihao et al., 2016).

RESULTS AND DISCUSSION

16 (sixteen) ethnomedicinally important plants of Manipur namely *Scutellaria discolor, Curcuma caesia*, *Paris polyphylla*, *Centella asiatica*, *Alium odorum*, *Catharanthes roseus*, *Achryranthes*

aspera, Kaempferia rotunda, Celtis timorensis, Plectranthes ternifolius , Phlogocanthes jenkensii , Goniothalamus sesqeupedalis, Plantago asiatica , Oroxylum indicum , Eclipta alba and Tinospora cordifolia were sampled from various parts of the state based on their folk medicinal use and subjected to isolation procedures for endophytic bacteria.

198 (one hundred and nighty eight) endophytic bacteria were isolated and screened for biocontrol (antagonistic) against indicator rice fungal pathogens and plant growth promoting (PGP) traits such as IAA, Siderophore, and Ammonia production and Phosphate solubilisation. 21(Twenty one) isolates were found to have antifungal activity against one or more of the test organisms namely *Curvularia oryzae*, *Rhizoctonia solani* , *Aspergillus niger, Bipolaris oryzae*, *Fusarium oxysporium* and *Pyricularia oryzae*. 10 (ten) isolates namely CcRz1, CcRz21, CcRz6, CcRz9, VrS4, CtR2, PtS3, GsL7, AoS1 and CaS4 showed positive results for all PGP traits.

These 10 (ten) bioactive endophytic bacteria were shortlisted for *in vitro* seed germination test (Vigor Index) on rice (Variety: ***Jatra***) seeds. Rice seeds treated individually with the bioactive isolates, VrS4, CcRz1 and CtR2 showed higher vigor indices 251.75, 199.8 and 199.8 respectively and germination percentages 95, 90 and 90 respectively and exhibited enhanced growth of seedlings under gnotobiotic conditions compared to the control. The rice seeds treated with the isolates VrS4 and CtR2 showed the highest average fresh weight (0.564 g and 0.562 g respectively) and average dry weight (0.223 g each) of the rice seedlings.

The 7 (seven) best isolates showing the good vigor indices were further assayed for rice plant growth promotion under net house conditions. The rice plants treated with the endophytic isolates showed higher root and shoot lengths over the control, the highest readings of CcRz1 (15.5 cm and 64 cm), CtR2 (11.5 cm and 72 cm) and VrS4 (10.1 and 66 cm).

CONCLUSIONS

10 (ten) isolates (CcRz1, CcRz21, CcRz6, CcRz9, VrS4, CtR2, PtS3, GsL7, AoS1 and CaS4) showed positive results in all the PGP traits. The isolates VrS4, CcRz1 and CtR2 showed highest vigor indices. VrS4 treated seeds showed higher germination percentages, vigor indices and significant increases in root and shoot lengths over the control. Furthermore, the isolate CtR2 and VrS4 showed the maximum average fresh weight of rice seedlings and enhanced growth of rice seedlings under gnotobiotic conditions. The rice plants treated with these bioactive endophytic isolates showed higher root and shoot lengths over the control under net house conditions. VrS4 and CtR2 showed more potential as a plant growth promoter for rice seedlings. These two bioactive isolates will be assayed for rice growth under limited field trial conditions.

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IRC/TM-1/PP-67

GENOTYPE X ENVIRONMENT INTERACTION IN RICE UNDER COASTAL SALINE SOILS

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Rice is an important cereal crop in India. The productivity of rice is being affected by biotic and abiotic factors. Among the various abiotic factors, coastal salinity rice crop during different growth stages. The salinity at reproductive stage has adverse effect on spikelet fertility and thus limits grain yield (Matsushima *et al*., 1982). Hence, it is necessary to evolve high yielding salt tolerant rice varieties stable across coastal saline ecosystem. Stable genotypes help to achieve predictable performance through the wider adaptability of genotypes (Allard and Bradshaw, 1964). In the present study, an attempt was made to assess the GxE interaction of 16 rice genotypes and their 48 hybrids with one check under salt affected soils.

MATERIALS AND METHODS

The experiment was conducted at Coastal Soil salinity Research Station, Danti, Umarat and Samany N.A.U., Navsari, Gujarat during *kharif* 2014with ECe as 4.1, 4.3 and 4.0 dS/m, respectively during flowering stage. Three complete sets of 65 entries comprised of 48 F_1's, 4 females, 12 males were evaluated for their yield performance under saline soils. The experiment was laid out in a randomized block design replicated three times. The parents and F_1's were represented by a single row plot of 10 plants placed at 20 cm x 15 cm spacing. During the investigation grain yield plant^{-1} (g) alongwith yield contributing traits were studied. Statistical technique suggested by Eberhart and Russell (1966) has been employed to assess the stability. The stability parameters *viz*., mean performance (µ), regression coefficient (bi) and individual squared deviation from linear regression (S^2di) for parents as well as crosses were estimated to assess the stability over the environments. The S^2di values if significantly deviates from zero then the genotype is considered to be highly unstable.

RESULTS AND DISCUSSION:

The analysis of variance for phenotypic stability revealed mean squares due to genotypes as well as environments were highly significant when tested against pooled error as well as pooled deviation. The mean squares due to environments (linear) were highly significant against pooled error and G x E was found to be significant when tested against pooled error and pooled deviation.

G x E (linear) was found to be significant indicating differential performance of genotypes under diverse environments but with considerably varying norms, *i.e.*, the linear sensitivity of different genotypes is variable. The mean squares due to pooled deviations were significant indicating that performance of different genotypes fluctuated significantly from their respective linear path of response to environments. On comparison relative magnitude of G x E (linear) found to be high than linearity (non-linear) indicating that linear component contributed more towards the G x E interactions.

The population mean grain yield of 48 experimental crosses was 22.84 grams per plant; while the same for 16 parents including checks for this trait was 19.78 g plant^{-1}. Twenty nine crosses and seven parents displayed higher mean grain yield plant^{-1} than mean yield of respective groups (22.84 and 19.78 g)

Table 1.: Average stable crosses and parents for grain yield plant^{-1} (g) under salt affected soils

Genotypes	Grain yield plant^{-1} (g)		
	Mean	b_i	S^{2}di
GNR 3 x NVSR 6108	23.69	0.15	-0.60
NAUR 1 x CSR 27	28.70	0.18	-0.64
GAR 13 x Kala Rata	23.66	1.50	-0.98
GAR 13 x IR 76346-B-B-10-1-1-1	23.93	1.08	-0.67
Panvel 1 x NVSR 6108	26.02	0.74	-1.02
Panvel 1 x NVSR 6100	23.07	1.20	2.37
Panvel 1 x Kala Rata	25.13	1.30	-0.84
Panvel 1 x IR 76346-B-B-10-1-1-1	23.99	2.35	-0.82
Cross mean	22.84		
Panvel 1	22.36	0.94	-1.00
GNR 3	21.82	1.65	-0.68
CSR 27	21.41	-0.09	-0.97
IR 76346-B-B-10-1-1-1	20.94	0.09	0.28
Parental mean	19.78		

in respect of grain yield plant^{-1} hence considered as desirable for interpretation of stability parameters.

Group-I (High mean, bi = 1 (NS), S^{2}di = NS) : Average stability was observed for eight crosses and top three stable crosses with highest mean grain yield plant^{-1} were NAUR 1 x CSR 27, Panvel 1 x NVSR 6108 and Panvel 1 x Kala Rata. The parent Panvel 1, GNR 3, CSR 27 and IR 76346-B-B-10-1-1-1 exhibited average stability across the environments. .

Group-II (High mean, bi > 1, S^{2}di = NS) : Four crosses *viz*., Panvel 1 x Dandi, Panvel 1 x IR 71907-3R-2-1-2, NAUR 1 x Kalarata and GNR 3 x Kalarata and parent GAR 13 registered higher means coupled with bi greater than unity and non-significant deviation of S^{2}di from zero. Hence, possess below average stability indicating their suitability for cultivation under favorable environmental conditions only.

Group-III (High mean, bi < 1, S^{2}di = NS) : Five crosses *viz*., NAUR 1 x NVSR 6108, GAR 13 x NVSR 6108, Panvel 1 x CSR 27, NAUR 1 x IR 71895-3R-9-3-1 and GNR 3 x CSR 27 with one parent viz., NAUR 1 were observed to have regression coefficient (bi) below unity and linear regression (S^{2}di) nearly equal to zero and thus exhibits above average stability for cultivation in poor environments.

Group-IV (High or low mean, bi =1or >1 or < 1, S^{2}di = Significant) : Six genotypes recorded significant deviation from zero and were considered as unpredictable.

In general, the female and male parents behaved differently in different environments as observed by Bose *et al*. (2012). However, it was noticed that one of the best general combiner in this experiment, CSR 27 (male parent) found to be stable for grain yield plant^{-1}. This has increased its potential use towards high yielding in combination with quality grain and stable performance under salt stress conditions. Among four females, only two *viz*., Panvel 1 and GNR 3 were found to be stable for grain yield plant^{-1}.

CONCLUSION :

The parents Panvel 1, GNR 3, CSR 27 and IR 76346-B-B-10-1-1-1 could be better exploited to obtain stable recombinants for coastal saline soils. The recombinants of the top three stable cross combinations *viz*; NAUR 1 x CSR 27, Panvel 1 x NVSR 6108 and Panvel 1 x Kala Rata could be further investigated to obtain high yielding stable cultivars for salt affected soils.

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IRC/TM-1/PP-68

ENHANCEMENT OF SECONDARY BRANCHING: A MAJOR BOTTLENECK FOR GRAIN FILLING IN RECOMBINANT INBREED LINES (RIL) OF RICE

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Rice is the staple food for majority of the World's population and it is the only source of human calories intake in most of the developing and underdeveloped countries across the Globe. The introduction of dwarfing gene, release of IR-8 during 1960s and subsequent improvements of IR-8 parented semi-dwarf rice cultivars have been accounted for a quantum jump in rice production and ensured food security. However, rice production from these high yielding semi-dwarf cultivars has attained almost a plateau since last 2-3 decades and creating a major bottleneck to feed all the mouths in the present scenario of expanding population growth. In this context, rice breeders have targeted to increase grain number within the panicle to improve the yield potential of the crop. Increase in grain number within the panicle of modern super rice cultivars has caused the enhancement of secondary branching of the panicle to accommodate more numbers of grains leading to change of panicle architecture from loose to compact. Further, increase in grain number in the compact panicle cultivar did not improve the overall grain yield of the plant because of poor partitioning of biomass to all the grains due to strong competitions for resources and space, ultimately leading to the production of many barren or poorly filled grains on basal panicle branches, unsuitable for human consumption. Under the circumstances, Recombinant inbred lines (RIL) can provide a means of genetic variations for the study of variability in grain filling in rice. In the present work, two RIL rice lines contrast for their sterility percentage and variations in secondary branching like SR-159 (high sterile) and SR-157 (low sterile) have been used to analyse the mystery of differential grain filling and its consequent reduction in grain yield.

MATERIALS AND METHODS

Two Recombinant Inbreed Lines (RIL) rice genotypes such as SR-159 (high sterile) and SR-157 (low sterile) have been used in the present work during the wet season of 2017 under open field conditions at NRRI, Cuttack, Odisha, India to understand the morpho-physiological basis of differential grain filling in rice. All recommended agronomic practices were followed from seed germination to transplanting in the field and up to grain maturity. Mother tillers in different hill reaching anthesis at the same time in the filled were tagged and sampling was done at 5 days interval from anthesis to grain maturity stage. Apart from measuring the dry mass accumulation and analysis of soluble sugars and starch concentrations of the apical and basal grains at 5 days interval, other morphological parameters such as panicle length, filled and unfilled grain number, individual grain weight, grain density within the primary and secondary branches, primary and secondary branch density of the panicle and other biochemical parameters like soluble carbohydrates and starch concentrations at different spikelet positions within the panicle were also measured at grain maturity. Ethylene production from the grains of panicles at anthesis and 3 days post-anthesis was also measured in a Gas chromatograh equipped with a FID detector (Kariali and Mohapatra, 2007).

RESULTS

Results showed significant differences in secondary branch density, total length of secondary branches, filled and unfilled grain number, individual grain weight and % sterility, though the panicle length and number of primary branches are more or less similar. Large numbers of grains were accommodated in more numbers of secondary branches in high sterile genotype SR-159 compared to lesser secondary branching in low sterile SR-157. Apart from more secondary branching and total grain numbers, the high sterile genotype SR-159 also exhibited more number of unfilled grains and higher sterility percentage compared to SR-157. The difference in the apical and basal grain dry wt. was relatively lower in SR-157 compared to SR-159. High sterile SR-159 produced more ethylene than that of low sterile SR-157. The production of ethylene was quite higher in basal spikelets compared to apical ones in both the genotypes. Apical spikelets accumulated relatively lower amount of sugars than basal spikelets in both the rice genotypes. The difference in sugar accumulation between the apical and basal spikelets was quite higher in high sterile SR-159 compared to low sterile SR-157. Basal spikelets accumulated less amount of starch than apical spikelets in both the genotypes and starch accumulation was higher in the low sterile genotype SR-157 compared to high sterile SR-159.

DISCUSSION AND CONCLUSION

It has been shown that down regulation of genes encoding ethylene receptors and signal transducers (Sekhar et. al., 2015) and poor expression of ethylene precursor like S-adenosyl methionine and proteins related to endosperm cell division (Das, et.al., 2016) are crucial for limiting grain yield in rice. High ethylene production also slackens grain growth in rice (Panda et. al., 2009). The sterile genotype SR-159 produced more ethylene compared to the fertile SR-157. Accumulation of sugars was more in the basal spikelets compared to apical ones and more in SR-159 compared to SR-157 which might be indicative of unused assimilates in sterile genotype and in the basal grains which in turn might be mediated by ethylene inhibition of starch biosynthesis in developing grains. Though there is a good correlation between secondary branching and grain sterility in rice panicle, literature citing enhancement of secondary branching is the cause of grain sterility are scant and more investigation is required in this regard. However, it may be concluded from the present work that RIL rice lines exhibiting poor grain filling properties in high sterile lines and also at basal positions might be due to more secondary branching attributable to poor conversion of soluble sugars into starch, mediated by the action of ethylene. Further, rice genotypes with more secondary branching, having proper grain filling especially in the basal part of secondary branches of the panicle may be a desirable trait to obtain future elite cultivars for improved grain yield.

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HETEROSIS STUDIES FOR YIELD AND QUALITY COMPONENT TRAITS IN AROMATIC RICE HYBRIDS

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Aromatic rices are very popular in South Asia and recently have gained wider acceptance in USA, Europe and China. Aromatic rice occupies a prime position in Indian culture not only because of their high quality but also of its auspicious nature. The traditional aromatic cultivars are tall in stature (about 160 cm or more), poor grain yielders and lodge under high doses of nitrogenous fertilizers but were famous for aroma and cooking qualities (Siddiq *et. al.*, 1997). The success of hybrid rice programme depends upon the magnitude of heterosis, which also helps in the identification of potential cross combinations to be used in the conventional breeding programme to create wide array of variability in the segregating generations (Krishna Veni and Shobha Rani, 2003). In the present study the main objective was to assess the magnitude of heterosis in the aromatic rice hybrids for fourteen yield and quality component traits.

METHODOLOGY

Four aromatic rice cultivars were selected as females and single crosses were made randomly with twelve non-aromatic, dwarf high yielding rice cultivars (male lines) to derive 19 hybrids at Agricultural Research Farm, Banarus Hindu University, Varanasi during Kharif, 2005. Among 4 female parents, 2 long grained aromatic rice (Pusa Basmati-1 and Taraori Basmati) cultivars were crossed with commercial high yielding rice varieties, the other two aromatic varieties (GR-32 and Kalanamak), which are short grained and susceptible to lodging were crossed with dwarf disease resistant high yielding lines selected from IRRI material. Experimental material for the study comprised of 37 rice genotypes (4 female lines, 12 male lines and 19 hybrids along with two checks HUBR 2-1 and Taraori Basmati). Seeds of hybrids and their parents were germinated in petri plates, when satisfactory germination was observed on the 4th and 5th day of soaking, the seedlings were transferred to small raised beds, covered with a layer of sand and sufficient care was taken to avoid water logging and complete drying up of the nursery beds. All the recommended practices were followed to raise and maintain the healthy crop in the nursery. Healthy and vigorous 25 days old seedlings were transplanted in to the main field with 20 x 15 cm spacing for heterosis studies. These genotypes were evaluated in a randomized block design with three replications. Each entry consisted of two rows of 5 m length. Observations were recorded for days to 50 % flowering, plant height (cm), ear bearing tillers per plant, panicle length (cm), number of grains per panicle, spikelet fertility (%) , 1000 - grain weight (g), grain yield per plant (g), milling recovery (%), head rice recovery (%), kernel length (mm), kernel breadth (mm), kernel L/B ratio and kernel length after cooking (mm) by following standard procedures. The magnitude of heterosis in hybrids was estimated in relation to better parent and the checks (Taraori Basmati and HUBR 2-1) as percent increase or decrease of hybrid over better parent (Heterobeltiosis) and the checks (standard heterosis)

RESULTS

The analysis of variance for 37 rice genotypes (4 females, 12 males, 19 hybrids and 2 check varieties) with regards to yield and quality component traits revealed that the existence of significant differences among the genotypes studied for all the traits indicating that good amount of variation for effective selection. Heterobeltiosis, standard heterosis and best heterotic crosses for yield and quality component traits in rice genotypes was given in Table 1. Three hybrids Pusa Basmati x Jaya, Taraori Basmati x Malviya 36 and GR 32 x IR 73004 exhibited significant negative (desirable) heterobeltiosis and standard heterosis for days to 50 % flowering, indicating early flowering in these hybrids than the parents and checks. Almost all the hybrids exhibited tallness as compared to their parents, so the negative heterosis, which is desired for plant height was not observed in any of the hybrids with regards to heterobeltiosis. The hybrids in general recorded high grain yields with increased performance in the yield contributing traits *viz.*, more ear bearing tillers, greater panicle length, increased number of grains per panicle and high spikelet fertility per cent as compared to parents. Maximum number of superior hybrids was observed in the crosses involving Pusa Basmati-1 as female parent followed by Taraori Basmati. Among the females Pusa Basmati-1 recorded maximum grain yield per plant with this best parent, the best hybrid (Pusa Basmati-1 x BPT 5204) was observed. Among the yield contributing traits the maximum expression of significant and desirable heterobeltiosis and standard heterosis was observed for grain yield per plant followed by ear bearing tillers, number of grains per panicle and spikelet fertility. Most of the hybrids in the present study exhibited significant and positive standard heterosis and heterobeltiosis for milling per cent and head rice recovery. Among grain quality characteristics of hybrids, the milling per cent and head rice recovery were observed to be more in hybrids as compared to parents whereas for other quality traits the performance was in negative direction. A perusal of the results of the present investigation revealed the production of superior hybrids from the crosses involving tall late duration aromatic females with semi dwarf high yielding non-

Table 1 Heterosis and best heterotic crosses for yield and quality component traits in aromatic rice genotypes

Character	Heterosis (%)			Best hybrids			
	HB	SH(1)	SH(2)	Based on mean performance	Based on BP heterosis	Based on SC (I) heterosis	Based on SC (II) heterosis
Days to 50% flowering	-4.77 to 6.00	1.91 to 17.64	-12.10 to 5.87	Pusa Basmati-1 x Jaya	Pusa Basmati-1 x Jaya	Pusa Basmati-1 x Jaya	Pusa Basmati-1 x Jaya
Plant height (cm)	1.79 to 45.21	-19.32 to 31.76	-32.91 to 24.00	Taraori Basmati x BPT 5204	Pusa Basmati-1 x Malviya 36	Taraori Basmati x BPT 5204	Taraori Basmati x BPT 5204
Ear bearing tillers per plant	-11.11 to 50.61	-33.80 to 37.55	-17.46 to 45.18	Taraori Basmati x BPT 5204	Taraori Basmati x WGL 23064	Taraori Basmati x BPT 5204	Taraori Basmati x BPT 5204
Panicle length (cm)	-8.71 to 11.17	-16.62 to 9.58	-10.21 to 14.55	Pusa Basmati-1 x Malviya 36	Taraori Basmati x Jaya	Pusa Basmati-1 x Malviya 36	Pusa Basmati-1 x Malviya 36
Number of grains per panicle	-40.43 to 38.31	-45.85 to 37.45	32.49 to 71.05	Pusa Basmati-1 x WGL 23064	Pusa Basmati-1 x Jaya	Pusa Basmati-1 x WGL 23064	Pusa Basmati-1 x WGL 23064
Spikelet fertility (%)	-34.77 to 19.16	-37.34 to 18.60	-34.14 to 20.50	Pusa Basmati-1 x Malviya 36	Pusa Basmati-1 x Jaya	Pusa Basmati-1 x Malviya 36	Pusa Basmati-1 x Malviya 36
1000-Grain weight (g)	-56.82 to 21.68	-74.87 to 8.85	-81.81 to 5.23	Kalanamak x TOX85C	Taraori Basmati x Malviya 36	Kalanamak x TOX85C	Kalanamak x TOX85C
Grain yield plant^{-1} (g)	-82.56 to 52.06	-26.31 to 55.64	-24.42 to 56.30	Pusa Basmati-1 x BPT 5204	Pusa Basmati-1 x BPT 5204	Pusa Basmati-1 x BPT 5204	Pusa Basmati-1 x BPT 5204
Milling recovery (%)	-2.25 to 11.36	-5.98 to 7.25	2.15 to 14.37	Pusa Basmati-1 x BPT 5204	Pusa Basmati-1 x WGL 23064	Pusa Basmati-1 x BPT 5204	Pusa Basmati-1 x BPT 5204
Head rice recovery (%)	-1.85 to 12.56	0.12 to 15.21	18.23 to 30.58	Pusa Basmati-1 x BPT 5204	Pusa Basmati-1 x BPT 5204	Pusa Basmati-1 x BPT 5204	Pusa Basmati-1 x BPT 5204
Kernel length (mm)	-44.53 to -1.94	-81.95 to 1.53	-103.60 to -10.18	Pusa Basmati-1 x Malviya 36	Taraori Basmati x Malviya 36	Pusa Basmati-1 x Malviya 36	Pusa Basmati-1 x Malviya 36
Kernel breadth (mm)	1.00 -to 32.51	-13.66 to 19.02	-5.59 to 24.77	Pusa Basmati-1 x BPT 5204	Taraori Basmati x IET 17298	Pusa Basmati-1 x BPT 5204	Pusa Basmati-1 x BPT 5204
Kernel L/B ratio	-68.46 to -7.63	-97.93 to 5.65	-139.69 to -14.25	Pusa Basmati-1 x Malviya 36	Kalanamak x U20	Pusa Basmati-1 x Malviya 36	Pusa Basmati-1 x Malviya 36
Kernel length after cooking (mm)	-47.55 to 6.68	-65.43 to 3.08	-63.88 to -3.25	Pusa Basmati-1 x Malviya 36	GR 32 x YN 1850	Pusa Basmati-1 x Malviya 36	Pusa Basmati-1 x Malviya 36

aromatic males. The hybrids Pusa Basmati-1 x BPT 5204 (34.63 g), Pusa Basmati-1 x Malviya 36 (31.21 g), Taraori Basmati x Jaya (30.76 g) and Pusa Basmati-1 x Swarna (30.16 g) recorded higher per plant yields with increased performance in yield attributing traits.

CONCLUSIONS

Out of the nineteen aromatic rice hybrids studied, four hybrids Pusa Basmati-1 x Malviya 36, Pusa Basmati-1 x BPT 5204, Taraori Basmati x Jaya and Pusa Basmati-1 x Swarna were identified promising for their high mean performance and high magnitude of heterosis for yield and quality component traits. These hybrids could be effectively utilized in the conventional breeding programme, which would be helpful to develop high yielding varieties with better grain quality.

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IRC/TM-1/PP-70

GENETIC STUDIES IN RICE (*ORYZA SATIVA* L.) MAPPING POPULATION FOR HIGH GRAIN ZINC CONTENT

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Rice is the source of energy for majority of global population. Rice grain being the poor the source of zinc and iron content in its polished form, resulted in malnutrition at aggravated level (Pradhan *et al*., 2020). Zinc deficiency causes diarrhea and respiratory diseases and is associated with poor growth, loss of appetite, skin lesions, impaired taste acuity, delayed wound healing, impaired immune response etc (Rao *et al*, 2020). Increasing grain iron and zinc content in rice through breeding efforts is cheaper and easiest option to lessen malnutrition in developing country (Pradhan *et al*., 2020). QTL mapping for identification of genomic regions responsible for high grain zinc content is one of the prime breeding effort in this direction. F_2 mapping population is important for preliminary screening genomic loci for studying any new trait. Improvement in grain zinc content can impact positively on large section of population dependent on rice.

So present study was undertaken to study with following objective

1. To study variability parameters in given mapping population.
2. To study different genetic parameters in given mapping population

METHODOLOGY :

F_2 Mapping population (size 312) for high grain zinc content was developed by advancing seeds obtained from individual true F_1 hybrid of cross between Rajendrakasturi and URG-30 (high zinc donar). F_2 population was raised in Kharif 2018 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi with spacing of 40×30 cm row to row and plant to plant (double than normal recommended spacing). Crop was raised by following recommended package of practices of given area and all morphological observations were recorded trait wise for yield relate and grain quality traits.. Individual F_2 plant was harvested separately and grains were analyzed for grain zinc content by XRF machine facility available at Harvest Plus lab, ICRISAT, Hyderabad. Data was subjected to analysis, variability and different genetic parameters were calculated using Windostat 9.3.

RESULTS

Wide spectrum of genetic variability is essential for the success of every breeding program. F_2 population offers good opportunity for studying parameters of variability, such studies are equally promising as F_2 population contain wide range of variability resulting out of segregation and recombination. In present evaluation of mapping population derived from single true F_1 plant represented higher phenotypic variability for various yield and grain quality traits. By cluster analysis using Tocher's method, 312 F_2 individuals were divided into 8 clusters. Intra cluster value ranges from 0.0 to 3546.12. Higher intra cluster value was found for cluster 4 indicted diversity among the individuals under cluster 4. Inter cluster distance ranges from 3426.97 (between cluster 1 and 7) to 78025.52 (between cluster 6 and 4). Cluster mean ranges from 22 for cluster 7 to 49 for cluster 5 for grain yield per plant, from 22 (cluster 7) to 27.04 (cluster4) for grain zinc content. Out of 15 characters studied, relative contribution of total grains per panicle was higher to total genetic divergence (51.6%) followed by fertile grains per panicle (26.83%) and plant height (14.73%). Least contributing traits for genetic divergence were panicle length and grain iron content (0.01% each).

Estimates of coefficients of variability, heritability and genetic advance were computed for given F_2 mapping population revealed higher value of phenotypic coefficient of variation than genotypic coefficient of variation for all the traits studied. Higher GVC and PCV were recorded for number of total tillers per plant, effective tillers per plant, grains per panicle, fertile grains per panicle and grain yield per plant while low GCV value coupled with low PCV value were recorded for days to flowering, moderate GCV and PCV values observed for grain zinc and iron content. Heritability and genetic advance estimates as percent of mean were higher for grain yield per plant, fertile grains per panicle, grains per panicle, effective tillers per plant, tillers per plant, 1000 grain weight, plant height, grain iron and zinc content and kernel length to breadth ratio, lowest estimate of genetic advance as percent of mean was reported for kernel breadth.

CONCLUSION

Findings from present study provides way forward for more conclusive studies in mapping population for cluster analysis based on genotypic data obtained from molecular marker analysis. Outcomes of QTL mapping studies supported by the findings of genetic parameters and variability studies increases authenticity and applicability of the results in breeding programme.

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IRC/TM-1/PP-71

SCREENING OF RICE GERMPLASM FOR RESPONSE TO LOW LIGHT INTENSITY DURING KHARIF SEASON IN KONKAN

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Rice (*Oryza sativa L.*) is most important staple food India has the largest rice growing area. India ranks second in rice production followed by China. In India, it is cultivated on an area of 44.1 million hectares which is maximum among all rice growing countries , annual production of about 107.40 million tonnes of rice during 2015 (Anonymous -2015). The total area under rice in the state is 15.57 lakh ha with an annual rice production of 36.54 (52.95 rough rice) lakh tones and the average productivity is 2.35 (3.40 rough rice) t/ha. (Maharashtra State Statistics Dept. Pune (2015-16) Konkan region is major rice producing area of Maharashtra. Nearly 3.69 lakh hectare area of Konkan is under rice crop with production of 10.83 lakh tones .The average productivity of Konkan region is 2.93 tons per hectare (Maharashtra State Statistics Dept. Pune (2015-16). Among these stresses, low light stress during Kharif season in Konkan region is emerging as one of the important biotic stresses for rice crop mainly grown in kharif. This problem of low light stress could aggravate in near future as total rainfall and rainy days are increasing frequently in recent years. Hence, exploring the available inherited potential in different popular varieties and to identify the suitable rice varieties for low light stress was a major aim of this study.

OBJECTIVES

1) To screen the rice varieties for the inherited potential to sustain yield under low light stress.

2) To identify the low light stress resilient rice varieties suitable for growing under Kharif seasons of konkan.

METHODOLOGY

The experiment was conducted during Kharif 2012, 2013 and 2015 with 50 rice Varieties released by four Agril. Universities of Maharashtra. The experiment was laid randomized block design 1.5m x 0.60m plot size with 20cm x 15cm in two replications under shade net and without shade net condition.The plots were artificially shaded by using 50 percent shade net, such 50-60 percent of natural light was only received by the crop canapy. Fourty five plants were transplanted of each varieties in shade net and without shade net condition. The chlorophyll content of leaves was calculated by using formula given by Arnon (1949).The static statistical analysis of trial was carried out according to Panse and Sukhatme (1967).

RESULTS

There was less reduction in yield in rice variety Karjat-7(2.68%),followed by Karjat-3(6.32%), Palghar -2 (7.95%), Karjat -2 (9.31%), Karjat -8 (10.09%), Palghar – 1 (10.29 %), Karjat – 6 (10.5 %) under shade net than control (without shade net). There was higher reduction in yield of rice variety Phule Radha (37.38 %), SYE – 1 (35.01 %), Ambika

Table no : 1 Average light intensity during crop duration.

Time	Under Shade Net (50 %) (LUX)	Without Shade Net (Control)
9.00 am	8766	19952
12.00 pm	14127	30553
3.00 pm	9201	20705

Table 2. pooled data of (gm/plant) grain yield resilient varieties.

Grain yield (gm/plant)	1st year(kharif-2012)		2nd year(kharif -2013)		3rd year(kharif -2015)		Pooled	
	WS	US	WS	US	WS	US	WS	US
Karjat-7	20.13	19.37	19.2	19.02	17.38	16.8	18.90	18.40
Karjat-3	17.35	14.8	18.25	17.95	15.35	14.95	16.98	15.90
Palghar-2	15.07	13.64	15.60	13.57	14.07	13.88	14.91	13.70
Karjat-2	17.51	13.54	13.65	16.36	15.75	16.72	15.09	9.31
Karjat-8	13.39	11.28	15.07	13.88	15.39	14.37	14.62	13.18
Palghar-1	13.19	10.31	13.99	13.88	14.19	13.02	13.79	12.40
Karjat-6	12.31	9.64	14.61	12.37	13.31	11.5	13.41	11.17

Table no.3 Resilient and non resilient varieties to grain yield under low light intensity.

Low light stress resilient varieties to Grain Yield	Low light stress non resilient varieties to Grain Yield
Karjat-7 (2.68%)	Phule Radha (37.38%)
Karjat-3 (6.32%)	SYE-1 (35.01%)
Palghar-2 (7.95%)	Ambika (33.79%)
Karjat-2 (9.31%)	Phule Samrudhi (32.79%)
Karjat-8 (10.09%)	SYE-75 (31.77%)
Palghar-1 (10.29%)	Parag (31.76%)
Karjat-6 (10.5%)	Pawana (31.19%)

(33.79 %) under shade net than control (without shade net). The 50 % flowering and maturity was delayed by 2-5 days under shade than control in above varieties. The total Chlorophyll and Spikelet fertility was increased under shade net than control (without shade net).

CONCLUSION :

Amongst 50 varieties Karjat-7, Karjat-3, Palghar-2, Karjat-2, Karjat-8, Palghar-1 and Karjat-6 developed by Dr.Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli found to be resilient rice varieties for giving stable yield under low light stress conditions of Kharif season in Konkan. while Phule Radha, SYE-1, Ambika, Phule Samrudhi, SYE-75, Parag and Pawana found to be highly sensitive rice varieties as their growth and yield was highly reduced under low light stress conditions.

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IRC/TM-1/PP-72

EVALUATION OF SENSORY AND PHYSICO-CHEMICAL PROPERTIES OF SOME QUALITY RICE VARIETIES

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Rice (*Oryza sativa* L.) a premium staple food for the majority of people around the world. The grain is usually processed as brown rice (dehusked), polished rice (milled) and parboiled polished rice. In recent days, pigmented rice varieties (black & red) are being appreciated due to their better nutritional quality as compared to white rice. Pigmented rice are such varieties which have large amount of anthocyanin pigment that are deposited into the rice bran to form it's black, brown and red colours. Nine rice cultivars (black, red and white) namely (i) Manipuri Black, Chakhao, Mamihunger (black), (ii) Balam, Annapurna (red) (iii) Naveen, CR Dhan310, Govindbhog & Swarna (white) were taken for this study. The objective of this study was to analyze the raw and parboiled rice grain with respect to different parameters like physico-chemical properties, colour, texture, viscosity and antioxidant properties, which are directly related to human preference as well as health.

METHODOLOGY

Physico-chemical properties of raw grains include hulling, milling and head rice recovery percentage. It also includes grain amylose content and different cooking parameters like elongation ratio, alkali spreading value, kernel length after cooking, gel consistency, volume expansion ratio etc (Pal et al,2019). The colour parameters of the grain were determined by CIE colour scales L*, a* and b* using Hunter Lab digital colorimeter (Model: ColourFlex EZ , Hunter Associates Laboratory, Reston, VA). The L* indicates the degree of lightness or darkness of the sample extended from 0 (black) to 100 (white), a* indicates degree of redness (+ a) to greenness (- a) whereas b* indicates the degree of yellowness (+ b) to blueness (- b), respectively (Pal et al.,2019). Hardness of grains was done using texture analyzer

Table1. Sensory and antioxidant parameters of raw and parboiled pigmented and non-pigmented rice.

Sl.	Parameters	Pigmented rice			Non-pigmented rice		
Colour parameters of grain		Raw	Parboiled	% change due to parboiling	Raw	Parboiled	% change due to parboiling
1	L*(Lightness)	23.57 to 36.3	22.2 to 31.8	-(0.05 to 0.12)	57.01 to 71.5	53.11 to 55.87	-(0.06 to 21.8)
2	a*(Red to green)	4.8 to 14.45	3.13 to 9.49	-34	2.48 to 5.83	6.38 to 7.38	+(26 to 157)
3	b*(Yellow to blue)	5.15 to 23.34	3.95 to 12.82	-(23 to 45)	7.59 to 22.31	24.13 to 26.97	+(20 to 217)
Viscosity of rice flour							
4	Peak viscosity(cP)	808 to 2132	230-2154	0.01 to - 71	1876 to 2951	358 to 1047	-(64 to 80)
5	Final viscosity(cP)	734 to 3443	412 to 2839	-(17.5 to 44.0)	2375 to 4680	815 to 1776	-(62 to 66)
Texture of rice grain							
6	Hardness (g force)	6274 to 15933	37181 to 46760	+(167 to 604)	7299 to 14133	41766 to 48259	+(217 to 509)
7	Phenolics (mg CE/g DW)	1.97 to 4.26	1.27 to 1.93	-(35 to 54)	1.22 to 1.44	1.28 to1.35	NS
8	Flavonoids(mg CE/g DW)	0.59-1.42	0.54 to1.38	-(10 to 15)	0.47 -0.63	0.45 to0.56	NS

* (+) Increase (-) Decrease of values; (NS) Non-significant

Fig1. Unmilled rice of different pigmented and non-pigmented rice cultivars. AN-Annapurna, GB-Gobindabhog, MH-Mamihunger, BA- Balam, CRD310- CR Dhan310, CH-Chakhao, SW-Swarna, MB- Manipuri Black, NA- Naveen.

model TA.XT plus (Stable Micro Systems Ltd, Surrey, UK) as per method of Pal et al.,2019. This measurement was performed in three replications by using cylindrical probe (p75) with diameter of 10 cm and the single sample was placed on a metal plate for each test. Viscosity of rice sample was accomplished by Rapid Visco Analyzer (Model- RVA4800; Perten Instruments) taking 4.5 to 5 g rice flour depending upon their moisture content. Analysis of antioxidant compounds like total phenolics and flavonoids content was done according to Eberhardt et al. (2000).

RESULT

Significant difference in the physio-chemical & cooking quality of these rice cultivars ($p- <0.0001$) were observed. According to the Hunter colorimeter analysis, the L* value (whiteness to darkness) was highest in Naveen (parboiled) and CR Dhan 310 (Raw). Highest a* value (redness to greenness) was obtained from Balam (parboiled) and Mamihunger (Raw).The b* value (yellowness to blueness) was recorded highest in Swarna (parboiled) and Manipuri Black (raw). The color changes indicate that some components move during soaking from the inner layers to the surface, while others, specially bran compounds, move in the direction the endosperm. Amongst different pasting properties accomplished by Rapid Visco Analyzer, the highest final viscosity of parboiled brown rice flour was observed in Balam followed by Manipuri black and Chakhao but lowest was obtained from Annapurna whereas the peak viscosity was highest in Chakhao and Balam. In case of grain hardness parameter, measured by Texture Analyzer, the raw brown rice has lower values than the parboiled rice due to solidification of starch. In case of raw rice, the highest hardness was found in the red rice variety Balam followed by Swarna whereas Manipuri Black rice possessed lowest. But in case of parboiled rice CR Dhan 310 ranked first and lowest was obtained in Chakhao. The reduction of antioxidant capacity along with total phenolic and flavonoid content was observed in parboiled brown rice as compared to raw rice.

CONCLUSION

Phenolics and flavonoids content reduced due to parboiling whereas grain hardness increased due to parboiling. Lightness (L*value) reduced due to parboiling. Peak and final viscosity are generally lower in parboiled rice as compared to raw rice. Raw rice of CR Dhan 310 showed maximum viscosity value. Amylose content of pigmented rice is generally low as compared to white rice.

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IRC/TM-1/PP-73

ROLE OF SEDOHEPTULOSE-1, 7 BISPHOSPHATASE IN CONTRIBUTING LOW LIGHT TOLERANCE OF RICE (*Oryza sativa* L)

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Rice grain yield is significantly reduced during wet season (July-October), averaging around 2.1 t ha-^{1} in India due to the overcast skies that causes a low light (LL) stress (Panda et al. 2019). Cloudy weather during the grain-filling stage impairs grain yield and quality in rice. It affects the formation of grain by affecting photosynthesis, activities of antioxidant enzymes and other key enzymes involved in starch biosynthesis in rice grains, along with the translocations of photo-assimilates and nitrogen. This could be primarily attributed by the reduction in CO_2 assimilating potency of plants that acts as a fundamental process behind regulating the yield capacity and chiefly depends on light. The entire photosynthetic apparatus reorients and adapts to LL stress by undergoing several alterations in Calvin-Benson cycle enzymes and proteins and pigments. Therefore, identification of rice genotypes having better LL use efficiency as reflected in the minimum reduction in photosynthesis and grain yield during the WS has been a great challenge for the rice. Consequently, it is essential to maintain a balance between their participation in the process of carbohydrate biosynthesis and RuBP generation. To achieve this, the catalytic activity of certain enzymes like seudoheptulose-1,7-bisphosphatase need to be strictly regulated. This is achieved by the redox potential generated through the ferredoxin/thioredoxin system, which modulates the activity of SBPase in response to light or dark conditions. So far, the activity and expression of SBPase to track low light tolerance propensity of rice are not employed. We, therefore, studied SBPase activity and expression in low light tolerant and susceptible rice genotypes, with emphasis on its effect on the net photosynthetic rate, grain yield and other yield related traits under low light and normal light conditions.

OBJECTIVE:

Role of sedoheptulose-1, 7 bisphosphatase in low light tolerance of rice (*Oryza sativa* L)

METHODOLOGY:

Field experiments were conducted in the experimental plots of ICAR-National Rice Research Institute (NRRI) Cuttack, Odisha, India during the wet seasons (WS) of 2017 and 2018. Two tolerant cultivars, Purnendu and Swarnaprbha, one moderately susceptible cultivar, Sasarang and one susceptible cultivar, IR8 were used for study of expression and activity of SBPase and its overall impact on the net photosynthetic rate, grain yield and related traits. The net photosynthetic rate (P_n), stomatal conductance (g_s), rate of transpiration (T_n) and internal carbon dioxide to assimilated carbon dioxide ratio (C_i/C_a) of the flag leaf during 50% flowering were determined using a LI-6400XT portable photosynthesis system (LI-COR, Inc., USA). Activity of SBPase was determined using the coupled assay method. Total RNA was extracted from the flag leaf at 50% flowering stage using RNEasy Plant Mini Kit(Qiagen, USA) following the manufacturer's protocol. Four genotypes under study were evaluated for grain yield and related traits under normal light and low light conditions of WS 2017 and WS 2018 following randomized complete block design (RCBD) with three replications of each. Five hills were randomly selected from the middle of each plot and data for 6 traits, tiller/plant, panicle/plant, fertility%, 1000-grain weight, biomass/plant and grain yield/plant traits were recorded.

RESULTS :

Net assimilation rate (NAR), stomatal conductance (SC) and transpiration rate (TR) ($P<0.05$) were significantly decreased, whereas the ratio of internal CO_2 to ambient CO_2 (Ci/Ca) was significantly increased ($P<0.05$) for all cultivars under LL stress in comparison to NL condition. Tolerant cultivars, Purnendu and Swarnaprbha showed lesser decrease in the net assimilation rate (NAR), stomatal conductance (SC) and transpiration rate (TR) while a lesser increase in Ci/Ca ratio was observed as compared to moderately susceptible cultivar, Sasarang and susceptible cultivar, IR8 under low light stress. SBPase is the principal enzyme for RuBP regeneration during the Calvin cycle. We measured its activity in flag leaf Purnendu, Swarnaprahbha, Sasarang and IR8 under both NL and LL conditions. The SBPase activity was reduced significantly in all the four genotypes under LL stress as compared to NL during the WSs of 2017 and 2018 . In Purnendu and Swarnaprbha, SBPase activity (U/mg Protein) was constantly increased up to the 6th hour and then decreased after the 6th hour of incubation both under LL and NL. In contrast to this, the SBPase activity in Sasarang and IR8 was increased up to 4 hrs of incubation and then drastically reduced ($P<0.05$). However, SBPase activity was maintained significantly at higher level under NL as compared to LL condition in all the genotypes. Lower reduction in the SBPase activity under LL in comparison to NL in Purnendu and Swarnaparabha was observed. Significantly higher reduction was found in Sasarang and IR8 under low light as compared to normal light. There was an increase in enzymatic activity both under NL and LL conditions after 4rth hour of incubation in tolerant cultivars Purnendu and Swarnaprbha. In contrast to this, the enzyme activity was drastically reduced after the 4rth hour, both under LL conditions in Sasarang and IR8 as compared to LN condition. To further check if SBPase activity is influenced by LL stress, we investigated the expression pattern of *SBPase* transcript in rice plants using quantitative real-time PCR analysis. The data suggested that the primary process of biosynthesis of *SBPase* protein was optimum during 50% flowering, when the net photosynthetic rate is expected to be high. LL stress reduced the expression of the SBPase in all genotypes as compared to NL.

CONCLUSION:

The study clearly indicated that by tracking the expression and activity of SBPase, we can screen for the low light tolerant rice genotypes. It is, therefore, could be used as a marker enzyme for the screening process. However, it is not clear how exactly the expression and activity of SBPase is maintained under low light in tolerant genotypes and what is the exact physiological basis for the regulation of SBPase. Since photosynthesis is highly sensitive to the available light intensity, we proposed that SBPase could enhance tolerance to low light in rice the plants by precisely maintaining a delicate balance between its expression and activity by efficiently utilizing the available photons. The enhanced tolerance to low light stress could be due to over expression of SBPase *in vivo*. A further study of other light regulated Calvin cycle genes and their interaction with SBPase could provide information about the role of other enzymes for a better understanding of this complex process.

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IRC/TM-1/PP-74

GENOMICS ASSISTED BREEDING FOR ENHANCING DURABILITY OF RESISTANCE AGAINST RICE SHEATH BLIGHT UTILIZING WILD *ORYZA* SPECIES

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Sheath blight (SB) is one of the most serious diseases of rice (*Oryza sativa L.*) worldwide caused by a soil-borne fungus *Rhizoctonia solani Kühn* (R. solani), which poses a great threat to the rice grain yield and quality. *R. solani* is a soil-borne hemibiotrophic pathogen (Kouzai et al. 2018) that survives as sclerotia or mycelia in the debris of host plants during its necrotrophic phase. It causes severe losses in grain quality and yield in many rice-growing countries in both temperate and tropical climates. Breeding for sheath blight resistance is an economical and effective strategy for controlling diseases as compared to chemical control. Wild species germplasm of rice is an important resource for the enhancement of modern rice cultivars in terms of providing tolerance/resistance against various abiotic and biotic stresses (Khush et al., 1990). In the present study, nearly 500 accessions including wild *Oryza* species *Oryza nivara* and *Oryza rufipogon* was screened against sheath blight disease under artificial inoculation with *Rhizoctonia solani* and mapping studies were carried out.

METHOLODGY

***Plant materials* and inoculation with *R. solani* :** The plant materials consisted of 500 accessions of *Oryza nivara* and *Oryza rufipogon* were originally procured from International Rice Research Institute (IRRI), Manila, Philippines and National Rice Research Institute (NRRI), Cuttack, India. Standard protocol was used for isolation of *Rhizoctonia solani* from the susceptible cultivar PR121 showing the sheath blight symptoms. The maize meal sand (1:3) medium method was used for inoculation. Disease assessment was made 14 days after inoculation under field conditions. Ten plants from each accession in two replications were screened every year. Relative lesion height (RLH) was calculated using the formula given by Sharma *et al.*, 1990. We also genotyped 400 accessions of *Oryza rufipogon* using genotyping by sequencing and association mapping was performed.

RESULTS

Approximately, 100 accessions of *O. nivara* were screened for nearly five years 2016 to 2020. Twelve accessions showed constant moderate reactions to the sheath blight disease (Aggrawal *et al.*, 2019). The *O. nivara accession* IRGC81941A showed the maximum potential against sheath blight due to a least relative lesion height of 22.80% and was crossed with rice cultivar PR121 to generate the mapping population. The $F_{2:3}$ mapping population was inoculated and scored against sheath blight disease. The normal distribution was obtained for the RLH. The whole population was genotyped using GBS and QTL mapping was conducted. The major QTLs for relative lesion height were obtained on chromosome 1, 4 and 11. Further, work on development of linked markers is under way.

About 400 accessions of *Oryza rufipogoan* were screened during *kharif* 2015 and 2016 and moderately resistant (MR) accessions were further evaluated during the year 2017 and 2020. Finally, 19 accessions were identified as promising which showed continuously moderately resistant reaction for three years. The range of plant height varied from 84cm to 140cm, lesion length varies from 27cm to 36cm whereas the relative lesion length varies from 21 to31 percent among the studied moderate resistant accession of *O. rufipogon*. Based on the genotypic and phenotypic data of 400 accessions, we conducted association mapping for sheath blight resistance. We got strong association for plant height on chromosome 3 and chromosome 10 whereas for relative lesion height we got association on chromosome 2, 7 and 9.

CONCLUSION

Comprehensive phenotyping of large number accessions of wild species of rice leads to the identification of promising sources for transferring sheath blight resistance to the elite cultivars. We have initiated the transfer of sheath blight resistance to the elite cultivars using MAS from the identified sources of resistance in *O. nivara* and *O. rufipogon*.

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IRC/TM-1/PP-75

GENETIC VARIABILITY OF ANTIOXIDANT COMPOUNDS IN PIGMENTED RICE LANDRACES FOR CROP IMPROVEMENT

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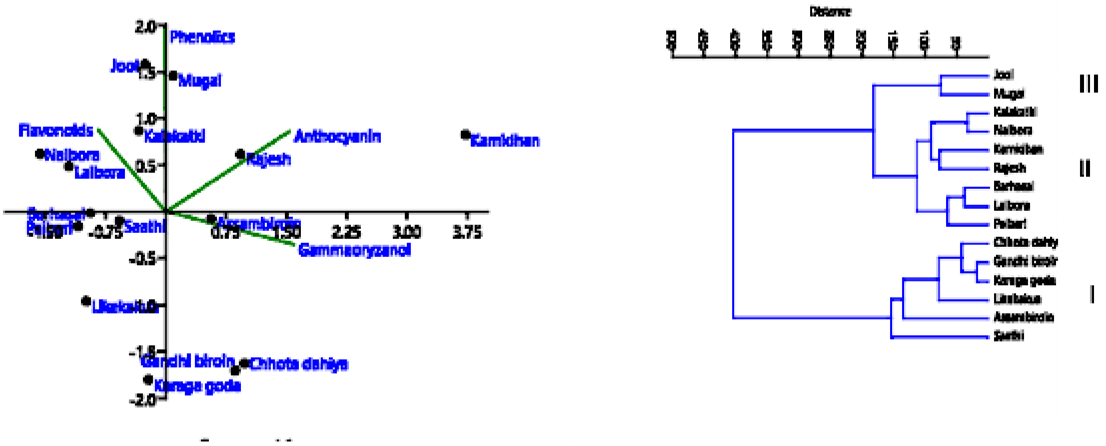
Nutritional superiority of pigmented rice over white rice owing to its richness in bioactive compounds such as anthocyanin, phenolic acids, flavonoids, pro-anthocyanidins, tocopherols, tocotrienols, oryzanol (Samyor et al. 2017; Sanghamitra et al., 2017,2018,Mbanjo et al.,2020) has made it essential for its inclusion in the rice breeding programme to achieve food and nutritional security of the world populace heavily dependant on rice as a staple food. Evaluating variability in phytochemical traits in the pigmented rice and identifying promising genotypes is needed to initiate and its successful utilisation in plant breeding programme.

METHODOLOGY

Fifteen pigmented rice genotypes used in this study were dehusked, grain samples were grounded by a grinding machine (Glen mini grinder), sieved through 100 mesh size and evaluated for phytochemical properties such as total anthocyanin contents(TAC) in the samples were determined using method described by Fuleki and Francis (1968) and expressed as mg 100 g^{-1}.Gamma-oryzanol (GO) was estimated according to Bucci et al., (2003) with minor modifications and expressed as mg 100 g^{-1}. Total phenolics compounds (TPC) was determined by modified protocol of Zilic et al., (2011) and expressed as mg Catechol equivalent(CE) 100 g^{-1}. Total flavonoid content (TFC) was determined according to Eberhardt et al., (2000) and expressed as mg Catechine equivalent(CEt) 100 g^{-1}. The test of significance was performed using Fisher's (F) test. Correlation,principal component analysis and clustering was done based on the mean values of the 15 genotypes using paleontological statistics (PAST) software version 4.02.

RESULT

Genotypes were found significant for all the phytochemical compounds studied. Karnidhan was observed with highest anthocyanin content (5.11 mg $100g^{-1}$),Gammaoryzanol(65.85 mg $100g^{-1}$) and total phenolics(638.36 mg CE $100g^{-1}$) . Total flavonoid content was highest in the genotype Assambiroin (245.60 mg CEt $100g^{-1}$). Correlation analysis observed significant positive correlation of anthocyanin content with gammaoryzanols and Total phenolics.PCA(Fig.1A) showed that PC1 and PC2 with Eigen value more than one exhibited maximum 73.77 % of total variation. Anthocyanin, gammaoryzanol in PC1 and Total phenolics in PC2 responsible for significant variation in the phytochemical properties.The PCA exhibited three groups of the genotypes. Three genotypes (Assambiroin, Gandhibiroin and Chhotadahiya) in the first quarter separated from other group based on gammaoryzanol. The second quarter consisting of three genotypes(Mugai,Rajesh and Karnidhaan) separated from other group based on phenolics and anthocyanin content. Whereas the third group was the largest group consisting of nine genotypes separated from other group based on flavonoids. The cluster analysis based on UPGMA(Fig 1B) also divided the genotypes into three groups at an Euclidean distance of 400 based on the



A

B

Fig1: PCA (A)and clustering(B) of pigmented rice genotypes

phytochemical properties.The group I consisting of six genotypes with Chhotadahiya and Saathi being the diverse one. Seven group constituting the group II found Kalakatki and Palbari the diverse genotypes.The third group consist of rest two genotypes Jool and Mugai.

CONCLUSION

The PCA and cluster analysis provide information about closeness of genotypes required for selection. Further the trait association identified will help in screening large number of germplasm for breeding superior varieties with enhanced grain and nutritional quality. The genotype Karnidhan was found promising having highest anthocyanin, gammaoryzanol and total phenolics content.Whereas Assambiroin was also found suitable with highest flavonoid content to be used in the plant breeding programme for development of improved lines and also could be utilized in value added products by the food industry.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-76

BLACK RICE: FOR BRIGHT FUTURE

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Black rice is a variety of rice which has several promising health benefits. The high antioxidant activity of black rice makes it a highly super nutritious food. Black rice *Zizania aqatica* (Kumar *et al*., 2020) is the native of the common rice species (*Oryza sativa*). Other common names of black rice are purple rice, forbidden rice, heaven rice, imperial rice, king's rice and prized rice. It is known as Chak-hao Ambi in Manipur (Chak-hao means 'delicious' and ambi means 'black'). In Odisha it is known as Kalabati (kala means 'black' and bati means 'rice' in Oriya). Black rice was initially grown in China before the Chinese dynastic period and was called as the 'luck rice' because it was believed that people consuming black rice would live longer. Black rice is formed by the mutation of Kala 4 gene that stimulates the production of the black pigment-anthocyanin (Oikawa *et al*., 2015).

The pericarp (outer covering) of black rice is black in colour due to the presence of the black colour pigment called anthocyanin which is rich in antioxidants and poses a variety of health benefits such as anti-aging, anticancer, anti-diabetes, lowering the risk of obesity *etc*. Black rice has high levels of protein, fiber, vitamins (Vitamin B_1, Vitamin B2, folic acid) and minerals (iron, zinc, calcium, phosphorus and selenium) compared to that of white rice. The major essential amino acids present in black rice are lysine and tryptophan.

In the world it is mainly cultivated in Southeast Asian countries like China, Thailand, India, Sri Lanka, India, Indonesia and Philippines. China accounts for 62% of black rice production in the world. There are more than 200 types of black rice varieties in the world. In India black rice is grown in North-eastern states like Manipur, Mizoram, Meghalaya, Assam and some parts of Odisha (Oikawa et al., 2015). Earlier people refused to consume black rice due to its black color as they considered it to be 'dirty' because of the black color (Takashi *et al*., 2001). Black rice has a low Glycemic Index (GI) of 42.3 compared to white rice, which has an average GI of 89, and brown rice that has an average GI of 50.

The types of black rice are Black Japonica Rice is a mix of short and medium sized rice grains has an earthy flavour with a mild sweet spiciness. Black Glutinous Rice (Black Sticky Rice) has a short unevenly coloured grain size and has a sticky texture, used to make sweet dishes in Asia. Italian black rice has long rice grains and has the characteristics of both chinese black rice and italian rice with a rich buttery aroma (Kumar *et al*., 2020). Thai black jasmine rice has a medium grain size and originated from Thailand that combines Chinese black rice with jasmine rice. Jasmine rice is native of Thailand and has a subtle floral aroma (Kumar *et al*., 2020).

Black rice helps in reducing the weight, because of high fiber content on the bran. On consuming it gives the feeling of fullness, so does not feel hungry and also decreases the fatty acid synthesis. It act as a Natural detoxifier. The phytonutrients present in black rice help cleanse the body of disease causing toxins (caused by free radicals). It was found out that anthocyanin present in black rice lowers the LDL (bad cholesterol) and increases the HDL (Good cholesterol) levels which decrease the chances for developing atherosclerosis and heart attack. The naturally low content of sugar and high fiber content in black rice prevents the occurrence of diabetes and it eases the bowl movement and cure chronic constipation (Thanuja and Parimalavalli, 2018).

CONCLUSION:

There is a direct need to include black rice as a novel ingredient in food processing to explore its complete benefits. Several researches suggested that black rice may have the capacity to reduce the likelihood of developing a number of diseases and illnesses, suggesting that black rice consumption may promote heart and liver health, weight loss, control on blood glucose level and lipid profile, prevention and control of inflammation and cancer.

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IRC/TM-1/PP-77

BREEDING FOR NITROGEN USE EFFICIENCY TO ENHANCE RICE PRODUCTIVITY

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Rice is the principal staple cereal crop securing half of the global population from food crisis. In order to satisfy the requirements of drastically growing global population, there is a need of significant rice yield potential under the circumstances of decreased arable lands, global climate change, natural disasters and frequent occurrence of pests and diseases. Nitrogen is an important soil macronutrient required for plant growth and development. But its availability limits the yields in most of the cropping areas. Therefore practice of excessive application of synthetic nitrogen (N) fertilizers may not only limits the yield but also leads to considerable negative impacts on human health and environment in the form of blue baby syndrome and soil acidification, air pollution, fertilizer burn, water eutrophication and green house effect. New solutions are therefore urgently needed to simultaneously increase yields by maintaining or preferably decreased applied N to maximize the Nitrogen use efficiency (NUE) in Rice.

NUE in rice is defined as "amount of biomass or grain production per unit of N applied". Plant NUE is integration of NUpE (Nitrogen Uptake efficiency) and NUtE (Nitrogen Utilization efficiency). Enhanced NUE is achieved through genetically modifying plants and integrated agricultural management practices. In rice, two transporter families NPF (nitrate transporter 1/peptide transporter family) NPF 2 for uptake and translocation of nitrate were associated with enhancing nitrate uptake and root-to-shoot transport affinity. OsNPF genes of this family has a significant impact on NUE as well as on yield because they mainly expressed in root epidermis and hairs, rice panicle elongation, ammonium uptake, promotion of lateral root formation and finally increased grain yield.

Breeding for NUE in rice was extensively studied through several enzymes, N Transporters, genes and promoters. Bi *et al*., 2009 noticed that over expression of rice early nodulin gene- OsENOD93-1 had increased shoot dry biomass and seed yield up to 10% to 20%. Satisha *et al*., (2016) revealed that, Nitrogen Harvest Index (NHI) was high in T_0 (80.33%), compared to a T_1 (78.93%) indicating that the variation in nitrogen harvest index among 84 rice genotypes is mainly due to efficient uptake of N and re-assimilation of N to economic part.

By the replacement of Cytosine/Thyamine in NRT1.1B (nitrogen transporter) gene in rice, increased NUE which was confirmed by genome editing using CRISPR/Cas9 (Mishra *et al*., 2018). Over expression of OsATG 8a gene (responsible for increased expression levels of 'N' under starvation conditions) increased level of autophagy and resulted in number of effective tillers in transgenic rice line (Japonica variety) Shennong 9816 and it's biomass was increased by 22.9% or 10.62%, under N_{225} and N_{75} treatments respectively (Yu *et al*., 2019).

Rice NUE is the integration of NUpE and NUtE and governed by multiple interacting genetic and environmental factors. Improvement of genes, transporters and enzymes related to NUE are playing an immense role in enhancing Nitrogen use efficiency. Useful gene-based markers are provided to breeders for the production of Nitrogen efficient GM plants.

Finally, the road ahead for NUE crops appears bumpy, the necessity in creating crops that require decreased N fertilizer levels is the need and has been recognized in the call for a "Second green revolution".

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IRC/TM-1/PP-78

MARKER ASSISTED FORWARD BREEDING FOR MULTIPLE TRAIT RESISTANCE IN RICE

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Rice is the most important cereal crop occupying a prominent place in Indian agriculture and continues as a staple food crop for more than half of the global population despite the changing climatic, social and economic scenario. Productivity of rice fluctuates significantly from region to region; season to season due to various biotic and abiotic stresses. The yield loss due to biotic stresses varies depending on the severity of the stress prevailing in the specified region. The major biotic stresses like blast, bacterial leaf blight, brown plant hoppers, etc result in severe yield penalty in rice. In addition, abiotic stresses such as drought, salinity, heat, cold, submergence etc hinder growth and development of rice plant resulting in severe yield reduction in rice. Recent advances in breeding to transfer genes/QTLs with high precision have provided new opportunities to combat challenges arising from different biotic and abiotic stresses (Kumar et al.2018). Rice varieties improved with resistance to multiple biotic/abiotic stresses not only provide for preventing yield losses and increasing the income of rice farmers but also are a viable option for environmental sustainability.

Considering the yield losses caused due to various stresses, the present study aims at development of high yielding climate-resilient rice, using 11 genes conferring resistance against blast (BL) (*Pi2* and *Pi54*), bacterial leaf blight (BB) (*xa5, xa13* and *Xa21*), brown planthopper (BPH) (*Bph3*, *Bph17*, *Bph20* and *Bph21*), gall midge (GM) (*Gm4* and *Gm8*) and 4 QTLs for drought tolerance (*qDTY1.1, qDTY2.1, qDTY3.1* and *qDTY12.1*) through marker-assisted forward breeding (MAFB) approach.

METHODOLOGY

Breeding for multiple trait introgression employing marker assisted selection was initiated at ICAR-Indian Institute of Rice Research (ICAR-IIRR) during *Kharif* 2013 with two recurrent parents and 14 donors. A total of 9 donors *viz.*, RP Bio Patho-1 with *Pi2* and RP Bio Patho-2 with *Pi-54* for BL, Improved Samba Mahsuri (ISM) with *xa5, xa13* and *Xa21* for BB, Rathu Heenati with *Bph 3* and *Bph17* for BPH, RP 5924-23 for *Gm4* and RP 5925-24 with *Gm8* for GM resistance and IR 96321-1447-561-B-1 with *qDTY 1.1* and *qDTY 3.1*, IR 81896-96-B-B-195 with *qDTY 2.1* and IR74371-46-1-1-13 with *qDTY 12.1* for yield under drought stress were used for multiple genes/QTL pyramiding into ‘WGL14’. Similarly, 7 donors *viz.*, IRBB60 with *xa5*, *xa13* and *Xa21* for BB, RP Bio Patho-3 with *Pi2* and Tetep with *Pi 54* for BL, IR 71033-121-15-B with *Bph 20* and *Bph 21* for BPH and 3 donors for *qDTY* QTL same as for WGL14 were used in crossing with Krishna Hamsa.

F_1 crosses were made between recipient parent and each of the donor during *Kharif* 2013 (wet season) followed by all possible inter-crosses among F_1’s during *Rabi* 2014 (dry season). Tightly linked polymorphic SSRs were used in knowing different combinations of genes/QTL introgressions in IC_1F_1’s. Genotyping and inter-crossing of inter-crossed F_1’s was continued up to *Kharif* 2015 to get all the targeted genes/QTL into common background. IC_4F_1's were selfed and single plant selections were advanced from *Rabi* 2016 to *Rabi* 2018. Phenotypic evaluation (Yield under control-YC, yield under drought stress-YS, BL, BB, BPH and GM) of IC_4F_6 progenies (forward breeding lines-FBLs) was done in *Kharif* 2018 (YC, YS, BL, BB, BPH and GM), *Rabi* 2019 (YC), *Kharif* 2019 (YC, YS, BL, BB), *Rabi* 2020 (YC and YS) and *Kharif* 2020 (YC, BL and BB). Genotyping with foreground markers in FBLs was repeated in 2018 and 2019 to confirm gene/QTL introgressions.

RESULTS

In the background of Krishna Hamsa and WGL14, 256 and 253 FBLs respectively were subjected to repeated screening and phenotypically promising lines in various trait combinations were identified. With Krishna Hamsa as recurrent parent, 10 FBLs (KFBL19001, KFBL19030, KFBL19177, KFBL19210, KFBL19241, KFBL19246, KFBL19249, KFBL19378, KFBL19379, KFBL19471) were with high yield (6-8 t/ha) under control, resistant to both BL and BB (score d”3) and 13.2-22.34% yield improvement of over Krishna Hamsa under drought stress. 5 of them recorded intermediate amylose content (20-25%), high HRR (55-64.7%) and MS-LS grain type indicating on par/superior grain quality characteristics when compared to the recurrent parent Krishna Hamsa. A combination of five gene/QTL *xa5+Xa21+qDTY1.1+qDTY2.1+qDTY12.1* was recovered in KFBL19177 and 3 gene/QTL combination of *Xa21+Pi9+qDTY2.1* in KFBL19249. Further, 37 and 9 FBLs were found with very high level of BL and BB resistance (score d”3) respectively.

With WGL14 as recurrent parent, of the 253 phenotypically evaluated FBLs, 9 FBLs (WFBL19087, WFBL19088, WFBL 19090, WFBL19093, WFBL 19100, WFBL 19103, WFBL 19344, WFBL19347 and WFBL19451) have all the targeted trait introgressions in 5-10 gene/QTL combinations and showed high level of resistance to BL and BB (both score d”3), high yield (5-8 t/ha), yield advantage of 11.24 to 28.42% over WGL14 under drought stress, intermediate amylose content (20-25%) and high HRR (55-65.2%). In all the 9 FBLs, MS grain type akin to WGL14 was recovered. Further, 6 FBLs (WFBL 19101, WFBL 19104, WFBL19283, WFBL19285, WFBL19292 and WFBL19321) with BB+BL+GM and 11 FBLs (WFBL19067, WFBL19068, WFBL19072, WFBL19074, WFBL19091, WFBL19147, WFBL19154, WFBL19162, WFBL19349, WFBL19446 and WFBL19449) with BB+BL and yield under drought stress were identified. one FBL in the background of WGL14-WFBL19347, maximum introgression of 10 genes/QTL with a combination of *xa5+xa13+Xa21+Pi2+Gm4+Gm8+qDTY1.1+qDTY2.1+qDTY3.1+qDTY12.1* was observed followed by *xa5+xa13+Pi2+Gm4+Gm8+qDTY1.1+qDTY2.1+qDTY3.1+ qDTY12.1* (9 genes/QTL) in WFBL19344. Also, 16 and 40 FBLs showed very high level of resistance to BL and BB (score ≤ 3) respectively.

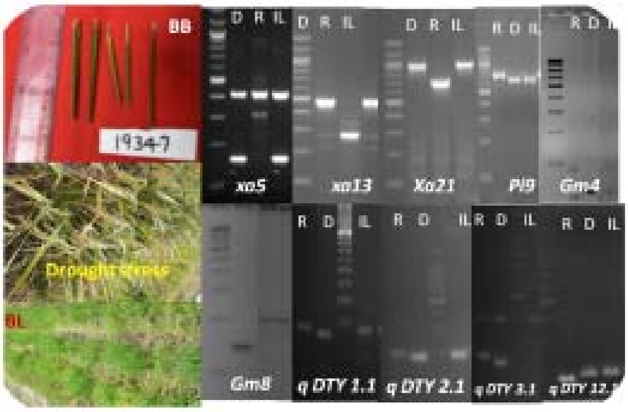

Fig 1. WFBL 19347 in the background of WGL14 positive genotypically and phenotypically for all the targeted traits (BB score-1; BL score-3; YC-5740kg/ha; YS-4066kg/ha). D-donor, R-WGL14, IL-WFBL19347

Bph 20, Bph21 for Krishna Hamsa, *Bph3, Bph17* and *Gm4* for WGL14 were found not effective as the lines possessing these genes showed susceptible reaction to BPH and gall midge respectively. Similar observations on BPH reaction in introgression lines with *Bph3* and *Bph17* was recently reported (Dixit et al 2020)

CONCLUSION

The present study demonstrates the success of marker assisted forward breeding in introgressing multiple trait resistance/tolerance and maintaining high yield levels and preferred grain quality. We developed FBLs with 3 to ten genes/QTL which showed improvement over their respective recipient parents in terms of multiple biotic and abiotic stress resistance/ tolerance together with yield advantages of 11.24 to 28.42% under drought stress conditions. The developed FBLs with resistance to multiple stresses would certainly benefit future rice breeding programs.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-79

GENETIC VARIATION AND MARKER AIDED SELECTION STRATEGY FOR FRAGRANCE IN A F_2 POPULATION OF RICE

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The Basmati rice is the gift of nature to India. India is an exporter of world class aromatic rice. Local aromatic tall indica rice varieties are low yielding due to insufficient partitioning of biomass and mostly susceptible to insects and a variety of abiotic stresses including drought, flood, and heat stress. Most of the aromatic varieties of rice including Jasmine and Basmati types reveal the 8-bp deletion on exon 7 of the BADH2 gene. Identification of this gene for fragrance (Amarawathi *et al.*, 2008) has created an opportunity to sort out aromatic plants from a large population of F_2. Therefore, a marker assisted breeding strategy was designed for success in aromatic rice breeding.

METHODOLOGY

The experimental material used in the present investigation comprised a cross HH-25-DT-20 x ORCZ 66. Among the parents, HH-25-DT-20 was non aromatic semi-dwarf plant type with high yield potential, while ORCZ 66 was a pre-release aromatic advanced breeding line characterized by tall, basmati type grain quality with moderate high yield potential. Evaluation of the F_2 population was carried out in the field for yield and yield attributes. Variation for agro-morphological and quality traits including status of aroma among individual F_2 plants has been worked out. Genotyping of parents, F_1 and F_2 plants were done following PCR using badh2 gene specific primer 'FMbadh2-E7(Shi *et al.*, 2008)'. The inheritance pattern of aroma was studied by Chi-square test.

RESULTS

The F_2 plants varied widely in days to flowering, maturity duration, number of ear bearing tillers, number of fertile grains/panicle, grain size, status of aroma and grain yield per plant. Number of ear bearing tillers/plant and grain number/plant had shown significant positive correlation with grain yield. Sensory test (1.7% KOH) of young leaves was initially carried out at seedling stage to reduce population size for effective confirmation of F_2 plants for aromatic status. Ten plants out of 120 F_2 plants in the cross qualified for presence of aroma ranging from average panel score of 0.7 to 4.0 in 0-4 scale (Table 1) resulting unimodal skewed distribution towards non-aromatic status parent, HH-25-DT-20. Those ten putative aromatic F_2plants along with ten randomly selected non-aromatic plants of F_2 alongside both the parents and F_1 were genotyped (Fig 1). The parent HH-25-DT-20, F_1 showed the non-aromatic allele (268bp) amplified by the badh2 gene specific primer 'FMbadh2-E7' while, the aromatic parent ORCZ 66 and eight out of ten above putative aromatic plants selected based on sensory test revealed homozygous recessive for the 260 bp allele linked to aroma. In contrast, two putative aromatic F_2 plants with average panel score as low as 0.7-0.8 and all randomly selected non-aromatic plants of F_2 showed either homozyosity for non- aromatic allele (268bp) or heterozygosity due to codominant status of 260bp and 268bp alleles. Further, matured seeds of the above eight aromatic F_2 were retested by chewing at maturity stage in the field and after harvest at 14% moisture using 1.7% KOH. All such plants continued to retain aroma status. In the present study, the F_2 population segregated into 15(Non-aromatic):1 (Aromatic) ratio for aroma in rice grains. The probability of exceeding the calculated chi-square value lies at fairly higher probability interval beyond 0.05 indicating non-significant ÷2-value. This clearly indicates that segregation pattern of plants in the generation satisfactorily agreed with the expected classical ratio of 15 : 1 for inheritance of aroma. Grain yield ranged from 4.86-45.9g per plant among the F_2 plants as compared to mean grain yield of 50.2 g/plant in HH-25-DT-20 and 30.5g/plant in ORCZ 66 and 48.4g/ plant in F_1

CONCLUSION

Marker assisted selection of F_2 plants for aromatic status at seedling stage and further selection of few high yielding F_2 plants coupled with acceptable quality features based on phenotyping seems to have greater advantage for genetic improvement in aromatic rice.

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IRC/TM-1/PP-80

ISOLATION OF IMPROVED LINE IN 'BADSHABHOG' THROUGH INDUCED MUTATION

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Non-basmati aromatic rice is very popular for its excellent grain quality with inbuilt aroma. But these cultivars have been ignored in the mainstream industrial agriculture due to low yielder. It is serious matter that most of these cultivars are fast disappearing from the scene of the locality. Among them *Badshabhog* is very popular cultivar of rice which is cultivated by the farmers from primitive period for their own consumption and ritual purposes in eastern India. This cultivar is handicapped by its tallness (167-177cm.), late maturity (150-155 days) and poor yielder (2.0 – 2.5t/ha). Therefore, there is an urgent need to improve the yield potential of this cultivar without disrupting its original grain quality and cooking quality features. Genetic improvement in specific traits like height of the plant, duration of maturity, yield and its component characters through hybridization and recombination often becomes difficult due to break-down of aroma and cooking quality characters. Mutation breeding is one of the options to improve/rectify of specific traits of these cultivars within very short period without break-down of in-built quality traits. The present investigation was carried out to isolation of semi dwarf, early maturity and high yielding line in *Badshabhog* through induced mutation.

METHODOLOGY:

Genetically uniform, disease free, healthy seeds of Badshabhog with 12 percent moisture weighing 100g were taken in six packets for the experiment. Five such packets were used for gamma irradiations. The seeds were placed inside the gamma radiation chamber to get the seeds irradiated with five different doses of gamma rays viz. 200Gy, 250Gy, 300Gy, 350Gy and 400Gy [Gy: Gray (1Gray = 1 joule per kg of matter undergoing radiations = 0.1kR)] from the Cobalt 60 gamma rays source for appropriate time for each dose based on the half-life of the source at Department of Atomic Energy, Board of Research in Nuclear Science, BARC, Trombay, Mumbai in India. The dose rate was of the order of 17Gy/min in radiation chamber. Sixth unexposed seed packet was used as control. The plants were grown in the M_1, M_2, M_3 and M_4 generations along with control. Throughout the programmes desirable mutant types have been identified, which was according to their performance against the controls.

RESULTS:

Optimal dose of gamma irradiation under *in vitro* and *in vivo* conditions were determined at 358.37Gy & 346.10Gy which were based on weighted mean of LD_{50} and GR_{30}/GR_{50} resulting from percent germination, percent seedling survival and seedling growth parameters. 200Gy and 250Gy dose was found more efficient. Higher efficiency at the lower dose of gamma ray may be occurred through increasing biological damage (lethality and sterility) within dose at a faster than the mutations (Konzak *et al.*, 1965). Desirable changes appeared through efficient mutagenesis with minimum undesirable effects. *Albina*, Chlorophyll mutant was highest. Different types of morphological mutations were also identified. In $\mathbf{M_2}$ generation, desirable mutants with short stature, earliness in maturity and other yield attributing traits were selected. The selected individuals tested for aroma with KOH solution under segregating progeny were collected separately and main panicle of the rest plants of this progeny were harvested as bulk and were grown in M_3 generation. Three type of early maturity mutants such as 10 days early, 20 days early and 30 days early and semi-dwarf mutants having desirable plant type with upto 50 cm. reduction in plant height as compare to their parent were selected in M3 generation. Seeds of all confirmed mutants under each character as well as each treatment were collected separately and were grown in M_4 generation with replicated trail to produce the near homozygous lines for the traits under consideration. Substantial genetic variability was observed for all economic characters studied in M_4. There was no consistency in the behaviour of selected mutants from various doses of mutagen. Majority of the mutants had combination of both positive and negative forms of important yield contributing characters. There was no apparent variation for different characters within the progenies of majority of the mutant families due to further increase in homozygosity. However, segregation for height continued in few mutant families. All the mutants retained apparently the same characteristic aroma of their respective mother genotypes. This was quite expected since aroma in these groups of rice is controlled by a single recessive gene (Kole 2005) and chances of mutation from recessive form of aroma gene to a dominant one are rare. Considering the performance of the mutants of agronomical important characters, three mutants {one for 20 days early and other two for short height (reduction up to 50 cm)} were promising. These mutants need further testing in multilocation trials for evaluation of their potential for direct release as varieties of aromatic rice. The other mutants may be used in cross breeding programmes of aromatic rice for utilization of agronomically useful mutant characters.

CONCLUSIONS:

The desirable mutants isolated in the experiment are characterized as semi-dwarf plant type, early maturation, having higher yield with desired level of aroma. The results demonstrated that there are great scopes for improving qualitative and quantitative traits by using appropriate mutation breeding approaches. The present study on mutagenesis has generated a good amount of genetic variability for economically and agronomically important characters. Mutation breeding is one of the most effective non-conventional methods of plant breeding to induce desirable character in locally adapted varieties. If these mutants are released for general cultivation, they may replace the low yielding local cultivars Badshabhog and there by promoting better socio-economic conditions of farmers.

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IRC/TM-1/PP-81

STABILITY ANALYSIS OF YIELD AND YIELD ATTRIBUTING TRAITS IN ADVANCED BREEING LINES OF RICE (*Oryza sativa* L.)

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In India rice is grown under a diverse set of agro-environments varying in seasons, temperature, rainfall, soil types, hydrology varieties an input management. This staple food contributes 43% of the total food. To meet the growing demand for food will require significant improvements in rice production. However the enhancement of rice productivity is not an easy job owing to the declining land area, water resources and occurrence of several biotic and biotic stresses. It is very much necessary to develop varieties having stable yield performance over diverse environments. Hence, knowledge on the nature and magnitude of genotype x environment interactions is important in understanding the stability of a particular variety before it is being recommended for a given situation. Testing of genotype under different environments differing in unpredictable variation is an accepted approach for selecting stable genotypes.

MATERIAL AND METHODS

The present experiment material comprised of seventeen long duration advanced breeding lines including one check (common check) developed at different rice research stations across Andhra Pradesh. The trials were conducted in a randomized Block design with two replications at two locations viz., Agricultural Research Station, Ragolu and Regional Agricultural Research Station, Anakapalle during *kharif* 2018 with plot size of 12 $m^{2.}$ Observations were recorded on ten randomly selected plants in respect of six quantative characters viz., days to fifty percent flowering, plant height (cm), panicle length , productive tillers per square meter, test weight (g) and grain yield per hectare (kg/ha). Advanced lines data over locations were subjected to pooled stability analysis as per Eberhart and Russell (1966). The genotype with high mean, unit regression coefficient and non-significant deviation from regression was considered to be stable over environments.

RESULTS AND DISCUSSION

The analysis of variance of stability using Eberhart and Russell model (1966) revealed that the genotypes and environments were significant for all characters except for panicle length and test weight indicating the diversity among the genotypes and environments studied. The GE interaction was not significant for all the traits indicating the absence of genetic differences among varieties for regression on environmental indices (Rashmi *et al*. 2017). The data pertaining to stability parameters for yield and its attributing characters presented in table 1. The entry L-609 recorded less mean value (110.50) for days to 50% flowering with regression coefficient value around unity (b_i=0.98) and less deviation from regression was identified as stable genotype over locations. Out of 17 lines tested for plant height (cm) the entry L-609 registered above general mean with b_i value around unity (b_i=0.97) and non-significant deviation from regression found to be stable under environments. No.of productive tillers/m^2 is the important trait for yield contributing character. None of the entry exhibited stable performance over two locations. The entry L-615 recorded highest (333) no.of productive tillers/m^2 with b_i more than unity, it was suggested to have less than average stability (good performance in favorable environments). The lines L-615 and L-

Table 1. Mean performance and stability parameters for yield and contributing characters

Entries	Days to 50 % Flowering			Plant Height (Cm)			No. of productive tillers/m²			Panicle length (cm)			Test Weight (g)			Grain Yield (Kg/ha)		
	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s²di	Mean	bi	s²di
L-605	114.50	1.86	0.00	114.50	0.90	0.00	294.75	2.77	0.00	22.23	1.37	0.00	19.14	1.07	0.00	6945.25	1.61	0.00
L-606	118.50	0.55	0.00	103.25	0.75	0.00	289.25	4.21	0.00	23.77	0.39	0.00	19.74	1.72	0.00	5654.50	1.42	0.00
L-607	102.50	2.08	0.00	95.50	0.48	0.00	286.00	1.55	0.00	22.19	0.95	0.00	18.11	-1.5	0.00	4855.50	0.03	0.00
L-609	110.50	0.98	0.00	101.75	0.97	0.00	289.75	-1.97	0.00	21.21	0.97	0.00	19.42	0.96	0.00	6780.75	0.61	0.00
L-610	122.50	2.08	0.00	96.00	0.88	0.00	267.00	2.09	0.00	20.91	0.64	0.00	18.58	1.84	0.00	4549.75	0.95	0.00
L-611	103.00	1.75	0.00	89.25	0.86	0.00	274.75	-0.47	0.00	21.02	1.10	0.00	13.10	-0.2	0.00	3192.25	0.69	0.00
L-613	134.25	0.05	0.00	115.50	1.58	0.00	296.50	-2.64	0.00	23.12	1.17	0.00	18.78	1.72	0.00	5630.50	1.81	0.00
L-614	127.00	0	0.00	93.25	1.05	0.00	292.50	3.59	0.00	20.79	0.64	0.00	16.59	2.31	0.00	5054.75	1.26	0.00
L-615	119.50	0.33	0.00	104.25	1.34	0.00	333.00	2.09	0.00	24.04	0.97	0.00	18.63	1.69	0.00	5869.50	0.86	0.00
L-616	119.00	0.44	0.00	91.75	1.12	0.00	309.75	2.02	0.00	23.40	0.98	0.00	19.81	0.34	0.00	6031.75	1.06	0.00
L-617	115.25	1.69	0.00	103.25	0.42	0.00	265.50	-0.3	0.00	23.56	0.83	0.00	16.48	2.13	0.00	5184.25	0.38	0.00
L-619	102.00	1.53	0.00	93.50	0.81	0.00	232.75	1.77	0.00	21.55	1.2	0.00	12.91	-0.7	0.00	3311.00	0.47	0.00
L 620(C)	122.75	0.05	0.00	103.25	1.42	0.00	297.25	-0.77	0.00	26.20	1.11	0.00	18.80	1.38	0.00	6882.00	1.42	0.00
L-621	124.00	1.31	0.00	104.25	1.45	0.00	276.50	0.1	0.00	22.11	0.85	0.00	16.99	1.38	0.00	4986.50	0.95	0.00
L-623	130.75	0.82	0.00	109.00	1.18	0.00	252.75	1.52	0.00	24.54	1.33	0.00	17.01	1.72	0.00	4244.25	1.04	0.00
L-624	129.50	0.11	0.00	98.00	1.43	0.00	259.75	1.17	0.00	21.64	1.49	0.00	19.82	2.72	0.00	5772.25	1.78	0.00
L-625	114.75	1.37	0.00	79.25	0.35	0.00	295.75	0.27	0.00	19.25	0.99	0.00	16.85	-1.6	0.00	4623.75	0.67	0.00

616 were found to be stable for panicle length (cm) with above general mean, bi value around unity (b_i= 0.97 and b_i=0.98) and non-significant deviation from regression. For the character test weight the line L-609 exhibited more mean value than general mean, regression coefficient value is around unity (b_i= 0.96) and less deviation from regression. The entry L-605 indicated less than average stability (b_i= 1.07) with good performance in favorable environments. The breeding lines L-615 and L-616 were found to be stable for Grain yield (kg/ha) with mean above general mean, bi value around unity (b_i= 0.86 and b_i=1.06) and non-significant deviation from regression. The entries L-605, L-620 and L-624 recorded highest mean more than general mean with b_i more than unity indicating good performance in favorable environments. Advanced lines L-609 recorded regression less than unity (b_i=0.61) with mean more than general mean representing good performance in poor environments.

CONCLUSION

The lines L-615 and L-616 with yield more than general mean were stable for panicle length over locations. The high yielding line L-609 was stable for days to fifty percent flowering, plant height (cm) and test weight in two locations. These stable lines may be exploited for commercial cultivation in rice growing areas in North coastal zone of Andhra Pradesh.

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IRC/TM-1/PP-82

STABILITY ANALYSIS OF YIELD AND YIELD CONTRIBUTING TRAITS IN RICE (*ORYZA SATIVA* L.)

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Rice (*Oryza sativa* L.) is the staple food of about more than one third population of the world. Its demand is increasing day by day as per the increase in the population, hence varietal adaptability to environmental fluctuations is important for the stabilization of crop production over both the regions and years. The present investigation was carried out at Agriculture Research Station, Palghar with seven rice varieties released by DBSKKV, Dapoli.

OBJECTIVE

The aim of this research work to identify the most stable rice variety for north konkan region of Maharashtra state.

MATERIALS AND METHODS

The experimental material comprised of seven released rice varieties *viz.*, Karjat-3, Karjat-7, Palghar 1, Palghar 2, Ratnagiri 5, Ratnagiri 24 and Karjat 184. The verities were evaluated during four consecutive *kharif* seasons from *kharif* 2015 to *kharif* 2018 at Agriculture Research Station, Palghar. The experiment was laid out in RBD with three replications. All the cultivation packages of practices were followed. Observations on five characters were recorded.

The analysis of variance for each season was conducted the mean genotypic values for each season was taken for analysing the data over the seasons. The characters which recorded significant G x E were used for stability analysis of Eberhart and Russell model (1966).

RESULTS AND DISCUSSION

The analysis of variance for stability showed that the genotype (G) and environment (E) differences were highly significant to days to flowering; plant height, panicle length, spikelets per panicle except grain yield per ha (Table 1) which indicated a wide range of variability among the genotypes performance. The variation in both linear trend and non-linear trend relative to all the traits were significant, where it was corroborated by Kulkarni *et al.*, (2000).

Table 1: Analysis of variance for stability performance for five components in rice

Source	DF	Days to 50 % flowering	Plant height (cm)	Panicle length (cm)	Spikelets per panicle	Grain yield (t/ha)
Variety	6	6.82**	20.35**	4.01**	161.17**	0.05
Environment	3	184.18**	14.55**	18.17**	1513.40**	0.99
Var. X Env.	18	18.07**	32.34**	4.65**	153.54**	0.04
Env.+Var. X Env.	21	41.80**	29.79**	6.58**	347.81**	0.18
Env. (Linear)	1	552.52**	43.64**	54.52**	4540.20**	2.97
Env. X Var. (Linear)	6	23.64**	21.66**	8.44**	359.80**	0.03
Pooled Deviation	14	13.10**	32.29**	2.36*	43.21**	0.04
Pooled Error	48	4.81	9.13	2.20	63.50	0.03

* & ** Significant at P=0.05 and P=0.01 respectively when tested against pooled error.

Table 2: Stability parameters of yield and yield contributing traits in rice

Genotype	Days to 50 % flowering			Plant height (cm)			Panicle length (cm)			Spikelets per panicle			Grain yield (t/ha)		
	Xi	Bi	S^2di	Xi	Bi	S^2di	Xi	Bi	S^2di	Xi	Bi	S^2di	Xi	Bi	S^2di
Karjat-3	91.25	-0.09	49.25**	98.04	2.21	35.98**	24.83	1.76	1.18	190.67	1.52	51.84**	3.89	1.27	0.07
Karjat-7	94.00	1.16	9.15**	99.99	2.00	20.86**	24.49	2.02	0.61	194.83	1.41	-12.56**	3.75	0.94	0.00
Palghar-1	90.50	1.13	10.55**	97.58	2.26	46.87**	23.54	1.87	0.83	189.00	1.83	2.09	3.80	1.07	0.00
Palghar-2	91.83	1.53	6.30**	94.41	1.47	30.70**	23.21	1.67	1.08	191.00	1.57	42.38**	3.62	1.41	-0.02
Ratnagiri-5	91.33	1.50	3.66*	96.70	2.35	27.85**	24.56	0.01	2.14	180.25	0.34	75.88**	3.69	0.81	0.02
Ratnagiri-24	89.33	0.78	-0.42	93.78	-1.02	5.51**	24.89	-0.12	3.36*	180.33	0.33	13.89**	3.59	0.72	0.08
Karjat 184	90.25	0.99	1.97	98.72	-2.27	36.97**	22.28	-0.20	0.56	179.33	0.01	-19.19**	3.61	0.78	0.05

* and ** significant at p- 0.05 and p-0.01 respectively, Xi- mean, bi-regression coefficient and S^2di-deviation from the regression

The divergence from regression for days to 50 per cent flowering was highly significant in all the varieties except Ratnagiri 24 and Karjat 184. It revealed that, Ratnagiri 24 is stable variety for earliness. For plant height, the divergence from regression was highly significant in all the varieties under study. Similar results reported by Sarawgi *et al.* (2000).

The divergence from regression for panicle length was non-significant in all the varieties except Ratnagiri 24. The data showed that (Table 2), highest panicle length with regression coefficient near unity and low S^2di value for Palghar 1 (Xi-23.54, bi- 1.87 and S^2di-0.83) followed by Palghar 2 (Xi-23.21, bi- 1.67 and S^2di-1.08) and Karjat 3 (Xi-24.83, bi- 1.66 and S^2di-1.18). It revealed that, these three varieties considered to be stable for panicle length over the seasons. Similar results reported by Singh *et al.* (1995).

For spikelets per panicle, the divergence from regression (S^2di value) was highly significant in all the varieties except Palghar 1. From Table 3, Karjat 7 exhibited highest number of spikelets per panicle (194.83) with regression coefficient near unity (1.41) and low deviation from regression (-12.56). Hence, Karjat 7 is presumed to be stable over the season for the same trait. Similar results reported by Kumar *et al.* (2010).

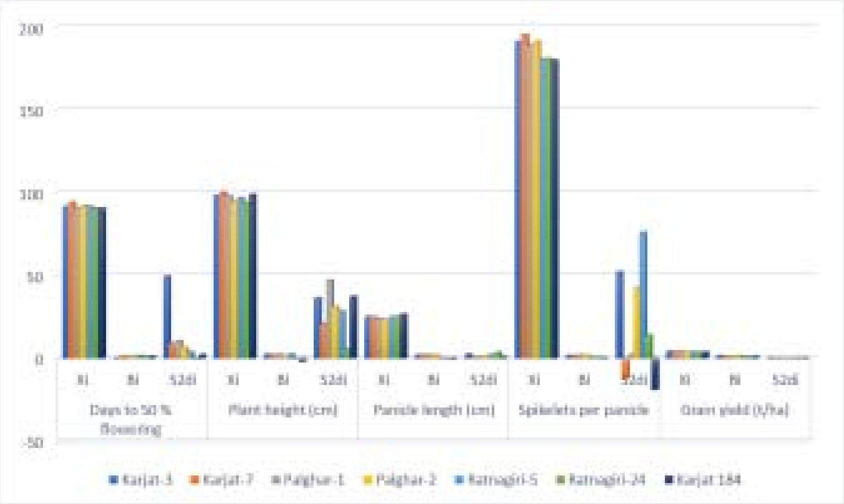

Figure 1: Stability parameters of yield and yield contributing traits in rice

All the varieties showed non-significant deviation from regression for grain yield. The data of grain yield (t/ha) showed that (Table 2), the regression coefficient near unity and zero (approximately) S^2di value with highest grain yield (t/ha) for Karjat 3 (Xi-3.89, bi- 1.27 and S^2di-0.07) followed by Palghar 1 (Xi-3.80, bi- 1.07 and S^2di-0.00), Karjat 7 (Xi-3.75, bi- 0.94 and S^2di-0.00), Ratnagiri 5 (Xi-3.69, bi- 0.81 and S^2di-0.02), Palghar 2 (Xi-3.62, bi- 1.41 and S^2di--0.02), Karjat 184 (Xi-3.61, bi- 0.78 and S^2di-0.05) and Ratnagiri 24 (Xi-3,59, bi- 0.72 and S^2di-0.08). It revealed that, these all the varieties opined to be stable for grain yield over the seasons. Similar results reported by Kumar *et al.* (2010), Reddy and Choudhary (1991), Singh *et al.* (1995) and Vijaya Lakshmi (2014).

ILLUSTRATION

Karjat 7, Karjat 184 and Palghar 1 are ideally adaptable, stable and may be recommended for cultivation for *kharif* season in north konkan region of Maharashtra state.

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IRC/TM-1/PP-83

FREQUENCY DISTRIBUTION STUDY OF GRAIN YIELD AND QUALITY TRAITS IN RICE

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Rice is food grain crop of global importance with special preference in Asian countries. India was the largest exporter of rice in 2017-18 followed by Thailand and Vietnam and Pakistan. As consumer preferences in Asia and all over the world are diverse due to varied demographics and culture, defining uniform attributes to capture regional grain quality preferences becomes more challenging (Butardo *et al*., 2019). Skewness refers to asymmetry of the frequency distribution curve. In a normal distribution, skewness is zero. Skewed distribution towards positive indicating more proportion of segregants present in low end of distribution and negative indicating more segregants present in higher end of distribution. Kurtosis is a measure of how flat the top of a symmetric distribution when compared to normal distribution of same variance. A normal distribution has kurtosis exactly zero is called mesokurtic. A distribution of kurtosis with less than zero is called platykurtic. A distribution of kurtosis with more than zero is called leptokurtic.

MATERIALS AND METHODS

This experiment was carried out at the Department of Plant Breeding and Genetics of Agricultural College and Research Institute, TNAU, Madurai. The F_2 generation of ASD 16/Improved Pusa Basmati 1 (cross 1), ASD 16/Improved Samba Mahsuri (cross 2), ADT 37/RNR 15048 (cross 3) and ADT 37/Improved Samba Mahsuri (cross 4) were raised. Seven yielding contributing traits *viz.*,Days to first flowering, plant height, number of productive tillers per plant, panicle length, flag leaf length, hundred grain weight, single plant yield and Fifteen grain quality traits *viz*., hulling percentage, milling percentage, head rice recovery, kernel length, kernel breadth, kernel L/B ratio, milled rice length, milled rice breadth, kernel length after cooking, kernel breadth after cooking, linear elongation ratio, breadthwise expansion ratio, alkali spreading value, gel consistency and amylose content were observed.

RESULTS AND DISCUSSION

The genetics of the trait in segregating generation can be easily understood by skewness and kurtosis. To get maximum genetic gain, intense selection is required from the existing variability. Kurtosis is a measure of the peakness of the probability distribution.

In grain yield and yield contributing traits, a positive and significant skewness was observed for days to first flowering in all the four crosses which indicated that early flowering segregants were obtained and selection can be done for earliness.

For panicle length, negative significant skewness was recorded in cross 1 which implied that more segregants having high panicle length was distributed in the population and significant negative skewness was obtained for flag leaf length in cross 4 and hundred grain weight in cross 1 which indicated that more segregants having high flag leaf length and hundred grain weight was distributed in the population.

Regarding kurtosis of grain yield contributing traits, wide range of variability was observed for days to first flowering in all the four crosses. Significant and leptokurtic nature of distribution was recorded for plant height in cross 2 which indicated that distribution of segregants for plant height was widely distributed.

Number of productive tillers per plant in cross 2, cross 3 and cross 4 showed platykurtic nature of distribution. Panicle length in cross 3 and cross 4, number of filled grains per panicle in cross 3, hundred grain weight in cross 1 and single plant yield in all the four crosses showed significant platykurtic. Parents involved in these crosses were highly contrasting type for yield and yield contributing traits. Hence, wide ranges of segregants were obtained in all the four crosses for yield and yield contributing traits.

For grain quality traits, negative significant skewness was obtained for kernel L/B ratio and milled rice length in cross 1 which indicated that segregants with high kernel L/B ratio and high milled rice length were obtained from this population. Positive significant skewness was observed for milled rice breadth in cross 3 indicating more segregant having less kernel breadth was distributed. In cross 1, negative significant skewness was obtained for kernel length after cooking which indicated that more segregants with high kernel length after cooking were obtained in this cross. It may be due to the male parent of that cross which was Improved Pusa Basmati 1 having high length wise expansion during cooking.

In kurtosis, Platykurtic nature of distribution was obtained for breadth wise expansion ratio in cross 1, kernel L/B ratio in cross 2, milled rice length and kernel breadth after cooking in cross 3 and kernel length after cooking in cross 4 which indicated that wide range of distribution was recorded for these traits. Hence, intense selection on these traits will give high grain quality segregants.

CONCLUSION

In frequency distribution studies, days to first flowering showed positive significant skewness and platykurtic nature of distribution in all the four crosses. Hence, early flowering segregants were obtained in all the four crosses. In grain quality traits, less kernel breadth segregants was distributed and intense selection for this trait will give slender grain type segregants.

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IRC/TM-1/PP-84

GENETIC VARIABILITY ANALYSIS FOR YIELD AND GRAIN QUALITY CHARACTERS IN SLENDER GRAIN RICE (*ORYZA SATIVA* L.)

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Rice is one of the major food grain crops in the world, particularly in Asian countries. The current rate of population growth of India (annually 1.09%) would set an annual requirement of rice of about 120 million tons by 2030 and 140 million tons by 2050. There is possibly little hope to allocate additional land for growing rice as the total cultivable area is diminishing day by day due to increased requirements for basic infrastructure like housing, roads; industry etc. Therefore, the task of increasing rice production to meet the anticipated demand is quite challenging.

In recent decades as the purchasing power of people have increased, demand for high-quality rice is continuously on rise. Quality rice is not only in big demand for domestic consumption, but also have great export potential and can earn a lot of foreign exchange for the country. The milling percentage, hulling percentage, grain dimensions and various cooking qualities such as gelatinization temperature, gel consistency and amylose-content constitutes the quality traits in rice. Like grain yield, quality is also not easily amenable to selection due to its complex nature. Therefore, efforts to enhance rice productivity with keeping grain quality must receive top priority. Keeping in view of the above perspectives the present experiment was carried out to estimate the genetic variability parameters for various yield attributing traits and quality traits in rice.

MATERIALS AND METHODS:

The present experiment was carried out using 32 genotypes (including 3 check varieties) from the experimental materials of SYT (Slender Grain) at O.U.A.T., Bhubaneswar. The experimental materials were put in a RBD Design with two replications. Observations were recorded for nine different yield-attributing metric traits as well as nine important grain quality traits.

RESULTS AND DISCUSSION:

From the analysis of variance, it was observed that there exist high significant differences among the test genotypes for all the morphological characters under study. The mean sum of squares due to genotypes was significant for all the characters, indicating ample scope for selection of different quantitative characters for rice improvement. In general, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) suggesting the influence of environment on the expression of the characters. Among all the characters studied, GCV ranged from 6.06 for days to 50% flowering to 23.32 for no. of filled grains/panicle and PCV ranged from 6.12 for days to 50% flowering to 23.99 for no. of filled grains/panicle. High PCV & GCV was observed for number of filled grains/panicle (23.99, 23.32) and moderate for flag leaf area (19.40, 18.21), grain yield (18.75, 17.82), 100-grain weight (13.47, 13.40), plant height (11.68, 11.21) and number of effective tillers/plant (13.98, 9.73).

All the characters showed high heritability except no. of effective tillers/plant which showed moderate heritability. A high degree of heritability estimates was associated with high degree of genetic advance for filled grains per panicle, flag leaf area, grain yield, 100-grain weight indicating the presence of

Table 1. Mean & Range of nine grain quality characters for the 32 genotypes under study

Genotypes	Kernel Length (mm)	Kernel Breadth (mm)	L/B Ratio	Grain Type	Head Rice Recovery %	Milling %	Hulling %	Amylose Content %	Alkali Spreading Value	Gel Consistency (mm)
OR2659-5	5.26	1.63	3.22	SS	50	67	76	23.1	3	49
OR2659-7	5.3	1.69	3.13	SS	52	67	78	22.65	4	50
OR2674-13	5.41	1.65	3.27	SS	63	68	78	21.22	3	55
OR2674-14-1	6.28	1.52	4.13	LS	48	68	78	22.5	3	51
OR2675-1-1	6.4	1.73	3.69	LS	55	67	75	23.02	4	47
OR2675-1-2	6.49	1.69	3.84	LS	55	67	78	19.57	4	59
OR2675-2-1	6.57	1.6	4.1	LS	46	64	74	21.67	7	53
OR2675-2-2	6.48	1.6	4.05	LS	47	62	74	21.82	7	54
OR2675-2-3	6.27	1.5	4.18	LS	45	66	75	22.12	4	50
OR2675-2-4	6.48	1.61	4.02	LS	45	65	75	21.67	7	52
OR2675-2-5	6.53	1.5	4.35	LS	50	65	75	22.2	7	55
OR2675-2-6	6.57	1.6	4.1	LS	48	66	75	21.67	4	57
OR2675-3-1	6.29	1.61	3.9	LS	44	66	76	19.5	3	60
OR2675-3-2	6.52	1.85	3.52	LS	48	69	79	20.3	3	61
OR2675-4-1	6.38	1.6	3.98	LS	42	61	73	19.95	4	61
OR2675-5-1	5.88	1.66	3.54	SS	55	64	78	21.37	3	57
OR2675-5-2	6.47	1.6	4.04	LS	50	63	76	21.52	3	58
OR2675-6-4	5.82	1.55	3.75	SS	46	61	76	21.3	4	59
OR2675-6-7	6.23	1.75	3.56	LS	40	65	75	23.25	4	49
OR2676-1-1	6.23	1.5	4.15	LS	44	63	75	21.9	3	58
OR2676-1-2	6.08	1.6	3.8	LS	50	65	75	22.72	3	51
OR2676-1-4	6.17	1.53	4.03	LS	42	63	75	21.22	4	56
OR2676-2-3	6.34	1.58	4.01	LS	46	60	78	21.9	3	57
OR2676-2-4	6.19	1.81	3.41	LS	45	64	76	20.77	3	59
OR2676-2-5	6.12	1.46	4.19	LS	54	62	77	20.4	3	60
OR2676-2-6	6.2	1.45	4.27	LS	44	63	74	20.7	3	59
OR2676-3-1	6.11	1.44	4.24	LS	46	65	76	19.5	4	60
OR2676-3-2	6.33	1.51	4.19	LS	50	61	76	19.65	5	59
OR2676-4-2	6.1	1.55	3.73	LS	49	65	76	19.27	4	61
Ranidhan	5.1	1.96	2.6	MS	48	66	76	19.72	3	61
Sambamahsuri	4.96	1.77	2.8	MS	50	63	75	24.1	4	63
Jajati	5.39	1.85	2.91	MS	36	67	77	19.72	6	59
Range Max.	6.57	1.96	4.35		63	69	79	24.1	7	63
Range Min.	4.96	1.44	2.6		36	60	73	19.27	3	47
Mean	6.09	1.62	3.77		47.90	64.62	75.93	21.31	4.03	56.25

**SS- short slender, LS- long slender, MS- medium slender

additive gene effect and hence selection based on phenotypic performance would be effective.

Grain yield showed moderate PCV & GCV, high heritability and genetic advance indicating that it is a simply inherited trait possessing additive gene effects and selection based on phenotype will be effective. The plot yield varied from 21.24 q/ha in OR 2674-14-1 to 51.22 q/ha in OR2676-2-3 with overall mean of 37.37 q/ha. Filled grains/panicle showed high PCV, GCV, heritability and genetic advance indicating that it is a simply inherited trait possessing additive gene effects and selection based on phenotype will be effective. The observed range for no. of filled grains/panicle was 96.15-303.00 and the overall mean was 187.85.

The range of variability for the grain physical characters of 32 test genotypes was, kernel length 4.96 mm to 6.57 mm, kernel width 1.44 mm to 1.96 mm, kernel L/B ratio 2.6 to 4.35. Most of the genotypes were long-slender grain type with kernel length e”6 mm and L/B Ratio e”3.0. The range of variability for HRR, milling %, hulling % was from 36% to 63%, 60% to 69%, and 73 % to 79 % respectively. Most of the genotypes had intermediate amylose content ranging from 19.27% to 24.1% and an average of 21.3%. It indicated that most of the genotypes would cook dry and fluffy and will have moderate to high volume expansion upon cooking. Most of the genotypes had intermediate alkali spreading value of 3 or 4, which corresponds to intermediate gelatinization temperature of (70-74 ºC). It indicated that rice would cook at a moderate pace and would take less to moderate time to cook. The overall mean gel length was 56.25 mm with the range varying from 47 mm to 63 mm corresponding medium to soft gel consistency. It indicated that rice would cook soft initially and would take more time to get hardened.

On the basis of yield the genotypes OR2676-2-3, OR2675-6-7, Ranidhan, OR2659-7, OR2676-2-6 were found promising and they also showed appreciable, if not best, grain quality characters.

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RATOON RICE (*Oryza sativa* L.) GENETIC VARIABILITY STUDIES FOR YIELD, ITS COMPONENTS AND QUALITY TRAITS

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Rice (*Oryza sativa* L.) is one of the staple cereal food crops of India. About 90% of the world's rice is grown and consumed in Asia. According to the projections made by the Population Foundation of India, the country's population will be 1546 million by the end of 2030 and 1824 million by the end of 2050. It is estimated that the demand for rice will be 121.2 million tonnes by the year 2030 and 137.3 million tonnes by the year 2050. (CRRI -VISION 2050). Due to various socio-economic constraints, a chance of bringing more area under rice cultivation is very remote. Hence, to achieve the target of increased rice production, it requires raising the production per unit area. Emphasis is being diverted towards the maximum utilization of land by producing more rice yield per unit area per unit time for which there is a need to improve different traits related to grain yield. Hence to achieve the target of increased rice production, it requires raising the production per unit area. Emphasis is being diverted towards the maximum utilization of land by producing more rice yield per unit area per unit time for which there is a need to improve different traits related to grain yield. Hence, ratooning, the ability of the rice plant to regenerate new panicle-bearing tillers after harvest, could be a practical approach to increase rice production per unit area and per unit time. Agronomic practices such as harvesting main crop at correct stage and at optimum cutting height were found to influence ratoon crop performance (Chauhan *et al.* 1985). Ratooning ability is a potentially important but complicated varietal character. Considerable progress has been made in the field of genetics of quantitative and qualitative traits in this crop, but not much had been accomplished with regard to inheritance of ratooning ability. It is imperative, that enhanced ratoon rice crop yield is totally dependent upon the ratooning ability. The adaption of hybrids /varieties towards the improvement of the ratooning trait can contribute to increase production and productivity (Mishra, 2001), by developing high yielding varieties, which requires a thorough knowledge of genetic variation in yield contributing characters. Observed variability is a combined estimate of genetic and environmental causes whereas genetic variability alone is heritable. Moreover, estimates of genetic variability across different environments helps to exploit complete genetic variability to exercise selection for development of yield contributing traits.

OBJECTIVE

The success of any breeding programme depends upon the quantum of genetic variability present in the population. In addition to the genetic variability, knowledge on heritability and genetic advance helps the breeder to employ the suitable breeding strategy. Therefore, it is necessary to have knowledge of genetic variability, heritability and genetic advance present in the available genetic material.

METHODOLOGY

Twenty popular varieties (varieties grown by farmers + pre released cultivars), were used for

Table 1. Mean performance of ratoon crop of 20 varieties in rice (*Oryza sativa* L.) for yield, yield components traits

Varieties	DFF	DM	PH (cm)	TNTP	NRTP MCT	NVBA HMC	TEB TP	NRPT PMCPT	PL (cm)	NGPP	TW (g)	LAI	GYPP(g)
MTU 1121	51.67	81.67	104.64	9.00	77.02	11.00	7.00	75.19	24.82	162.20	18.34	1.69	19.51
MTU 1001	45.33	71.67	110.87	11.67	100.00	13.00	6.33	79.17	21.64	125.53	21.20	1.70	18.98
MTU 1075	55.00	86.67	110.60	10.00	71.33	11.33	5.67	68.52	23.33	166.50	18.92	1.78	22.22
MTU 3626	43.67	68.00	90.55	4.33	43.00	7.67	2.33	31.22	18.37	109.50	22.62	1.97	5.68
MTU 7029	51.00	81.33	98.65	9.00	77.27	10.00	6.00	72.22	22.91	135.06	18.04	2.34	18.25
MTU 1061	55.00	88.00	111.74	9.67	76.71	12.00	8.67	77.22	23.32	153.67	18.61	2.41	21.89
MTU 1064	52.33	86.33	110.56	10.33	86.25	12.67	8.20	87.93	23.66	143.50	18.38	2.29	26.07
MTU 2077	47.67	75.67	108.06	5.00	57.87	6.67	2.67	46.67	25.05	123.10	16.96	1.83	5.87
MTU 2716	45.00	73.00	107.38	7.33	66.21	9.33	3.33	38.42	21.23	129.23	19.41	2.40	9.36
MTU 1140	53.33	81.00	111.42	8.67	77.78	10.33	7.33	84.72	22.02	153.63	21.10	2.15	24.01
MTU 1112	56.00	91.00	116.06	9.00	69.29	11.00	4.33	65.08	22.24	181.10	15.48	2.48	9.68
MTU 4870	48.67	78.33	112.79	9.67	75.03	11.33	3.67	57.94	22.36	144.80	19.52	3.03	12.24
BPT 3291	45.33	73.00	93.87	9.33	93.33	11.33	5.67	81.35	21.17	158.49	19.76	1.72	17.63
BPT 5204	49.00	79.33	90.36	9.00	72.86	10.00	4.00	52.38	20.25	181.50	15.39	2.11	6.71
PLA 1100	50.33	81.33	96.59	7.00	67.88	8.33	4.67	61.31	21.52	152.10	17.46	2.23	14.98
MTU 1166	49.00	79.00	111.17	9.67	74.66	11.67	4.33	59.72	22.75	167.12	15.21	1.91	8.30
MTU 1078	48.67	77.67	94.32	8.33	72.74	11.00	3.33	45.24	20.92	136.47	14.96	2.31	9.28
MTU 2067	46.67	75.00	108.00	9.00	71.31	11.00	4.00	61.11	24.68	99.18	19.56	1.83	7.05
MCM 100	51.00	82.00	104.71	9.33	75.43	10.67	7.00	72.59	22.09	167.00	18.96	2.00	18.49
MTU 1071	50.00	80.33	115.04	9.00	67.40	9.67	5.33	69.64	24.31	186.60	16.51	2.45	16.46
Overall													
Mean	49.73	79.52	105.37	8.72	73.67	10.50	5.19	64.38	22.43	148.81	18.32	2.13	14.63
C.V.	2.07	3.45	3.03	13.78	14.75	13.48	14.40	16.11	3.03	6.07	2.65	12.33	8.14
S.Em	0.59	1.58	1.84	0.69	6.27	0.82	0.43	5.99	0.39	5.21	0.28	0.15	0.69
C.D. 5%	1.70	4.53	5.28	1.98	17.96	2.34	1.24	17.14	1.12	14.93	0.80	0.43	1.97

DFF: Days to 50% Flowering; **DM:** Days to Maturity; **PH:** Plant Height; **TNTP:** Total Number of Tillers per Plant; **TEBTP:** Total number of Ear Bearing Tillers per Plant; **NRTPMCT:** Number of ratoon tillers as percentage of main crop tillers; **NRPTPMCPT:** Number of ratoon ear bearing tillers as percentage of main crop ear bearing tillers **NVBAHMC:** Number of vegetative buds after the harvest of main crop; **PL:** Panicle Length per plant; **NGPP:** Number of Grains Per Panicle; **TW:** Test Weight; **LAI:** Leaf Area Index at maximum tillering stage; **GYPP:** Grain Yield per plant

ratoonability screening (ratooning rate-Samson, 1980 and ratooning ability-Chauhan *et al.*, 1989) at APPRI & RARS, Maruteru, W.G district, A.P., were raised in randomized complete block design (RCBD), with three replications, each entry was planted in five rows of three meters length at 20 cm x 15 cm spacing during kharif and rabi as main crop and its ratoon crop, respectively. The main crop was harvested at the time of physiological maturity, leaving a stubble height of 30 cm above the ground level. Stubbles left over were then allowed to regenerate. Fertilizer application was one fourth of the main crop recommendations were applied to the ratoon crop two days after the harvest of the main crop. Observations were recorded on ten randomly chosen plants in the ratoon crop for twenty four quantitative characters of which 10 yield attributing characters viz., days to 50% flowering, days to maturity, plant height (cm), total number of tillers per plant, number of ear bearing tillers per plant, panicle length per plant (cm), number of grains per panicle, test weight (gm), leaf area index at maximum tillering stage, grain yield per plant; 6 physical quality traits such as hulling per cent, milling per cent, head rice recovery per cent, kernel length (mm), kernel breadth (mm), L/B ratio;

Table 1. Mean performance of ratoon crop of 20 varieties in rice (*Oryza sativa* L.) for quality traits

Varieties	HP	MP	HRR %	KL (mm)	KB (mm)	L/B ratio	KLAC (mm)	KBAC (mm)	KLER	VER	WU (ml)	GC (mm)	ASV (mm)	AC (%)
MTU 1121	77.85	73.10	70.48	5.42	1.95	2.79	9.36	2.50	1.73	5.20	170.83	55.91	3.06	21.37
MTU 1001	77.82	68.48	66.72	5.83	2.32	2.52	10.13	2.80	1.74	4.84	264.17	54.76	5.89	25.26
MTU 1075	75.18	69.29	65.02	5.54	1.88	2.96	10.04	2.55	1.82	4.74	222.50	60.00	2.89	24.07
MTU 3626	79.04	62.80	54.84	5.55	2.27	2.44	8.80	2.62	1.58	4.54	231.83	39.92	5.89	22.23
MTU 7029	78.98	68.29	65.24	5.22	2.16	2.42	9.29	3.34	1.78	4.73	170.83	45.58	3.00	22.76
MTU 1061	79.89	71.59	70.82	5.45	1.93	2.83	9.42	2.80	1.73	4.88	215.17	62.78	6.94	21.05
MTU 1064	79.39	73.97	69.50	5.33	2.14	2.49	9.15	2.48	1.72	4.89	184.17	62.15	6.83	24.92
MTU 2077	77.46	70.51	63.36	4.91	2.07	2.37	7.05	2.88	1.44	4.83	207.50	55.53	3.50	25.04
MTU 2716	79.93	73.18	70.36	5.54	1.98	2.81	9.20	2.62	1.66	4.73	160.17	57.14	3.00	21.65
MTU 1140	80.48	72.50	69.83	5.39	2.13	2.54	9.57	2.70	1.77	5.34	200.83	45.29	4.67	24.62
MTU 1112	78.69	72.20	67.00	4.95	1.82	2.72	9.53	2.46	1.93	4.89	199.17	48.90	4.39	24.91
MTU 4870	79.76	71.79	65.57	5.44	2.15	2.53	8.71	2.70	1.60	4.92	233.00	42.13	6.78	23.01
BPT 3291	78.62	72.91	69.53	5.32	2.03	2.62	9.21	2.51	1.73	4.56	202.50	52.69	4.00	24.20
BPT 5204	79.44	69.90	65.13	4.84	1.78	2.72	8.66	2.25	1.79	4.74	170.83	48.07	3.73	23.58
PLA 1100	78.79	73.95	63.71	4.89	2.05	2.39	8.34	2.73	1.71	4.79	170.00	49.10	3.11	20.49
MTU 1166	78.63	72.74	65.71	4.82	1.73	2.79	9.32	2.17	1.93	5.02	196.83	55.14	4.22	24.55
MTU 1078	76.65	74.42	68.29	4.90	2.06	2.37	8.07	2.38	1.65	4.76	159.67	47.98	2.89	24.27
MTU 2067	80.00	66.46	64.89	5.23	2.14	2.44	8.37	2.82	1.60	5.26	140.50	63.83	2.89	25.00
MCM 100	76.69	74.80	69.08	5.28	2.16	2.45	9.28	2.92	1.76	4.22	157.50	56.00	3.47	21.06
MTU 1071	77.03	71.76	66.70	4.95	1.93	2.56	8.68	2.36	1.76	5.14	220.17	60.88	3.11	24.48
Overall Mean	78.52	71.23	66.59	5.24	2.03	2.59	9.01	2.63	1.72	4.85	193.91	53.19	4.21	23.42
C.V.	1.66	1.54	1.94	3.33	2.90	5.02	1.39	2.24	3.45	6.48	3.41	2.73	3.49	4.37
S.Em	0.75	0.63	0.74	0.10	0.03	0.08	0.07	0.03	0.03	0.18	3.81	0.84	0.08	0.59
C.D. 5%	2.15	1.82	2.13	0.29	0.10	0.21	0.21	0.10	0.10	0.52	10.92	2.40	0.24	1.69

HP: Hulling percentage; **MP:** Milling percentage; **HRR:** Head Rice Recovery percentage; **KL:** Kernel Length; **KB:** Kernel Breadth; **L/B:** Kernel L/B ratio; **KLAC:** Kernel Length After Cooking (mm); **KBAC:** Kernel Breadth After Cooking (mm); **KLER:** Kernel Linear Elongation Ratio; **VER:** Volume Expansion Ratio; **WU:** Water Uptake (ml); **GC:** Gel Consistency (mm); **ASV**: Alkali Spreading Value; **AC (%):** Amylose Content (%).

and 8 cooking quality traits such as kernel length after cooking (mm), kernel breadth after cooking (mm), kernel elongation ratio, volume expansion ratio, water uptake value (ml), gel consistency, alkali digestion value and amylose contents. The data were subjected to statistical analysis and various genetic parameters such as PCV, GCV, heritability and genetic advance in ratoon crop to find the variability (Johnson *et al.*, 1955).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among all the 20 ratoon rice varieties for all the characters studied, indicating a high degree of variability in the material (Table 1 & 2). In the present study, the variation among genotypes was estimated as coefficient of variation (Table 3). The phenotypic coefficient of variance (PCV) was slightly higher in

Table 2. Analysis of variance for grain yield, yield component characters and quality traits of ratoon crop of 20 varieties in rice (*Oryza sativa* L.)

Source of variations	d.f	DFF	DM	PH (cm)	TNTP	NRTP MCT	NVBA HMC	TPTP	NRPTP MCPT	PL (cm)	NGPP	TW (g)	LAI	GYPP (g)
Mean sum of squares														
Replications	2	0.517	0.067	0.584	0.267	12.802	0.950	0.163	4.745	0.031	16.888	0.123	0.029	0.518
Treatments	19	37.389**	101.245**	205.102**	8.676**	417.627**	7.526**	9.955**	728.184**	8.359**	1709.850**	13.466**	0.354**	128.831**
Error	38	1.061	7.505	10.196	1.442	118.070	2.003	0.559	107.544	0.461	81.565	0.236	0.069	1.421
Total	59	38.967	108.817	215.882	10.385	548.499	10.479	10.677	840.473	8.851	1808.303	13.825	0.453	130.769

Source of variations	d.f.	HP	MP	HRR	KL(mm)	KB(mm)	L/B ratio	KLAC (mm)	KBAC (mm)	KLER	VER	WU(ml)	GC(mm)	ASV (mm)	AC (%)
Mean sum of squares															
Replications	2	0.650	0.104	0.114	0.011	0.002	0.012	0.002	0.000	0.001	0.053	6.679	0.114	0.002	0.014
Treatments	19	5.668**	26.787**	39.769**	0.257**	0.075**	0.095**	1.499**	0.213**	0.040**	0.205**	2993.241**	148.584**	6.322**	7.524**
Error	38	1.699	1.207	1.664	0.030	0.003	0.017	0.016	0.003	0.004	0.099	43.653	2.116	0.022	1.047
Total	59	8.018	28.098	41.548	0.299	0.080	0.124	1.517	0.216	0.044	0.357	3043.573	150.813	6.345	8.586

** Significant at 1% level

DFF: Days to 50% Flowering; **DM:** Days to Maturity; **PH:** Plant Height; **TNTP:** Total Number of Tillers per Plant; **TEBTP:** Total number of Ear Bearing Tillers per Plant; **NRTPMCT:** Number of ratoon tillers as percentage of main crop tillers; **NRPTPMCPT:** Number of ratoon ear bearing tillers as percentage of main crop ear bearing tillers **NVBAHMC:** Number of vegetative buds after the harvest of main crop; **PL:** Panicle Length per plant; **NGPP:** Number of Grains Per Panicle; **TW:** Test Weight; **LAI:** Leaf Area Index at maximum tillering stage; **GYPP:** Grain Yield per plant. **HP:** Hulling percentage; **MP:** Milling percentage; **HRR:** Head Rice Recovery percentage; **KL:** Kernel Length**; KB:** Kernel Breadth; **L/B:** Kernel L/B ratio; **KLAC:** Kernel Length After Cooking (mm); **KBAC:** Kernel Breadth After Cooking (mm); **KLER:** Kernel Linear Elongation Ratio; **VER:** Volume Expansion Ratio; **WU:** Water Uptake (ml); **GC:** Gel Consistency (mm); **ASV**: Alkali Spreading Value; **AC (%):** Amylose Content (%).

magnitude than genotypic coefficient of variance (GCV) for all the characters studied indicating the influence of environment on expression of these traits. Highest PCV and GCV (42.27 and 44.53) were exhibited by grain yield per plant, followed by total ear bearing tillers, alkaline spreading value and number of ratoon ear bearing tillers as percentage of main crop ear bearing tillers. Whereas moderate PCV and GCV was recorded for number of vegetative buds after the harvest of main crop, number of grains per plant, test weight, leaf area index, kernel breadth after cooking, water uptake and gel consistency. Total number of tillers per plant, Number of ratoon tillers as percentage of main crop tiller and total number of ear bearing tillers per plant, exhibited high PCV and moderate GCV. The rest of characters show low PCV and low GCV. The results are in accordance with the results reported by Allam *et al.* (2015).

Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. The estimates of heritability and genetic advance as per cent of mean were high for total number of tillers per plant, total number of ear bearing tillers per plant, number of ratoon ear bearing tillers as percentage of main crop ear bearing tillers, number of grains per plant, test weight, grain yield per plant, kernel breadth after cooking, water uptake, gel consistency, and alkaline spreading value indicating that these characters were less influenced by environment and governed by additive gene action

Table 3. Estimates of variability, heritability and genetic advance as per cent of mean for grain yield, yield components and quality traits of ratoon of 20 varieties in rice (*Oryza sativa* L.)

Character	Mean	Range		Coefficient of variation (%)		Heritability in broad sense (h^2_b)	Genetic advance (GA) (%)	Genetic advance as per cent of mean (GAM)
		Min	Max	Phenotypic (PCV)	Genotypic (PCV)			
DFF	49.73	43.67	56.00	7.30	7.00	91.90	6.87	13.82
DM	79.52	68.00	91.00	7.83	7.03	80.60	10.34	13.00
PH (cm)	105.37	90.36	116.06	8.23	7.65	86.40	15.44	14.65
TNTP	8.72	4.33	11.67	22.52	17.82	62.60	2.53	29.03
NRTPMCT	73.67	43.00	100.00	20.04	13.56	45.80	13.93	18.91
NVBAHMC	10.50	6.67	13.00	18.67	12.92	47.90	1.94	18.43
TEBTP	5.19	2.33	8.67	36.99	34.08	84.90	3.36	64.66
NREBTPMCEBT	64.38	31.22	79.17	27.54	22.34	65.80	24.03	37.33
PL (cm)	22.43	18.37	21.64	7.84	7.23	85.10	3.08	13.75
NGPP	148.81	99.18	186.60	16.79	15.66	86.90	44.75	30.07
TW (g)	18.32	14.96	22.62	11.77	11.46	94.90	4.21	23.01
LAI	2.13	1.69	3.03	19.01	14.48	58.00	0.48	22.70
GYPP (g)	14.63	5.68	26.07	45.27	44.53	96.80	13.21	90.24
HP	78.52	75.18	80.48	2.21	1.47	43.80	1.57	2.00
MP	71.23	62.80	74.80	4.38	4.10	87.60	5.63	7.90
HRR%	66.59	54.84	70.82	5.69	5.35	88.40	6.90	10.37
KL (mm)	5.24	4.82	5.83	6.21	5.25	71.30	0.48	9.12
KB (mm)	2.03	1.73	2.32	8.13	7.60	87.30	0.30	14.63
L/B ratio	2.59	2.37	2.96	8.00	6.23	60.60	0.26	9.99
KLAC (mm)	9.01	7.05	10.13	7.93	7.81	96.90	1.43	15.83
KBAC (mm)	2.63	2.17	3.34	10.29	10.04	95.30	0.53	20.19
KLER	1.72	1.44	1.93	7.25	6.37	77.30	0.20	11.54
VER	4.85	4.22	5.34	7.55	3.87	26.30	0.20	4.09
WU (ml)	193.91	140.50	264.17	16.53	16.17	95.70	63.21	32.60
GC (mm)	53.19	39.92	63.83	13.42	13.14	95.80	14.09	26.49
ASV (mm)	4.21	2.89	6.94	34.58	34.40	99.00	2.97	70.50
AC (%)	23.42	20.49	25.26	7.64	6.27	67.30	2.48	10.60

DFF: Days to 50% flowering; **DM:** Days to maturity; **PH:** Plant height; **TNTP:** Total number of tillers per Plant; **TEBTP:** Total number of Ear Bearing Tillers per Plant; **NRTPMCT:** Number of ratoon tillers as percentage of main crop tillers; **NREBTPMCEBT:** Number of ratoon ear bearing tillers as percentage of main crop ear bearing tillers; **NVBAHMC:** Number of vegetative buds after the harvest of main crop; **PL:** Panicle Length per plant; **NGPP:** Number of Grains Per Panicle; **TW:** Test Weight; **LAI:** Leaf Area Index at maximum tillering stage; **GYPP:** Grain Yield per plant. **HP:** Hulling percentage; **MP:** Milling percentage**; HRR:** Head Rice Recovery percentage; **KL:** Kernel Length; **KB**: Kernel Breadth; **L/B**: Kernel L/B ratio; **KLAC:** Kernel Length After Cooking (mm); **KBAC:** Kernel Breadth After Cooking (mm); **KLER:** Kernel Linear Elongation Ratio; **VER:** Volume Expansion Ratio; WU: Water Uptake (ml); **GC:** Gel Consistency (mm); **ASV:** Alkali Spreading Value; **AC (%):** Amylose Content (%).

which may be exploited through breeding methods involving simple selection like pedigree method, mass selection, ear-to-row method, etc. These findings were in agreement with the findings of Keya *et al.* (2015) and Sameera *et al.* (2015).

High heritability coupled with moderate genetic advance as per cent of mean was observed for Days to 50% flowering, days to maturity, plant height, panicle length, head rice recovery, kernel breadth, kernel length after cooking, kernel elongation ration and alkaline content. Whereas milling percentage and length-breadth ratio expressed high heritability accompanied with low genetic advance indicating the role of both additive and non-additive gene actions in the inheritance of these traits. Moderate heritability coupled with moderate genetic advance as per cent of mean was observed for number of ratoon tillers as percentage of main crop tillers, number of ratoon ear bearing tillers as percentage of main crop ear bearing tillers and leaf area index. Moderate heritability coupled with low genetic advance as per cent of mean was observed for hulling percentage. These findings are corroborated by Keya *et al.* (2015) and Sameera *et al.* (2015).

CONCLUSIONS

Grain yield per plant exhibited high PCV and GCV indicating the role of additive gene action and can be improved by population improvement methods involving selection, intermating among selected ones and reselection may help to improve these traits besides exploiting the methods of heterosis breeding. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. The estimates of heritability and genetic advance as per cent of mean were high for total number of tillers per plant, total number of ear bearing tillers per plant, number of ratoon ear bearing tillers as percentage of main crop ear bearing tillers, number of grains per plant, test weight, grain yield per plant, kernel breadth after cooking, water uptake, gel consistency, and alkaline spreading value indicating that these characters were less influenced by environment and governed by additive gene action which may be exploited through breeding methods involving simple selection like pedigree method, mass selection, ear-to-row method, etc.

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