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IDENTIFICATION OF GENOMIC REGIONS LINKED TO DORMANCY RELATED TRAITS USING BULK SEGREGANT ANALYSIS IN RICE (ORYZA SATIVA L.)

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A total of 119 $F_{6.7}$ recombinant inbred lines of a cross between BPT 2231 (non-dormant parent) and MTU 1001 (dormant parent) was analyzed to identify the markers associated with dormancy. Parental polymorphism survey with 188 SSR markers revealed 10 polymorphic markers between the parents. The bulk segregant analysis results revealed that four markers showed polymorphism between these bulks. The association of putative markers viz., RM346, RM22565, RM7051 and RM10793 identified based on DNA pooling from selected segregant was analyzed by Single Marker Analysis (SMA). The results of SMA revealed that RM22565 on chromosome 8 showed significant association with germination (%) at 5 days after harvesting indicating that the chromosomal region linking to marker RM 22565 on chromosome 8 may

be associated with dormancy. Out of the 4 polymorphic markers used in the present study, RM346 is notified as a dormancy linked marker from previous studies. The other 3 markers viz., RM22565, RM7051 and RM10793 identified as dormancy linked markers in the present study needs further validation on alternative set of population or a set of germplasm lines for their further utilization in the marker assisted breeding programme. Based on germination percentage, physiological parameters and genotyping studies, the lines SD 3, SD 12, SD 15 and SD 68 may be used in future breeding programme as donor parents for seed dormancy.

Keywords: SSR markers, Bulk segregant analysis, Single marker analysis

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MAPPING OF QTLS FOR ZINC DEFICIENCY TOLERANCE IN RIL POPULATION OF RICE (ORYZA SATIVA L.)

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Rice is one of the important cereal crops consuming more than half of the world's population and 95% of it is being produced and consumed in Asia. Zinc (Zn) deficiency is one of the major abiotic stresses limiting rice growth and its production. Among the cereals, rice is considered as highly sensitive to Zn deficiency and it is the most important micronutrient, restricted the rice growth and its yield. Zn deficiency in rice plants causes various symptoms that usually appear 2 to 3 weeks after transplanting (WAT) rice seedlings. Zn deficiency leads to develop brown blotches and streaks in leaves that may ultimately fuse to cover older leaves entirely, plants remain stunted and in severe cases may die. Plants with severe Zn deficiency undergo symptoms like leaf bronzing with stunting growth and ultimately leads to low grain yield. Zn deficiency is associated with a diverse range of soil conditions with high pH (>7.0) alkaline soil, low availability of Zn content, prolonged submergence in water (Neue and Lantin, 1994). Use of RIL populations for mapping of QTLs is considered to be highly advantageous due to the facts that multiple selfing events increase the recombination events which permit a finer mapping of QTLs. Once the RILs are established having fixed genotypes as homozygote, these lines are often repeatedly used for investigating QTLs of diverse phenotypes under different environments provided the parents involved were contrasting for the trait of interest. Therefore, the aim of this study was to

determine the response of RIL population with regard to Zn deficiency tolerance under Zn deficient soil conditions to identify and map QTLs associated with it using SSR markers.

OBJECTIVES

1. Estimation of zinc concentration in RIL mapping population.

2. Construction of genetic linkage map and identification of genomic regions having QTL for zinc deficiency tolerance.

METHODOLOGY

The experimental materials consisted of 236 RILs (F_{τ}) mapping population developed from a cross between Kinandang Patong and A69-1. The field screening under Zn deficiency was carried out at two locations viz., BHU, Varanasi, India and Acharya Narendra Deva University of Agriculture & Technology (NDUAT), Ayodhya. The experiment was laid out in an alpha lattice design with two replications at both the locations. The RILs mapping population and their parents were evaluated for traits associated with zinc deficiency viz., leaf bronzing score, plant mortality, root/ shoot zinc concentration for each replications at both the locations and their means were used for the statistical analysis in a Zn deficient field condition. The leaf bronzing (LB) was scored visually five times at 3 WAT and at late vegetative stage through 1-9 scales, along with parents and two sensitive checks. The total



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genomic DNA was isolated from the leaf of twentyone days old seedling using the method described by Doyle and Doyle, (1990) with some modifications. DNA of the two parents, Kinandang Patong (sensitive to Zn deficiency) and A69-1(tolerant to Zn deficiency) was extracted for polymorphism detection using 697 number of SSR markers. 81 SSR markers were polymorphic with the parents and used for genotyping the 236 RILs mapping population. Linkage maps were constructed using MAPMAKER/EXP version 3.0b (Lander et al., 2009) following Kosambi Function (Kosambi, 1944). Linkage between the markers and the QTL was detected by a statistical test called the Logarithm of Odds (LOD) score method. QTLs were detected by Composite Interval Mapping (CIM) procedure of Windows QTL Cartographer v.2.5 software (Wang et al., 2006).

RESULTS

The results of the analysis of variance (ANOVA) for, Varanasi and, Ayodhya revealed significant variation among the RILs for all the associated traits with Zn deficiency (P<0.01). Out of 697 SSR markers, 81 markers showed parental polymorphism however, only 74 markers were included in constructing a linkage map and 7showed unlinked of the remaining markers to the linkage map. About 11.62% of primers were exhibited parental polymorphism. The linkage map covered 1353.3 cM distance employing Kosambi mapping function, resulting in an average marker interval of 18.28 cM. QTL analysis was performed using WinQtlCart 2.5 for identification of QTLs related to Zn deficiency tolerance. The association of molecular markers and phenotypic data was performed using Composite interval mapping analysis with 3 as LOD threshold for detecting a QTL. A total of five [major (>10 R²) and one minor (<10 R²)] QTLs at Varanasi and four major

and one minor QTLs at Ayodhya for Zn deficiency tolerance with Logarithm of odd (LOD) threshold value higher than 3 were identified. A total of six QTLs at Varanasi and five QTLs at Ayodhya by CIM methods governing leaf bronzing, plant mortality, root Zn concentration and shoot Zn concentration were detected across two locations. These QTLs were located mostly in chromosome 2, 4 and 6.

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Leaf bronzing scored (1-9) was conducted five times at seedling to late vegetative stage in 236 RILs along with parents and two sensitive checks, IR-74 and Dular. Among the 236 RILs, 33 lines were highly tolerant at, Varanasi and 35 lines at, Ayodhya showing no symptoms of Zn deficiency and healthy growth with leaf bronzing score of 1 (Growth and tillering nearly normal; healthy). While 17lines and 21 lines which scored (9) were almost dead or dying at , Varanasi and , Ayodhya respectively.

CONCLUSION

The present study could identify major QTLs on chromosome 4 for all the zinc deficiency tolerant traits under studied in both the locations and one major QTL on chromosome 6 at BHU location. The identified QTLs were found to be novel and introgression of these new QTLs into elite rice breeding lines will be very promising.

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INTEGRATION OF C₄ PHOTOSYNTHETIC GENES FROM *SETARIA ITALICA* ENHANCES PHOTOSYNTHETIC EFFICIENCY OF C₃ RICE

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 C_4 plants are superior to C_3 plants in terms of photosynthesis, productivity and limiting photorespiration. Thus, higher nitrogen and water use efficiency, increased photosynthetic efficiency could be obtained by incorporating the C_4 photosynthetic genes in C₃ rice plants. Rice is one of the major food crops and thus yield potential of rice must be increased to fulfil the nutritional demand of world's rapidly growing population. Pyruvate orthophosphate dikinase [PPDK] and NADP-dependent Malic Enzyme [NADP-ME] are the two major chloroplastic genes in C_4 plants. These genes are tightly light-inducible, showed expression in green tissues, and their proteins products are involved in photosynthesis which converts light energy into sugar. In this study, PPDK and ME genes isolated from Setaria italica, a C₄ plant, were introduced to the C₃ Oryza sativa L.sp. Indica var. Naveen under the control of green tissue specific maize PPDK promoter through Agrobacterium mediated transformation. The developed rice transgenic plants would help us to understand the functionality of C_4 genes in rice and to further improve rice to develop climateready rice.

METHODOLOGY:

cDNA was prepared from the RNA samples of *Setaria italica* plant and PPDK and ME genes were amplified by reverse transcriptase PCR. Green tissue specific promoter ZmPPDKP and Nos terminator was cloned in binary vector along with PPDK and ME genes for the preparation of two distinct constructs (Figure.1A). Two individual constructs were transferred to rice calli for transgenic development. Screenings of transformed plants were done through PCR amplification. Expressions of transgenic plants were checked through real time PCR and stable gene integration was confirmed through Southern hybridisation. Physiological response of transgenic plants was analysed using Infra Red Gas Analyser as described by Kandoi et al., 2016.

RESULTS:

The semi quantitative real time PCR analysis showed that the desired PPDK and ME genes were successfully transcribed in their corresponding rice transgenic plant lines and had higher level of relative gene expression than in the control and vector control plants. The average PPDK enzyme activity were ~3 fold higher than untransformed plants. Similarly, the ME activity was ~2.6 fold higher in SiME carrying transgenic plants. The transgenic plant lines showed increased photosynthetic pigments (Fig1B), higher net photosynthetic rate (Fig1C), increased stomatal conductance and decreased internal CO₂ concentration. The CO₂ compensation point measured was lower than the control plants. The intrinsic water use efficiency of the transgenic plant lines was higher than the control and vector control plants. The chlorophyll fluorescence analysis indicated a declined Fv/Fm ratio and increased photochemical quenching in transgenic leaves. There was a considerable morphological and phenotypical variation seen among the transgenic plant lines as compared to non transgenic.

CONCLUSION:



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Fig 1: A. Schematic representation of Vector construct carrying PPDK and ME gene. B. Total chlorophyll accumulation of transgenic plant lines along with control and vector control plants. C. Net photosynthetic rate measured in the flowering stage of transgenic plants. *Asterisks* indicate the significant variance determined by statical analysis. (**P*<0.005, ***P*<0.001 and****P*<0.0001)

The transgenic plants with *PPDK* and *ME* genes were physiologically superior in terms of photosynthetic pigment accumulation, photosynthetic rate and related parameters compared to non transgenic.

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Indian Rice

GENERATING RICE MUTANTS FOR PEPC AND PPDK BY CRISPR/CAS9 MULTIPLEX GENOME EDITING

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INTRODUCTION AND OBJECTIVES

The CRISPR/Cas9 mediated genome editing has been demonstrated in several crops including rice. Rice provides food for more than half a billion population worldwide and serves as excellent model for functional genomics study. C4 plants are more efficient in terms of photosynthesis as compared to C3 rice by reducing photorespiration. PEPC (Phosphoenolpyruvate carboxylase) and PPDK (Pyruvate ortho-phosphate dikinase) are the two major photosynthetic genes involved in the C4 pathway. Although these genes are present in C3 rice, their functions and regulations are not understood and evaluated properly. Thus, we set out to perform targeted multiplex genome editing of PPDK and PEPC genes using CRISPR/Cas9 system to generate mutant rice plants. Analysis of mutants would help us to understand the exact role of PEPC and PPDK genes in rice plant and subsequently may assist in planning to improve photosynthetic efficiency.

METHODOLOGY

Ø PCR amplification of different fragments consisting of tRNA and gRNA using different sets of primers.

Ø Golden Gate Assembly of three different amplicons.

Ø Cloning of assembled product in pGEM-T vector.

Ø Clone confirmation by restriction enzymes and Sanger sequencing.

Ø Subcloning of assembled product into the binary vector.

Ø Agrobacterium mediated rice transformation.

RESULT AND DISCUSSION

In the present study, we have targeted two C4 pathways genes, namely PEPC and PPDK in rice through CRISPR/Cas9 multiplex genome editing tools. We have used PTG system (polycistronic tRNA-gRNA system) (Xie et al. 2015) for editing of PEPC and PPDK genes in rice. We have designed two guide RNAs for disrupting the PEPC and PPDK genes. For enhancing editing efficiency, we fused a tRNA upstream of each guide RNA. We assembled the tRNA-guide RNAs for the two targets through golden gate assembly. Successful assembly was validated through Sanger sequencing. Assembled product was cloned into binary vector harbouring Cas9 expression cassette (Figure



Figure 1a: Schematic representation of plant construct for *Agrobacterium* mediated plant transformation. Figure 1b: Selected calli on regeneration media. Figure 1c: Putative mutant rice seedling



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1a). Clone was confirmed through restriction digestion and Sanger sequencing. The binary vector was transformed into rice cultivar through *Agrobacterium* mediated transformation. *Agrobacterium* mediated plant transformation was performed using embryogenic callus as explants. Regenerated calli were subsequently transferred under light (16±8 hrs) (Fig1b), and putative germinated seedlings transferred into soilrite for hardening. (Fig1c) Screening of the plants are going on. Selected double and single mutant plants would be analyzed for physiological, biochemical and morphological parameters to ascertain the function of C3 PEPC and PPDK.

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PHYSIOLOGICAL CHARACTERIZATION OF TRANSGENIC RICE PLANTS DEVELOPED BY INTRODUCING CYTOSOLIC C₄ ENZYMES: CARBONIC ANHYDRASE AND PHOSPHOENOLPYRUVATE CARBOXYLASE

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INTRODUCTION AND OBJECTIVE:

Rice is the most widely consumed staple food for a large part of human population. Enhancement of photosynthesis in changing climate is crucial to increase yield potential of rice. Engineering C₄ photosynthetic traits into rice is one of the strategies to reduce photorespiratory loss and increase the radiation use efficiency to enhance photosynthesis that may lead to higher yield. Carbonic anhydrase (CA) plays a fundamental role in the photosynthesis of C_{4} plants, acting as the first enzyme in a pathway for the conversion of atmospheric CO₂ to HCO₃" which is then fixed by phosphoenolpyruvate carboxylase (PEPC) to produce C₄ acids. The transfer of these two key enzymes, CA and PEPC from C₄ plants to C₃ rice plants is thought to be primary step for improving the photosynthetic rate (Häusler et al., 2002).

METHODOLOGY:

CA gene was isolated from Sorghum bicolour and cloned in pBS-SK⁺ vector. SbCA was subcloned at downstream of the CaMV35S promoter of pBI121 vector to generate pBI121-CaMV35S-SbCA-NOS. Similarly, PEPC gene was isolated from Setaria italica, cloned in pTZ57R/T vector and further cloned at the downstream of the P_{ZmPPDK} promoter of pCAMBIA1301 to generate pCAMBIA1301-PZmPPDK-SiPEPC-nos construct. pCAMBIA1301 carrying both the gene constructs (Fig.1a and b) were transferred to LBA4404 separately which were used to infect the rice calli for development of transgenic plants. Integration and expression of transgene was confirmed by Southern hybridization and qRT PCR. Gas exchange parameters were measured in the fully expanded first leaf from the top of the plant at 50% flowering stage using a portable Infrared Gas Analyzer (IRGA) (LI-COR 6400XTportable photosynthetic system; Lincoln, NE).

RESULT AND DISCUSSION

In the present study, real time PCR analysis revealed the higher expression level of SbCA and SiPEPC in transgenic lines than in control plants. Photosynthetic pigment content, photosynthetic rate, light and CO₂ response curve were studied in CA and PEPC transgenic rice lines at flowering stage. Total chlorophyll accumulation was significantly more in some transgenic lines at flowering stage than control. IRGA data showed that the photosynthetic rate was significantly higher (11-17%) (Fig.1c) in transgenic plants than control. The net photosynthetic rate increased in the transgenic lines under high PAR > 1200 ìmol m^{"2}s^{"1} (Fig.1d) (Hu et al. 2012). The water use efficiency of transgenic plants was found to be significantly increased than control. More number of filled grains per panicles was obtained in SbCA and SiPEPC transgenic lines (26.19% and 23.86%, respectively). Total dry biomass increased up to 23% in transgenic CA and 27% in PEPC transgenic as a result of the increased tiller and panicle number per plant. Over all, the performance of the transgenic lines with CA and PEPC genes showed better performance in terms of photosynthesis and other physiological parameters. Both SbCA and SiPEPC transgenic rice



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Figure 1. (a) Schematic diagram and restriction map of the construct *CaMV35S-SbCA-NOS* (b) Schematic diagram of the gene construct P_{ZmPPDK} . *SiPEPC-NOS* (c) net photosynthetic rate observed at flowering stage of transgenic and control plants (d) Photosynthesis light response curve

lines showed higher radiation and water use efficiency. Overexpression of C4 *SbCA* and *SiPEPC* in transgenic rice plants enhanced the photosynthetic efficiency as well as showed better agronomic performance than the control non-transgenic plants.

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DECIPHERING SPECIFIC ROOT LENGTH (SRL) AND ROOT AVERAGE DIAMETER (RAD) INVOLVED TO COPE WITH WATER STRESS IN RICE (ORYZA SATIVA L.)

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Rice (*Oryza sativa* L.) is the most important primary crop associated with humid climate and cultivated nearly 44 Mha land (2018-19) (DES, 2019) in India. Different climate models predict that many rice grown areas will become drier in the coming decades (Rippke et al. 2016), exacerbating rice production weaknesses due to severe drought stress. To address these new challenges various strategies need to be developed. The design and distribution of root system can be seen as key factors for efficiently water uptake from deeper part of soil and thus managing the performance of rice production under drought stress.

Roots play a key role in anchoring the plant and absorb water and nutrients from the soil to control productivity (Uga et al., 2013). Plants can customize their root structure to accommodate different environments, including drought stress and survive accordingly (Jovanovic et al., 2010). Important root traits such as RDW/SDW, total root length (TRL), root surface area, root average diameter (RAD) and specific root length (SRL) are the key parameters associated with increased crop yield under drought stress (Fitter et al., 2002; Kadam et al., 2015). Thinner roots also enable for soil penetration ability than thicker roots and access the deeper soil water by resulting maximizes total root length (Wasaya et al., 2018). The results showed a complete information of root related traits at reproductive stage under both well watered and drought stress condition in rice. The main objective of this experiment is to characterize and evaluate the appropriate root parameters and to assess the variation of SRL and its related components which could be serving as the marker that could help in identification of tolerant genotypes under water stress.

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METHODOLOGY

The experiment was performed during the dry season -2019 at National Rice Research Institute, Cuttack (Odisha), India. Four rice genotypes, including two international popular checks (Sahabhagidhan as tolerant check and IR 64 as susceptible check) were taken for the establishment of experiment. The present experiment was performed in the pot containing 4 Kg of mixture including dried dust farm soil with farm yard manure (3:1 ratio) of 200 cm³ soil volume in a completely randomized design taking three replications. Drought stress was imposed to 15 of flowering by withdrawing the water and this situation continue until maturity stage with assured irrigation. Another set was maintained separately with well watered condition under the same climate. Sampling was done during flowering stage stress.

Roots without disturbing were taken from both the treatments in replication wise manner and washed by tap water repeatedly over a sieve. After washing the live roots were placed in iced water bath and immediately scanned using root scanner (Regent instrument Inc, LA 2400 scanner, EPSON). The analyzed roots were dried under oven at 60°C for 72 hours (Sandhu et al., 2017) and mean root dry weight was determined. The following are the important derived parameters based on computed data.

RESULTS

Under water stress different rice genotypes behaved different sensitivity limit through their root

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Figure 1. Root traits of 4 rice genotypes under well watered (WW) and water stress (WS) condition. Values shown are means of three biological replications \pm SE at the 5% level

performance. Our experimental findings showed that (Fig 1) under WS the tolerant check Sahabhagidhan able to maintain higher value of leaf water potential (-2.58MPa) followed by IC 516008 (-3.04MPa), where as susceptible check IR64 possessed lower value of WP (-4.17MPa) followed by Prasad (-4.49MPa). At the same time tolerant check Sahabhagidhan able to maintain higher value of RDW/SDW (0.269) followed by IC 516008 (0.239) while, IR 64 (0.069) and Prasad (0.121) had significantly (p<0.05) least amount of RDW/SDW under WS condition.

The genotype IC 516008 showed higher value of TRL (36843.25 cm) and SRL (4493.61 cm g⁻¹) with low RAD (0.46 mm) while, genotype Prasad was low in TRL (15227.15) and SRL (2978.87 cm g⁻¹) with higher RAD (0.60 mm). The check genotypes performed according to their sensitivity level (Fig 1). The genotypes having lower value of RAD possesses significantly (p<0.05) higher value of SRL and vice

versa under WS condition. With higher value of SRL and TRL the tolerant genotypes also possessed higher value of surface area and root volume compared to susceptible genotypes under WS condition to absorb water from deeper part of soil.

CONCLUSION

Morphological root traits such as total root length, root surface area, root volume, average root diameter and SRL showed strong differences between tolerant and susceptible genotypes. In the contrast to our findings, with the higher value of SRL, total root length, root surface area, root volume with lower root average diameter the genotypes IC 516008 would be superior genotype as compared with Prasad. Among these traits, SRL and average root diameter as a proxy to assign each root to a specific root order. SRL and average root diameter provides a new approach in rice plants under WS condition for promoting the root traits and establishing the individual genotypes. Again these

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two traits can improve our understandings towards different root function and maintain the accuracy by minimizing the errors with which our related root parameters can be predicted. Hence, SRL and average root diameter is the source of adaption to evaluate the genotypes under WS condition.

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GENOTYPE X PHOSPHORUS CONCENTRATION AND EXPRESSION PATTERN OF PHOSPHATE TRANSPORTERS IN RICE

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Phosphorus (P), an essential macronutrient, maintains proper symmetry of growth and development of plant. It is not only associated with several biochemical process, reproduction in plants but also forms the building block of most of the life biomolecules pointing its uniqueness. The non-renewability of phosphate reserve grims the scenario in this increasing population demand and intensive agriculture. To better understand the early response of genotypes to limitedphosphorus condition and the role of the phosphate transporter gene family in the presence of *PUP1* QTL, six genotypes were evaluated under low P condition.

METHOD

Three improved rice varieties such as Shabagidhan, PUP1 introgressed line IR64-Pup1 and IR64 and three land races Arupatham Kuruvai, Dular, and IC459373 were evaluated in different concentrations of P (0.5, 1, 2, 4, 6, 8 and 10 ppm) in hydroponics. Expression pattern of phosphate transporters were studied at 0.5, 4 and 10 ppm.

RESULTS

Trait and interactions of these traits were clearly distinguished among the various P rates. The shoot trait expression registered increased growth from 6.0 to 10.0 ppm of P. The major root-attributed traits in 0.5 ppm of P are significantly increased. In low P, maximum root length with shoot and root dry weight was observed in IC459373 than in Dular and IR64-Pup1 at 0.5 ppm of P. Among the 13 P transporter genes, PT1, PT2, PT6, and PT13 showed significant upregulation in IC459373, Dular, and IR64-Pup1.

CONCLUSION

The study indicated that the expression levels of the PUP1 and P transporter gene family at the early growth stages would be helpful in identifying superior donors to improve low-P tolerance in rice breeding program.

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SCREENING FOR DROUGHT RESISTANCE IN RICE (ORYZA SATIVA L.)

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Rice (Oryza sativa L.) consumed by ~50 % of the world's population, is one of the most globally important staple food crops (Shah et al. 2014) and it covers 9% of the earth's arable land. Drought stress is a major constraint to rice production and yield stability in the rainfed region (Evenson et al. 1996). Due to drought, there is an overall reduction of rice yield by 18 million tonnes at the global level (O'Toole, 2004). In Asia alone, it is estimated that a total of 20 million hectares of rice field both in upland and lowland conditions are drought-prone. In India drought is most prevalent in the eastern states viz ... Jharkhand, Odisha, and Chhattisgarh. In these areas, drought risk reduces productivity and leads to food insecurity (Pandey et al. 2008). Rice is particularly sensitive to drought stress during reproductive growth when slight stress can result in a drastic reduction in grain yield. However, drought adversely affects the growth of rice at all the stages, and the occurrence of drought during the early reproductive stage (anthesis) causes a significant loss of grain yield (Boojung and Fukai, 1996).

OBJECTIVES

1. To screen the rice genotypes for drought tolerance in the field condition

2. To validate the presence of droughtresistant QTLs in the rice genotypes through molecular studies

METHODOLOGY

A field experiment was conducted with 34 rice genotypes in two replications following randomized

block design (RBD) including three tolerant and one susceptible checks. The checks include IR 20 (Susceptible), and Mahulata, Selumpikit, CR-143-2-2 (Tolerant). The genotypes were tested under irrigated as well as reproductive stage drought stress condition in rainout shelter at ICAR- NRRI, Cuttack during Kharif 2016. The rice genotypes used in the present study were obtained from the Department of Plant Breeding and Genetics, OUAT, Bhubaneswar and ICAR- National Rice Research Institute (NRRI), Cuttack. Study of marker validation for the presence of drought resistant genes in those genotypes was also carried out in the molecular laboratory at ICAR-NRRI, Cuttack. The drought symptom like leaf rolling was recorded as per Standard Evaluation System (SES) of 1 to 9 scales (IRRI, 1995). Observations of yield and yield contributing traits were recorded on ten randomly selected plants per genotype per replication. The relative yield reduction (yield potential) under drought stress was calculated as the yield of specific genotypes under drought divided by that of the highest yielding genotype in the sample. The grain yield per plot was converted to q/ha.

RESULTS AND CONCLUSION

Yield attributing characters like Effective tillers per hill, Panicle length, Spikelet fertility percentage, Biomass per plant (gm) and Grain yield (q/ha) showed significance at 1% level of significance for the environment, variety, and Environment X Variety (E x V). Environment and Variety interaction was found significant for all the characters.



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Significant differences were observed in grain yield of rice varieties under moisture stress and control conditions. Yield decline in grain yield was observed in almost all the rice varieties grown under drought stress conditions. Variety mean yield ranged from 57.30 q ha⁻¹ to 26.60 q ha⁻¹ under non-stress irrigated condition and from 16.26 q ha⁻¹ to 3.53 q ha⁻¹under stress condition. Under control condition, high yielders were Jyotirmayee (57.30 q/ha), and Annada (56.80 q/ha), whereas IR 20 (3.59 q/ha) and Naveen (3.53 q/ha) were low yielders. Under stress situation, varieties namely Sahabhagidhan and Annada produced satisfactory grain yield as compared to the check varieties. The maximum soil moisture tension reached at the end of the 30th day stress period which was recorded to be -50kPa at 30cm depth. Thus, the level of stress could be classified as moderate to severe. Considering the stress tolerance indices like Stress tolerance level (STL), Stress Tolerance Index (STI) and Relative yield reduction (RYR%), varieties Khandagiri, Vandana, Heera, Mahulata, Selumpkit and CR 143-2-2 were found to be drought resistant.

Rice grown in drought stress conditions produced significantly less total biomass than irrigated rice. Similar trends were also observed for effective tillers per hill and spikelet fertility. Under drought stress conditions, varieties had lower biomass per plant than irrigated rice. Varieties Parijat, Jyotirmayee, Sarathi, Hiranmayee and Gouri showed high percent spikelet fertility than susceptible lines and checks. This result suggests that spikelet fertility is a reliable parameter for the screening of varieties for yield response subjected to water deficit stress at the reproductive stage. The depletion of soil moisture during the reproductive stage increased the percent spikelet sterility, which may result in decreased grain yield under stress conditions. Significant variations were observed among varieties for drought tolerance parameters namely leaf rolling.

Drought tolerant varieties *viz.*, Sarathi, Annada and Sebati had lesser leaf rolling as well as delayed leaf rolling.

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CONCLUSION

Variety Annada recorded satisfactory grain yield and no leaf rolling under moisture stress situation. Hence this may be considered as drought resistant variety. Based on other parameters such as stress tolerance indices and spikelet fertility varieties namely Sahabhagidhan, Vandana, Khandagiri, Heera, Jyotirmayee, Sarathi and Sebati were also found to be drought tolerant which may be recommended to the farmers for general cultivation in drought prone areas.

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RADIATION INDUCED MUTATION BREEDING FOR IMPROVEMENT OF TRADITIONAL RICE VARIETIES IN INDIA

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Rice, as a staple food for a majority of population in the world, holds a significant role to play in alleviating the global hunger problem. In India, it is the staple food for nearly half of the population. With the burgeoning size of population at an unprecedented rate, limited fertile land resources, climate resilience, emerging new races of pests and diseases and consumer preferences for quality attributes, it is imperative to increase crop diversity with better selection efficiency addressing the challenges of future rice production. India has a rich and diverse genetic wealth of rice and it has been estimated from various surveys that the country is endowed with large rice landraces/ germplasm lines, a rich biodiversity that no other country has. With advent of modern agriculture, and switch over to high yielding and hybrid varieties, has posed a great threat to the security of the age old practice of growing traditional varieties and landraces which had immense potential for different important traits. These diversity hotspots have been found mostly in Central, North-Eastern region, Eastern region and Southern India accompanying unique aroma, biotic and abiotic stress tolerance and quality attributes. Due to long duration, tall height (susceptible to lodging) and low yield potential these landraces are not able to compete with recent high yielding varieties, therefore are being marginalised and slowly going out of cultivation. There is need to revive these landraces by rectifying the undesirable agronomic traits without altering their original unique quality attributes.

Mutation breeding as proven tool in rice improvement: Mutation breeding is a very successful tool helping in increasing crop diversity and allowing plant breeders to exercise their skill in developing desirable crop varieties. The induction of mutations has been used to enhance the yield, better nutritional quality and wider adaptability of world's most important crops. Plant architecture including plant height, branching habit (tiller number), leaf shape and patterns, floral characters, grain traits and quality traits including aroma, cooking quality, etc are of tremendous importance for rice improvement programme. Bhabha Atomic Research Centre (BARC) in collaboration with State Agricultural Universities (SAUs) have started R&D work for revival of these traditional rice varieties adaptable to different agro-climatic regions of India through radiation induced mutation breeding. In collaboration with IGKV, Raipur, more than 50 traditional rice varieties are being improved. Mutant varieties viz. 'TCDM-1', 'Vikram TCR' and 'CG Jawaphool Trombay' have been released recently. In collaboration with DBSKKV-RARS, Karjat, 'TKR



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Kolam' has been released for Konkan region of Maharashtra. BARC and AAU, Jorhat have jointly developed early maturing, lodging resistant and photoperiod insensitive mutants in 'Kon Joha' rice and these are under evaluation. In collaboration with UBKV, Coochbehar WB), Improvement of 'Tulaipanji' and in collaboration with Vishwa Bharati University, Shantiniketan (WB), 'Badsahabhog', have been taken up and mutant lines are being evaluated for yield and other traits. Recently in collaboration with ANDUAT-CRS, Masodha (UP), improvement of Kalanamak rice (a premium aromatic rice of Tarai region of Eastern UP) through radiation induced mutation breeding has been initiated. Improvement of other traditional rice varieties are underway which will bring these varieties back into cultivation and help in improving the tribal and marginal farmer's economy.

Utilization of novel mutagens (proton beam) for rice improvement: Crop mutagenesis has gained significant momentum in recent years, driven by the up surging need for continuous improvement in crop production and availability of more efficient techniques. So far, a plethora of chemical and physical mutagens (viz. gamma rays, X-rays etc.) have been used to generate desirable genetic diversity, required to achieve targeted improvements which are not existing or rare in the natural population. In recent past, ion beam technology is being focussed upon to exploit the high mutagenic efficiency bestowed upon by higher LET values, as compared to X-rays and gamma rays being used since 1930's. Particulate nature, mass and charge possessed by ions results in their interaction being different and consequentially dense and local deposition of energy, that may lead to production of spectra of variations that are distinct from those produced through exposure to other mutagens. Larger local damage to DNA bears the possibility of breaking linkage drag between undesirable and desirable traits. The effects are subject to penetration to desired depth of plant propagule, without much energy loss in the medium. Proton (H⁺) beam accelerated to 14MeV energy using

BARC-TIFR Pelletron Facility, achieved penetration to the embryo of rice seeds. Proton beam irradiation technology was optimized in rice IBD-1 for increasing the efficiency of mutation and increasing the spectrum of mutants. This work is under progress.

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CONCLUSION:

In recent past, the genetic variability present in rice is narrowed using conventional breeding approaches and use of more popular and hybrid rice varieties in India for a long period. Induced mutagenesis is one of the most important approaches for broadening the genetic diversity in rice to circumvent the bottleneck conditions. This become more evident as the future rice production will have immense pressure from consumers' preferences, changing climatic conditions, resurgence of new races of pests and diseases, demand for bio-fortified rice etc. Induced mutagenesis has demonstrated the potential in broadening the plant genetic base and thereby avail plant breeders the raw materials required to address different problems related to rice production and consumer preferences. Rice varieties developed through mutation breeding will significantly contribute to national food and nutritional security and improvement of socio-economic conditions of the poor & marginal land holding farmers.

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VARIETAL SCREENING FOR ANAEROBIC GERMINATION, A TRAIT SUITABLE FOR WET DIRECT SEEDING IN RICE (*ORYZA SATIVA* L.)

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'Rice is life' for more than half of the world population and is a primary staple food for about 75% of the Indian population. Direct seeded rice (DSR) is becoming popular in recent years because of its lowinput demanding nature. Among the different DSR methods, Wet-DSR is most efficient as it can allows the early use of water and can reduce weed invasion. Anaerobic germination (AG) is an important trait for DSR to be successful. Rice usually has low germination under anaerobic conditions, which leads to a poor crop stand in Wet-DSR. The ability of rice to germinate under water reduces the risk of poor crop stand. Thus, AG is an important trait for a variety to be used in Wet-DSR... The present study is aimed at identifying the rice varieties with AG tolerance, which is further useful in developing DSR varieties through appropriate breeding programme.

METHODOLOGY

The present investigation was carried out at Regional Agricultural Research Station, Maruteru, Andhra Pradesh. The experimental material comprises 48 rice genotypes, including popular varieties and few germplasm lines. The experimental design used was Randomised Complete Block Design.

Ten pre-germinate seeds of each genotype were sub surface seeded in plastic cups filled with puddled soil, flooded for 14 days. Seedlings emerged above water level counted at 14 DAS and percent anaerobic germination was determined (as per, Manigbas *et al.* 2008). Analysis of variance of the character was done as per standard statistical procedure for randomized complete block design.

RESULTS

Significant variation for the character was recorded which was ranged from 30% (BPT 2270) to 100% (AC 39416A) with a mean of 67.40. The estimates of PCV (21.73) and GCV (16.79) for this Anaerobic germination were high and moderate respectively (Table. 1).

Moderate heritability (59.68%) coupled with high genetic advance as per cent of mean (26.72) was observed for the trait indicating the prevalence of non additive gene action and further improvement of this character would be possible through heterosis breeding rather than simple selection.

CONCLUSION

Designing crossing programme with other distant varieties in the present study with AC 39416A, after determining its combining ability would result in varieties with high AG tolerance which can be used in DSR upon confirming other yield traits.

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Table.1. Mean performance and genetic variability parameters of 48 genotypes of rice for Anaerobic germination

S. No.	Genotype	Anaerobic germination	Coefficient	of variation	Variance		Heritability broad sense	Genetic advance	Genetic advance as % of mean
		(%)	PCV(%)	GCV(%)	Phenotypic	Genotypic	(%)		
1	MTU 1010	65.00	21.73	16.79	214.52	128.01	59.68	18.01	26.72
2	MTU 3626	70.00							
3	MTU 1075	75.00							
4	MTU 1121	80.00							
5	MTU 1156	70.00							
6	MTU 1166	65.00							
7	MTU 1081	60.00							
8	MTU 1112	70.00							
9	MTU 1061	85.00							
10	MTU 1064	80.00							
11	MTU 2077	60.00							
12	PLA 1100	65.00							
13	MTU 1140	75.00							
14	MTU 1078	65.00							
15	BPT 5204	65.00							
16	BPT 2270	30.00							
17	BPT 3291	60.00							
18	IR 36	60.00							
19	IR 50	60.00							
20	IR 64	75.00							
21	IR 72	70.00							
22	MTU-sel-1	70.00							
23	PS-140-1	95.00							
24	MTU-sel-2	65.00							
25	AC 39416A	100.00							
26	AC 39397	75.00							
27	AC 34280	40.00							
28	AC 34245	90.00							
29	AC 39813	75.00							
30	AC 34345	70.00							
31	AZUCENA	65.00							
32	N 22	70.00							
33	SABITA	85.00							
34	RNR 15048	65.00							
35	JGL 17004	60.00							
36	NAVEEN	45.00							
37	VANDANA	55.00							
38	ANNADA	65.00							
39	ANJALI	35.00							
40	WAYRAREN	1	70.00						
41	IRS-3	70.00							
42	E412	60.00							
43	SHABAGIDI	HAN	60.00						
44	KALINGA-II	Ι	75.00						
45	RATNA	70.00							
46	RGL2332	70.00							
47	JGL 384	65.00							
48	RGL2537	65.00							
Range]	Lowest	30.00							
Range	Highest	100.00							
Mean	67.40								
C.V. (%)	13.80							
F ratio	3.96								
S.E.	6.58								
C.D. 5%	6	18.71							
C.D. 1%	6	24.97							



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PHOTOSYNTHETIC GAS EXCHANGE AND STOMATAL TRAITS VARIATION IN CHROMOSOME SEGMENT SUBSTITUTION LINES OF RICE UNDER DROUGHT STRESS

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Drought is one of the most damaging environmental disasters and has significant environmental, economic and social impacts around the world. Many factors threaten the global food security and drought stress is one of the major factor that affects rice physiology in many ways by affecting net photosynthetic rate, transpiration rate, stomatal conductance, water use efficiency, and all these above parameters are reduced (Ding et al, 2014) under stress. In the process of photosynthesis, microscopic pores called stomata plays important role to regulate CO, uptake with the concomitant release of water vapour through transpiration. Several studies in different plants including rice showed the importance of stomatal density, size and their association with higher photosynthetic rate. Wild species are known to have a high degree of drought tolerance because they have never been cultivated under ideal situations and they may serve as a source of superior drought-tolerance alleles for improving cultivated rice. A wild species of rice O. meridionalis Ng, with AA genome, was reported to have drought avoidance along with better adaptation to arid climatic conditions than O. sativa L (Somanthri, 2001).

The objective of the present work is to identify the variations in the leaf photosynthetic characteristics and stomatal traits in chromosome segment substitution lines (CSSLs) of rice under drought stress which may help in crop improvement programme for developing climate resiliencence rice varieties.

METHODOLOGY

Thirty two CSSLs of rice derived from cross between Curinga and wild derivative *O. meridionalis* (OR 44)(MER) developed in Cornell University, USA by Prof. Susan Mc Couch and received through SCPRID Programme along with and three checks [IR64- drought sensitive, CR 143-2-2 - drought tolerant and Curinga -recurrent parent] were grown in the field for the experimental purpose. Stress trial (DS) was conducted under rain out shelter and well watered (WW) trial in the nearby field. All the measurements were performed in maximum tillering stage before stress and stress was imposed on 45 days old seedlings for 14 days.

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Leaf atmosphere CO_2 and H_2O exchange measurements were recorded using LI-6400 XT a portable photosynthetic gas analyzer. The stomatal traits were measured in fully expanded top leaf of three plants. A nondestructive leaf impression was made from both abaxial and adaxial surface by applying nail varnish in the mid area of the leaf and the number of stomata were counted under light microscope system.

i)Stomatal size (S) was calculated based on the assumption that stomata are elliptical in shape with their major axis equal to guard cell length (L), and their minor axis equal to guard cell width (W) (Xiong et al., 2018): $S = L/2 \times W/2 \times \pi$

ii)Leaf stomatal density (D) expressed as the no. of stomata/unit leaf area

RESULTS

Wide variation was observed within the studied CSSLs for leaf gas exchange parameters (Table 1). Under drought stress among the lines, the range of photosynthetic rate (PN) in MER-25, MER-14 and MER-20 (15.58-16.37 μ mol CO₂ m⁻² s⁻¹) and stomatal conductance (gs) in MER-32, MER-30 and MER-14 (0.24-0.28 mol H₂O m⁻² s⁻¹) was found significantly higher than other lines. Water use efficiency





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Traits	Unit	Condition	Average	SE+	Min	Max	Range
Leaf structural traits							
Stomatal size							
<u>A</u> daxial lamina surface(S_{ada})	μm ²	WW	218.02	11.58	159.15	254.93	95.78
aua		DS	151.67	7.10	107.31	225.42	118.11
<u>Abaxial lamina surface(S_{aba})</u>	μm ²	WW	163.33	8.32	112.27	234.55	122.28
aba'		DS	127.86	7.74	62.75	204.65	141.90
Stomatal density							
<u>A</u> daxial lamina surface (D_{1})	mm^2	WW	259.38	9.17	187.30	380.10	192.80
		DS	238.03	7.65	209.33	258.91	49.58
<u>Abaxial lamina surface(D_{aba})</u>	mm^2	WW	309.64	9.68	218.51	495.79	277.28
aba'		DS	286.03	6.37	192.81	459.06	266.25
Leaf functional traits							
Photosynthetic rate (P_{y})	μ mol CO ₂ m ⁻² s ⁻¹	WW	21.27	0.47	14.55	25.54	10.99
	• 2	DS	12.76	0.41	8.61	16.37	7.76
Stomatal conductance(g)	mol H ₂ O m ⁻² s ⁻¹	WW	0.43	0.03	0.26	0.66	0.40
10 s ²	2	DS	0.17	0.01	0.09	0.28	0.09
Transpiration rate (E)	mmol H ₂ O m ⁻² s ⁻¹	WW	12.05	1.01	7.66	15.70	8.04
	2	DS	5.33	0.74	3.32	7.80	4.48
Internal CO_2 concentration(C_1)	μ mol(CO ₂) mol ⁻¹	WW	266.09	5.96	194.97	295.52	100.56
2	• 2	DS	245.56	11.05	168.90	288.51	119.62
Water use efficiency (WUE)	μ mol(CO ₂) mmol ⁻¹ (H ₂ O)	WW	1.80	0.17	1.31	2.44	1.12
• ` ` /	• • 2 • 2 /	DS	2.50	0.27	1.60	3.56	1.96

Table: 1 Intraspecific variation in stomatal traits and photosynthetic parameters in CSSLs

(WUE) was observed to be higher under drought stress than under well watered condition. MER-13, MER-14, MER-25 and CR 143-2-2 (3.47-3.56 μ mol (CO₂) mmol⁻¹(H₂O)) had highest WUE.

Stomatal features varied greatly among the CSSlines. Generally, stomatal size was smaller for abaxial side (lower surface- S_{aba}) than adaxial side (upper surface- S_{ada}), inversely, stomatal density was higher for abaxial side (D_{aba}) than adaxial (D_{ada}) side (Table 1). Under drought stress, the stomata size S_{aba} and S_{ada} ranged from 63 to 205 μ m² and from 107 to $225 \,\mu m^2$, while the density ranged from 193–459 mm² and 209–259 mm^2 for $D_{_{aba}}$ and $D_{_{ada}}$ respectively. On average, for both sides of the leaf stomatal size was 27% and stomatal density was 79% larger in well watered compared to drought stress condition. Stomatal size and density were negatively correlated for each side of the leaf. Under drought stress MER-20, MER-32, MER-14 and CR 143-2-2 were identified with smaller size (S) as well as minimal stomatal density (D) in both sides of the leaves.

CONCLUSION

The present study provides insight in the variation of leaf stomatal (structural) and photosynthetic gas exchange (functional) traits in CSSLs of rice. MER-14, MER-20, MER-25, MER-32 and CR 143-2-2 were identified as potential donors having maximum leaf photosynthetic rate, gas exchange and WUE with minimum size and density of stomata under drought stress condition suggesting their utilization in breeding programme for development of climate resilient variety.

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UNIQUE CORE SET OF MOLECULAR MARKERS BETWEEN ORYZA COARCTATA AND ORYZA SATIVA COMPLEX

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O. coarctata is the most difficult species for using in rice breeding and it belongs to tertiary gene pool. But utilization of this species will be worthy to address the issues of increasing salinity stress and recently it was possible to produce partially fertile progenies. Beside *O. sativa*, other species may serve as bridge species. Polymorphic and codominant markers distributed throughout the genome can expedite the utilization of the species.

METHODOLOGY

O. sativa (includes both indica and japonica ecotypes), other seven species of O. sativa complex and O. coarctata were used in the study. O. coarctata genome sequence was downloaded from local genome database of ICAR-National Institute for Plant Biotechnology, New Delhi, India (Mondal et al. 2018). Genome sequences of O. sativa, O. nivara, O. rufipogon, O. glaberrima, O. barthii, O. glumaepatula and O. meridionalis were downloaded in FASTA format (chromosome-wise) through Gramene database and O. longistaminata from the NCBI database. 23,499 rice STMS markers were chosen from Gramene database (McCouch et al. 2002) and literature search (Parida et al. 2009). In silico crosstransferability study of STMS makers was performed following a bioinformatics pipeline designed by us. This is an improved and modified version of a bioinformatics pipeline earlier used by us with relatively lesser number of markers (Ray et al. 2016). The modified pipeline can screen thousands of markers from multiple genomes sequences simultaneously with predefined commands.

RESULTS

This marker identification strategy is highly reproducible and band sizes or polymorphism prediction among different species is possible before in-vitro validation. Out of 23,499 markers, only 359 STMS were cross-transferable to O. coarctata and 77 were common with all the species of Oryza sativa complex. These core markers were distributed over 11 chromosomes of O. sativa complex. Nearly 76% of core markers were located within various genes of rice. The markers also showed unique genome specific polymorphism pattern with high levels of inter- and intraspecific variations in 'AA' genome and complete absence of Intra- or inter-population variations in O. coarctata (KKLL). The number of microsatellite motifs, number of repeats in different motifs and contribution of SSR sequences towards the amplicon length were substantially lesser in O. coarctata leading to the exceptionally high level of polymorphism with AA genome. Two markers are also useful for species identification. The hyper-variable markers are a useful resource for pre-breeding of O. sativa, O. glaberrima and new rice for Africa with O. coarctata or with any species of O. sativa complex.



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CONCLUSION

The markers are useful resource for the prebreeding of *O. sativa*, *O. glaberrima* or new rice for Africa (NERICA) involving all species of AA genome and *O. coarctata*. Excellent polymorphism level and wide applicability makes these 77 STMS markers as a useful resource for breeders in utilizing wild rice in their research. This novel and simple methodology for identification of core marker set may also be utilized in different other crops and their crop wild relatives.

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Rice Research and Development for Achieving Sustainable Development Goals

Theme - I : Enhancing rice productivity and quality



Indian Rice

CROP ENGINEERING BY SYNTHETIC GLYCOLATE METABOLISM

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Rice (Oryza sativa L.) is central to the lives of billions of people around the world and approximately 90% of the rice is produced and consumed in tropical Asia. In C3 plants like rice, photosynthetic productivity is limited by lower assimilation of CO₂ into organic carbon compounds because Ribulose-1,5bisphosphate carboxylase-oxygenase (RuBisCO) poorly discriminates between CO₂ and O₂, leads to photorespiration and the loss of fixed carbon and nitrogen. Despite these disadvantages, photorespiration has important role in plant because it recovers 75% of the carbon from phosphoglycolate as well as efficiently removes potent inhibitors of photosynthesis. Moreover, photorespiration dissipates excess photo-chemical energy under high light intensities, thus protecting the chloroplast from over-reduction. By using advantage of knowledge of synthetic biology, it is now feasible to design and introduce biochemical pathways in vivo in rice for bypassing photorespiration. The present work is an attempt to introduce chloroplast-targeted bacterial genes in plant for establishment of the photorespiratory bypass pathway.

METHODOLOGY

Five chloroplast-targeted bacterial genes encoding glycolate dehydrogenase (GDH), glyoxylate carboligase (GCL) and tartronic semialdehyde reductase (TSR), have been amplified by PCR from *E. coli* gDNA using suitable oligonucleotides and cloned in pGEMT vector. All sequences are available from the *E. coli* K12 genome sequence (gi49175990). Rice RuBisCO smaller subunit (rbcs) transit peptide (~300 bp) nucleotide sequence have been also amplified and cloned in pGEMT vector. The transit peptide sequence is used for tagging into the *GDH*, *GCL* and *TSR* in order to facilitate transferring integrated genes product from nuclear genome to chloroplast genome. Gene constructs were designed under constitutive promoter, tagged with transit peptide and transfer into binary vector (pCAMBIA-1302). These gene constructs were transferred into *agrobacterium* using tri-parental transformation method with the support of helper plasmid. Using stepwise (*agrobacterium* mediated) nuclear transformation with these chloroplast-targeted *E.coli* genes, we are going to generate rice plants in which chloroplastic glycolate is converted directly to glycerate.

RESULT

Gene constructs of synthetic glycolate metabolism pathway were designed and introduced into *agrobacterium*. These chloroplast-targeted bacterial genes need to introduce in plant for establishment of the photorespiratory bypass pathway. This will generate plants in which chloroplastic glycolate would be converted directly to glycerate. This will reduce, though may not eliminate, flux of photorespiratory metabolites through peroxisomes and mitochondria while increasing the rate of carbon fixation.

CONCLUSION

Introduction of photorespiratory bypass pathway into rice will generate plants in which chloroplastic glycolate would be converted directly to glycerate. This would reduce, though may not eliminate, flux of photorespiratory metabolites through peroxisomes and mitochondria while increasing the rate of carbon fixation. Diversification of chloroplastic glycolate from photorespiratory will improve the



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Plants passing selection were tested for gene insertion using PCR of gDNA. Primers were used to amplify the transperso GC, TSR, GlcD, GlcE and GlcF.



Representative photograph of selected transgenic plants(T0)

productivity of crops with C3 photosynthesis. By increasing photosynthetic productivity, the strategy of photorespiratory bypass could have a significant economic impact for rice production. The aspect of increasing nitrogen use efficiency is another aspect which can lead to significant reduction in fertilizer application and lower the environmental cost of agriculture.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-99

Indian Rice

HETEROSIS FOR MILLING QUALITY CHARACTERS IN RICE (ORYZA SATIVA L)

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Heterosis has been reported in rice for agronomic characters, physiological traits and low temperature tolerance and productivity, but reports of heterosis for the physicochemical grain quality characters in rice are limited. On the other hand knowledge on these genetic aspects is very important for maximum exploitation of heterotic effects in rice and for building up of gene pools to be employed in breeding programmes. Hence, present investigation was undertaken on heterotic manifestations in six milling quality traits involving high yielding genotypes susceptible to bacterial leaf blight disease as 'lines' and five donors for the said disease as 'testers'.

OBJECTIVE

To estimate the heterosis in milling traits

MATERIALS AND METHODS

The experiment was conducted at Plant Breeding and Genetics Unit of Tamil Nadu Rice Research Institute,Aduthurai during 2010. Five testers and 12 lines were grown and at flowering stage, they were crossed with each other in a line × tester manner as described by Kempthorne (1957) to produce 60 hybrids. The resultant 60 F1s together with 17 parental lines were grown in the second year in a Randomized Complete Block Design with three replications. Milling quality traits were recorded for all the hybrids and parents. Genotype means were used for the analysis of variance. Mid-parent based heterosis (MP) and better-parent based heterosis(BP) and standard parent based heterosis were estimated for the six grain quality traits . The heterosis per cent estimated for six grain quality traits over mid parent, better parent and standard check (ADT 43) and three best crosses are given hereunder . For hulling percentage, the mid parental heterosis, better parental heterosis and standard heterosis ranged from -11.72 (TNAU Rice ADT 49/ IRBB 21) to 22.60 (CO 47/Imp. Samba Mahsuri), -16.99 (ADT 39/Pusa 1460) to 12.15 (ADT (R) 47/ IRBB 21) and -14.78 (ADT 39/Pusa 1460) to 16.87 (CO 47/Imp. Samba Mahsuri) respectively. For hulling percentage, CO 47/Imp. Samba Mahsuri, ASD 16/ Ajaya, ADT (R) 47/ IRBB 21 and ASD 16/IRBB 21 showed high heterotic values for all the three types of heterosis. Similar results for this trait was reported by Sahai *et al.* (1986).

For milling percentage, the mid parental heterosis ranged from -12.08 (ADT 42/ Imp. Samba Mahsuri) to 27.80 (CO 47/Imp. Samba Mahsuri) per cent. The range of better parent heterosis varied from -15.64 (ADT (R) 46/ Ajaya) to 20.08 (CO 47/Imp. Samba Mahsuri) per cent. The standard heterosis ranged from -15.29 (TKM12/Pusa 1460) to 33.79 (CO 47/Imp. Samba Mahsuri) per cent. For milling percentage, CO 47/Imp. Samba Mahsuri, ASD16/ IRBB 21, ASD 16/Ajaya and ASD 16/IRBB 60 exhibited good amount of heterotic vigour for all the three categories of heterosis. The hybrid TNAU Rice ADT 49/IRBB 21 showed relative heterosis and heterobeltiosis. This is in confirmity with the results of Hassan *et al.* (2011).

For head rice recovery percentage, the per cent relative heterosis ranged from -31.15 (ADT 42/

RESULTS AND DISCUSSION



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Pusa 1460) to 16.57 (ASD 16/Ajaya) for this trait. The heterobeltiosis ranged from -39.03 (ADT 42/Pusa 1460) to 15.30 (ASD 16/Ajaya) per cent. The standard heterosis ranged from -28.64 (ADT 42/Pusa 1460) to 18.90 (ASD 16/ Ajaya) per cent. For head rice recovery percentage, ASD 16/Ajaya and ASD 16/ IRBB 21 were found to be with good amount of heterotic vigour for all the three categories of heterosis. Similarly, the hybrids ADT (R) 47/Imp. Samba Mahsuri and CO 47/Imp. Samba Mahsuri also had good heterotic vigour over mid parent and standard parent. This is in close agreement with the findings of Mahalingam and Nadarajan (2010).

The heterotic vigour for kernel length was from -11.48 (ASD 42/Pusa 1460) to 17.96 (CO 47/Imp. Samba Mahsuri) for relative heterosis; -22.12 (CO 47/ Pusa 1460) to 15.38 (TKM 11/Imp. Samba Mahsuri) for heterobeltiosis and -7.91 (ASD 16/Ajaya) to 28.25 (TRY 2/Pusa 1460) per cent for standard heterosis. Higher magnitude of relative heterosis was also observed in TKM 11/Imp. Samba Mahsuri, TRY 2/ IRBB 60 and TRY 2/IRBB 21; heterobeltiosis in CO 47/Ajaya, TRY 2/IRBB 60 and TRY 2/IRBB 21 and standard heterosis in TRY 2/IRBB 60, TKM 11/Pusa 1460 and TRY 2/IRBB 21 for this trait. The hybrids TRY 2/IRBB 60 and TRY 2/IRBB 21 produced significantly positive heterosis, under relative heterosis, heterobeltiosis and standard heterosis for kernel length while TKM 11/Imp. Samba Mahsuri also had good heterotic vigour over mid parent and better parent. Venkanna et al.(2014) reported similar positive heterosis for this trait.

For the trait Kernel breadth, heterosis in negative direction is desirable for quality rice. The relative heterosis for kernel breadth ranged from -11.56 (ASD 16/IRBB60) to 14.48 (ASD 16/IRBB 21) per cent; heterobeltiosis from -20.00 (ASD 16/Pusa 1460) to 12.31 (TKM 12/IRBB 21) per cent and standard heterosis from -2.59 (TNAU Rice ADT 49/Imp. Samba Mahsuri) to 43.10 per cent (ASD 16/IRBB 21). The heterotic vigour was found to be significantly negative for kernel breadth in the hybrids ASD 16/ IRBB 60, TKM 12/Ajaya and ADT (R) 45/Ajaya for relative heterosis and heterobeltiosis. This is in close agreement with the findings of Venkanna *et al.*(2014). None of the hybrids showed lesser kernel breadth than standard check ADT 43.

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The heterotic vigour for Kernel length/breadth ratio was from -19.49 (ASD 16/IRBB 21) to 22.69(TKM 12/IRBB 60) for relative heterosis; -31.63 (ASD 16/IRBB 21) to 17.42 (TKM 12/IRBB 60) for heterobeltiosis and -34.24 (ASD 16/IRBB 21) to 19.96(TRY 2/Pusa 1460) per cent for standard heterosis. High heterotic vigour was found to be existing in all the three types of estimation for kernel length/ breadth ratio in the hybrid TKM 12/IRBB 60 while TKM 11/Ajaya and TRY 2/IRBB 60 expressed highest relative heterosis and heterobeltiosis for kernel length/ breadth ratio. This is in confirmity with the findings of Venkanna *et al.*(2014).

CONCLUSION

A study was conducted on heterosis, yield and yield components in rice. Twelve lines were crossed with five testers in line × tester manner to produce 60 F1.hybrids. Kadambavanasundaram (1980) suggested that computing standard heterosis based on best cultivar for commercial exploitation of hybrid vigour is a primary need.For milling quality traits, among the top ranking hybrids, the hybrids CO 47/ Imp. Samba Mahsuri for hulling percentage (16.87 per cent) and milling percentage (33.79 per cent), ASD 16/Ajaya (18.90 per cent) for head rice recovery percentage, TRY 2/Pusa 1460 for kernel length (28.25 per cent), revealed highest standard heterotic values.

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Rice Research and Development for Achieving Sustainable Development Goals

Theme - I: Enhancing rice productivity and quality

IRC/TM-1/PP-100

Indian Rice

PHENOLOGICAL TRAITS GOVERNING DROUGHT TOLERANCE AT DIFFERENT GROWTH STAGES IN RICE

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Rice plays a significant role as a staple food. Drought stress critically hampers rice production and it can appear at any period of the crop growth stage. Although drought at the reproductive stage is more detrimental, still drought at the vegetative stage is also a determining factor for reproductive growth in rice. During the vegetative stage, drought stress decreases the leaf and tiller formation that ultimately reduces yield by affecting panicle development (Swain et al, 2017). However, when drought stress occurs during the reproductive growth phase, it remarkably reduces rice grain yield due to abortion of ovule and formation of partially filled grains (Pantuwan et al, 2002). Plant metabolism is primarily dependent on water status and it is measure through relative water content (RWC) and leaf water potential (LWP). RWC and LWP are highly correlated with plant height, days to flowering, panicle length, and harvest index besides grain yield (Gutierrez et al, 2010). Drought score and drought recovery score are also used to measure the degree of tolerance to oxidative damage and show lack of hydration of the plant tissue related to its RWC (Cabuslay et al, 2002). Drought decreases rice biomass accumulation at the vegetative stage (Zhang et al., 2018), which is directly related to the grain yield reduction at the reproductive stage (Fukai et al, 1999).

In this present study, twenty-one selected rice genotypes were evaluated both under vegetative and reproductive stage drought to identify suitable donors for a breeding programme to develop drought resilience genotypes best suited for upland and drought-prone areas.

METHODOLOGY:

This experiment was conducted at National Rice Research Institute (NRRI), Cuttack, Odisha during the dry season of 2017 and 2018 with twenty-one rice genotypes (including tolerant and susceptible check). The genotypes were grown in the field condition under well-watered (WW) and drought stress (DS) conditions in a randomized block design with three replications. The well-watered plot was maintained with nearly 5cm standing water from 30 days of germination to maturity.

Vegetative stage drought stress was imposed by withholding irrigation for 30 days when seedlings were 30 days old and stress was released by irrigating the experimental field. For reproductive stage drought, irrigation was withdrawn 10 days before flowering, and surface irrigation was provided when soil moisture content dropped below 17% and soil moisture tension dropped below -65kPa. The obtained data were calculated and evaluated using Microsoft excel, CROPSTAT ver 7.2, and XLSTAT evolution 2020.1.1. **RESULTS:**

The outcome of two years SES score showed that 7 genotypes with drought score '1', 11 genotypes with drought score '3', 2 genotypes with score '5' and IR 20 had '7' score in both the seasons. After 24 hrs of stress release, except IR 20 (not recovered), other genotypes recovered (4 genotypes with score '1', 11 genotypes with score '3', and 4 genotypes with score '5' in both the seasons. In response to drought at the vegetative stage, Mahamaya, Samaleswari, Poornima, IBD-1, Safri 17, Sahabhagidhan, and N22 had higher



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LWP (>-3.50 MPa) with > 70% leaf RWC whereas MTU1010, IR 64, and IR 20 had the lowest LWP (< -4.5 MPa) with less than 60% RWC under drought condition. Mahamaya, N22, Samleswari, Sahabhagidhan, and IBD1 had TDM> 0.68 t/ha whereas the lowest value (0.48 t/ha) was found in IR20.

In DS condition, minimum DFF was recorded in N22 (59 days) whereas maximum DFF was found in susceptible check IR-20 (112 days). All genotypes except N22 and Anjali (flowered early by 7 days and 5 days respectively) delayed in their DFF in DS as compared to WW condition and the range of delayed was 1 day (Danteshwari and Vandana) to 9 days (IR64 and IR-20).

The pooled data of two dry seasons showed that grain yield suffered a mean yield loss of 62.19% and associated reductions in PH by 11.87%, TN by 25.72%, TDM by 54.80%, HI by 19.15%, GF% by 43.33%, and GW by 3.39% under DS as compared to WW condition. Under DS condition, higher grain yield was recorded in Mahamaya (2.42 t.ha⁻¹), while the lowest recorded in susceptible check IR20 (0.66 t.ha⁻¹). Minimum RYR was exhibited by Danteswari (39.11%), while maximum RYR was observed in IR20 (86.28%) under DS condition over WW condition.





Agglomerative Cluster analysis based on Pearson correlation coefficient and unweighted pair group analysis by considering grain yield and yieldrelated traits classified 20 genotypes (except Safri 17), which explained the existence of a significant amount of diversity among the genotypes. The 4 genotypes of Cluster IA comprises drought-sensitive genotypes which have longer DFF, and lowest tillers number, total dry matters, grain yield, harvest index, and grain filling percentage and Cluster IB consisted of 4 genotypes which have moderate to lower tiller number, total dry matters, and grain filling percentage. 7 genotypes of Clustered IIA are with high tiller number, total dry matter, grain yield, and grain filling percentage indicating drought tolerance, and 5 genotypes of cluster IIB are characterized with moderate to lower value of DFF and higher to moderate value of plant height and harvest index (Fig 1.).

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CONCLUSION:

The present study identified that Sahabhagidhan, Poornima, Vandana, and N22 genotypes showed tolerance to both vegetative as well as reproductive stage drought stress, and these genotypes can be used further for the development of drought tolerant varieties suited for different growth stages and help to maintain stable grain yield in the drought-prone area under the prevailing unpredictable climatic situations.

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Theme - I : Enhancing rice productivity and quality

IRC/TM-1/PP-101

Indian Rice

ASSOCIATION STUDIES AMONG GRAIN QUALITY AND MICRONUTRIENT CONTENT OF POPULAR RICE VARIETIES OF ANDHRA PRADESH

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Inherent quality characteristics rule rice grain quality. These quality traits are controlled by rice genotype, environmental components, and traditional practices (Kale et al., 2017). The introduction of biofortified staple crops such as rice cultivars bred for improved mineral concentration should accomplish prevailing nutritional approaches. Food and nutritional security envisage the identification of rice varieties with high nutritional value. Rice lines with higher nutrient profiles need to be identified so that people consuming rice diets are supplied with adequate minerals (Ashraf et al., 2017). The objectives of the study are to screen rice varieties for physicochemical characteristics and micronutrients (Fe, zinc), the effect of degree of polishing on iron and zinc in polished rice, and association of physicochemical characteristics and mineral (Fe and Zn) content in rice varieties

METHODOLOGY

The experiment material constituted 20 popular rice varieties (16 released and four pre-released varieties) collected from Regional Agricultural Research Station, Maruteru, and West Godavari District. Observations were recorded on seven physical quality traits *viz.*, hulling %, milling %, head rice recovery, kernel length (mm), kernel Breadth, length/breadth ratio and 1000 kernel weight (g), three chemical quality traits *viz.*, amylose content (%), gel consistency) (mm) and alkali spreading value) five cooking quality traits *viz.*, kernel length after cooking (mm), water uptake (ml), volume expansion ratio (VER), elongation ratio (ER), and two nutritional traits like iron (Fe) (ppm), zinc (Zn) (ppm).

RESULTS

Chandra, Bhavapuri Sannalu, Indra, Swarna, and Samba Mahsuri among released varieties and MTU 1210, MTU 1224 pre-released varieties recorded high percent hulling, milling, and HRR with intermediate amylose, ASV, soft gel and higher VER and minimum ER.

All the varieties have shown a significant variance of iron and zinc content at polishing levels. Iron and zinc content were higher in brown rice than polished rice (5% and 10%). In this study, the varieties presented a wide range for iron (1.9 to 22.95 ppm) and zinc (8.22 to 34.07 ppm) among all the varieties at different polishing levels.

Among 20 varieties evaluated, three varieties containing low iron and zinc category, 11 varieties under medium iron, 12 varieties under medium zinc categories, and six varieties such as MTU 1210, MTU 1224, MTU 1262, Swarna, Sri Dhruthi, and Indra under high iron, five varieties Chandra, Swarna, Samba Mahsuri, MTU 1224, MTU 1262 were under high zinc categories. Three varieties Swarna, MTU 1224, MTU 1262, were categorized as high iron and zinc category.

The percent loss was more in medium slender grains (61.90-74.02 %) followed by long bold (64.66-73.88%) and long slender (62.77-72.52 %) at 5% and 10% respectively for iron content, whereas for zinc content at 5% and 10% level the percent loss was between 29.29-42.37% (MS), 27.69-39.58% (LS), 28.81-41.09% (LB). Percent loss for zinc showed very low among all grain types than iron. As the percent polishing increased, the iron content showed a



Table -1 Correlation coefficients between the quality traits and iron and zinc

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Traits	Hulling	Milling	HRR	1000 g.	KL	KB	L/B	AC(%)	g	ASV	KLAC	ER	VER	WU	Fe	Zn
	(%)	(%)	(%)	wt (g)	(uuu)	(uuu)			(uuu)		(uuu)			(III)	(mdd)	(uudd)
Hulling (%)	1	0.490^{*}	0.1401^{*}	-0.004	-0.173	0.04	-0.257	0.109	0.177	-0.04	-0.246	0.319	0.067	0.082	-0.178	0.082
Milling (%)		1	0.256^{8}	0.103	0.212	0.064^{**}	0.182	0.143	0.3	0.139	0.277	0.159^{8}	0.334	-0.211	0.096^{**}	-0.006
HRR(%)			1	-0.048	-0.1118	-00.00	-0.135*	-0.055	0.015	-0.199	-0.237	0.251	-0.154	0.179	0.369	0.27
1000 g. wt (g)				1	0.843^{**}	0.724^{**}	0.282	-0.123	0.021	-0.041	0.301**	-0.226	-0.256	0.072	0.262^{**}	-0.3
KL (mm)					1	0.653**	0.543*	0.028	0.056	0.028^{**}	0.068^{*}	-0.307	-0.299	0.044	-0.19	-0.262
KB (mm)						1	-0.279*	0.023	-0.092	0.136	-0.287	-0.152	-0.345	0.26	-0.172	-0.648**
L/B							1	0.011	0.148	-0.201	0.394	-0.24	-0.001	-0.199	-0.038	0.375
AC (%)								1	-0.392	-0.229	0.490*	0.424	0.093	0.064	0.284	-0.152
GC(mm)									1	0.338	0.075	-0.094	0.236	-0.068	-0.462*	0.047
ASV										1	0.151	-0.125	0.078	0.137^{*}	-0.166^{**}	-0.185^{**}
KLAC (mm)											1	0.059^{*}	0.387	0.138^{*}	0.135	0.008^{*}
R												1	0.379	-0.254	0.108	0.09
VER													1	-0.299	-0.385	-0.013
WU (ml)														1	0.37	-0.278
Fe (ppm)															1	0.183
Zn (ppm)																1

decreasing trend. At 10% polishing, more than 70% iron content was lost during processing because the iron is present only at the rice's outer layer, whereas zinc polishing could not influence % loss. Varieties such as MTU 1224, Swarna, MTU 1262, and Sri Dhruthi had shown less loss in iron, and Chandra, MTU 1224, Vijetha, Swarna had shown less reduction in zinc after polishing.

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The character hulling% showed significant and positive correlation with milling% ($r=0.490^*$) and HRR ($r=0.140^*$). A positive significant correlation was observed between the characters 1000 grain weight and KL ($r = 0.843^{**}$), KB (0.724^{**}). KL was significantly and positively correlated with KLAC ($r=0.068^*$) and ASV ($r=0.028^{**}$). Negative significant association of KB was observed with L/B ratio, ($r=-0.279^*$), Water Uptake ($r=-0.262^*$) and ASV ($r=-0.136^*$). KLAC had positive significant association with ER ($r=0.059^*$). ASV showed positive significant correlation with water uptake (r=0.137) and KL ($r=0.028^*$).

Positive and significant correlation were found between 1000 grain weight, KL ($r = 0.843^{**}$), KB ($r = 0.724^{**}$), KLAC ($r = 0.301^{**}$) and Fe ($r = 0.262^{**}$). Milling% was significantly and positively correlated with HRR ($r = 0.256^{*}$), KB ($r = 0.063^{**}$), ER ($r = 0.159^{*}$) and Fe ($r = 0.096^{**}$). A significant negative correlation was observed between the KB and Zn content of the grain ($r = -0.648^{**}$). Significant positive association were found between KLAC with ER ($r = 0.059^{*}$) and Zn ($r = 0.008^{*}$). ASV was significantly negatively correlated with Fe ($r = -0.166^{**}$) and Zn ($r = -0.185^{**}$).

CONCLUSION

Rice varieties such as Chandra, Indra, Sri Dhruthi, Swarna, Samba Mahsuri, MTU 1210, MTU 1224, and MTU 1262 recorded intermediate amylose, alkali spreading value, high iron, zinc which are desirable for rice consumers while counting for a better price with the best quality. The correlation coefficients





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obtained in the study show that improving anyone trait can either enhance or reduce other associated characters.

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IRC/TM-1/PP-102

. Indian Rice

ASSESSMENT OF GRAIN QUALITY, WAXY GENE POLYMORPHISMS AND MICROSATELLITE DIVERSITY IN STICKY RICE (ORYZA SATIVA L.) CULTIVARS OF ASSAM

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Sticky or glutinous rice is such a special group of rice cultivars grown for its culinary and cultural importance throughout South-east Asia. It is distinguished from non-glutinous rice by having no to low (<5%) amylose and a higher quantity of amylopectin in its starch. A "Glutinous Rice Zone" is distributed throughout the mountainous regions of the Indo-China Peninsula covering China, North-eastern region of India, Bangladesh, Myanmar, Laos and Philippines, where people showed a cultural preference for waxy starch. In the state of Assam, the sticky rice is classified in two groups: bora (glutinous) and chokuwa (semi-glutinous). The bora and chokuwa rices have been traditionally classified based on their stickiness after cooking (Dutta and Barua, 1978). These rice cultivars are considered as a speciality rice and have social and religious significance. Rice eating and cooking quality is mainly affected by apparent amylose content of the grains (Amy), gel consistency (GC), and gelatinization temperature (GT). The levels of Amy are controlled by Wx (Waxy) gene which encodes a GBSS1 enzyme crucial for amylose biosynthesis. Two wild type alleles, the indica-specific Wx^a , and the *japonica* specific Wx^b , have been reported to predominate at the Wx locus conditioning high (22-29%) and low (12-19%) Amy, respectively. The lower level of expression of the Wx^b allele has been shown to result from inefficient splicing of Wx intron 1

due to a single nucleotide variation at the intron 1 splice donor site (AG(G/T)TATA). Wx allelic diversity suggests that diversification occurred after divergence of the two subspecies. The objectives of this study were to assess the variability in grain quality traits in a set of sticky rices of Assam and study the nucleotide polymorphisms in Wx gene to understand causal association between Wx SNPs and Amy. Phylogenetic classification of *bora* and *chokuwa* cultivars was also done based on Wx sequence and genome wide SSR markers.

MATERIALS AND METHODS

Forty-six sticky rice accessions comprising of 37 *bora* and 9 *chokuwa* cultivars of Assam, India were taken from National Genebank, India. These were grown for two years at Shillong, Meghalaya. Sixteen grain morphological and quality traits were studied. The Amy of milled rice kernels were determined, and the accessions were classified as glutinous or waxy (0-5%), very low (5-12%), low (12-20%), intermediate (20-25%) and high (>25%) (Juliano 1992). Sequencing of the *Wx* gene was performed 24 (17 *bora* and 7 *chokuwa*) accessions. Overlapping *Wx* fragments were assembled and submitted to NCBI GenBank under MH880989-MH881012. Further, a set of 67 accessions from North-east India, 9 *indica*, 5 *aus*, and



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3 *japonica* genotypes were genotyped 40 SSR markers from the set of 50 primers suggested by GCP. The gene/ microsatellite diversity indices were calculated using DnaSP v5.0 and PowerMarker V3.25, respectively. Phylogenetic analysis was done in PAUP v4.0a.

RESULTS

The amylose content varied considerably (CV, 64%) among the cultivars, and it ranged between 2.2% -22.87%. Based on their Amy, 37 bora cultivars were categorized into four amylose classes: waxy, very low, low and intermediate. The Amy of Chokuwa cultivars varied between 5.12-20.4%, and three amylose classes were identified: very low to intermediate. The alkali digestion (AlkD) values varied from 3 to 7, and three classes were observed within both cultivar types. Most of the sticky cultivars (65%) showed brown furrows to brown coloured hulls with brown apiculus (60%). A few (17.4%) accessions showed small to long awns. The seed coat colour was predominantly white. Most of the rice accessions had medium to short grain length and medium grain shape. Awning, Awn Colour, Lemma palea colour and Apiculus colour showed high positive contributions in distribution of cultivars in principal component analysis. Lathing bora, Gomiri bora, Pakhari bora, Hukani bora, Nepali chokuwa, Kankoa bora and Kakoa bora were the most distinct cultivars based on grain morphology.

The *Wx* gene sequencing from 24 *bora* and *chokuwa* cultivars revealed several nucleotide variations that can explain the variation in the amylose phenotypes. Sixty-two segregating sites were detected in *bora* and 15 sites in *chokuwa*. Fifteen substitution and 7 indel polymorphisms were found in the intron 1. Three different CT_n microsatellite alleles: CT_{10} , CT_{11} and CT_{17} , were identified in the *Wx* exon 1 encoding the 5' untranslated region (UTR). The intron 1 G/T splice donor site mutation (G/T-int1) was observed in 7 glutinous *bora* accessions: Gorusika bora, Bora dhan,

Jeng bora, Silonia bora, Hukani bora, Kala bora and Dhol bao bora. These cultivars carried CT_{17} allele in exon 1. Three out of 10 glutinous *bora* cultivars and all non-glutinous *bora* and *chokuwa* cultivars had G-SNP at the splice donor site of intron 1 and CT_{10} or CT_{11} allele.

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The gene-tree constructed using 6 kb *Wx* gene sequences of 24 sticky cultivars and 30 reference accessions revealed that the *bora* cultivars with G/T-Int1 SNP were included in the *Japonica* clade. Rest of the *bora* and *chokuwa* cultivars showed a closer affinity to the *indica* varieties (Fig1A).

Altogether, 178 alleles were detected at 40 SSR loci in 67 rice cultivars with an average of 4.5 alleles. Average gene diversity and PIC was 0.55 and 0.50, respectively. Pairwise F_{st} values showed highly significant differentiation among the groups ranging from 0.053 (bora vs chokuwa) to 0.354 (chokuwa vs *japonica*). The *bora* cultivars showed lower differentiation with indica (0.070), than with aus (0.160). The chokuwa genotypes exhibited a higher degree of differentiation with both *indica*, aus $(F_{sr} =$ 0.142 and 0.188, respectively). Both bora and chokuwa were genetically distant from the japonicas. Both neighbour-joining tree and PCoA revealed a clear separation of bora and chokuwa cultivars from the japonica and distributed within the indica and aus groups (Fig1B).

CONCLUSIONS

Wide range of variation for grain amylose content, alkali digestion and other grain parameters exists in sticky cultivars of Assam. The glutinous phenotype is common in *bora* cultivars, while *chokuwa* cultivars are generally non-glutinous with very low to low amylose.

The sticky cultivars carried a general pattern of nucleotide polymorphisms in *Wx* gene as reported in Asian rice, especially in Bangladeshi *Beruin* cultivars. Seven out of 10 glutinous *bora* rice cultivars carried



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Fig. 1. Genetic diversity of sticky rice cultivars of Assam. A, Gene-tree based on *Wx* gene sequence placed the *bora* rice cultivars (bold faced) carrying G/T-Int1 SNP within *japonica* clade; B, Neighbour-joining tree using microsatellite diversity included the *bora* and *chokuwa* cultivars within *indica* or *indica-aus* varietal group

the G/T intron 1 splice donor site mutation. Rest of the glutinous and low amylose *bora* and *chokuwa* cultivars carried polymorphisms in the exon 4 and/ or exon 9, in addition to SNPs and indels in introns 5 and 10 which may affect the expression of the gene.

The *Wx* gene tree placed glutinous *bora* cultivars carrying G/T-Int1 SNP into *japonica* clade, while rest of the cultivars were included in *indica* clade. However, based on the genome-wide microsatellite diversity, all the *bora* and *chokuwa* cultivars were belonged to the *indica* or *indica-aus* varietal group.

Among the Wx polymorphisms, the CT_n microsatellite in exon 1 and G/T SNP in intron 1 (G/T-Int1) should be considered for marker assisted breeding involving glutinous *bora* cultivars of Assam.

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. Indian Rice

KEEPING AERATION INTACT: A CRUCIAL ADAPTATION STRATEGY TO WITHSTAND COMBINED STRESSES OF HYPOXIA AND SALINITY IMPOSED BY SALINE WATER FLOODING IN RICE

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Global climate change is a grim reality which has already started impacting agriculture worldwide. One of its major influences is supposed to be on the amount and distribution of precipitation, which in turn have pronounced impact on crop production; especially on the rain-fed agriculture constituting 60-95% of cultivated land in the developing world (Wani et al., 2006). Coastal rice cultivation possesses an inherent risk of saline water flooding which is intensifying further due to global climate change. The plant's response to fresh- and saline-water flooding seems to be different due added complexities of elemental toxicity of salinity. Flooding by sea water imposes salinity and hypoxia simultaneously. Salinity tolerance greatly depends upon initial acclimatization of plant cell with osmotic stress, followed by overcoming the ionic stress through ion exclusion and/or tissue tolerance strategy. Removal of Na⁺ from mass flow or its compartmentalization to vacuole helps avoiding direct interaction of Na⁺ with active cellular parts and thus avoiding Na⁺ cytotoxicity (Munns and Tester, 2008). Fortunately, a few rice genotypes, can withstand saline-water flooding which exerts combined stress of hypoxia and salinity. These can contribute to a great extent in understanding the physiological and genetic mechanisms required for conditioning tolerance to saline water flooding. So, in the present study we tried to find out (i) what makes a waterlogging tolerant genotype which is capable of handling hypoxia stress, susceptible to saline water flooding? (ii) What are the key physiological determinants for differential tolerance response under fresh- and saline-water flooding for rice? (iii) Among hypoxia and elemental toxicity, which one is more crucial for saline water flooding tolerance in rice?

METHODOLOGY:

In order to understand the mechanistic differences and their underlying molecular regulations, we analysed leaf sheath transcriptomes at late vegetative stage in two waterlogging tolerant rice genotypes, Varshadhan (salinity susceptible) and Rashpanjor (salinity tolerant) which differ in terms of their tolerance to salinity. We performed comprehensive transcriptome analyses under control condition (no flooding), fresh water flooding and saline water flooding and based on the obtained results developed a hypothesis regarding the mechanism of saline water flooding tolerance; which we further supported by providing several follow-up anatomical, physiological and molecular evidences. Flooding stress (both fresh and saline) i.e. waterlogging (fresh water flooding) and salinity + waterlogging (saline water flooding with 12.0 ± 0.2 dS m¹ NaCl) stresses were imposed in 45-day old plants in cemented tanks by maintaining the water level in the tanks at 45 ± 5 cm for 20 days. Another set of plants were maintained as control.

RESULTS:

Comparative transcriptome profiling showed that 1489 and 1028 genes were differentially expressed (DEGs) in Varshadhan and Rashpanjor, respectively under waterlogging stress, while fewer numbers of DEGs (748 and 840 in Varshadhan and Rashpanjor) were recorded under combined stress. Chlorophyll




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Fig. 1. Adaptation to waterlogging induced hypoxia and tolerance to flooding with fresh and saline water.

fluorescence analysis revealed more pronounced effect of combined stress on Varshadhan than Rashpanjor, but only waterlogging didn't show any negative impact on photosystem-II in both the cultivars. Early synthesis and accumulation of ethylene even in the absence of stress, up-regulated respiratory burst oxidase homolog (RBOH) mediated reactive oxygen species production and consequent aerenchyma formation in Rashpanjor, making it prepared to withstand fresh-, as well as, saline- water flooding. On the contrary, Varshadhan up-regulated signalling for aerenchyma formation only after encountering hypoxia by freshwater flooding, but under saline-water flooding, the action of metallothionein repressed the signalling. Hence, Varshadhan survived fresh water flooding but succumbed to saline water flooding.

CONCLUSION:

This suggests lysigenous aerenchyma formation process might be an innate or hypoxia stress induced

process in rice, which could be hindered due to salinity depending on the genotype (Fig. 1). Moreover, we found early preparedness to hypoxia stress, rather elemental toxicity tolerance, provides a preferential advantage to withstand saline-water flooding in rice.

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IRC/TM-1/PP-104

. Indian Rice

IMPROVING BPH RESISTANCE IN RICE HYBRID RAJALAXMI THROUGH MARKER ASSISTED BACK-CROSS BREEDING (MABB) STRATEGIES

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Rice is one of the most important and staple food crop that feed more than half of the world's population. However, its production is severely affected by several biotic and abiotic stresses. About 52% of the total global rice production is lost annually because of the damage caused by biotic factors, of which nearly 21% is attributed to the attack of insect pests. Brown plant hopper (BPH) Nilaparvata lugens (Stal) is one of the most destructive monophagous insect caused substantial yield loss in rice throughout Asian rice growing countries (Normile, 2008). This insect make damage by sucking plant sap thus resulting in "hopper burn" symptoms, besides, also helps in transmitting viral diseases like rice grassy stunt and ragged stunt (Cabauatan et. al. 2009). Application of pesticides is the most common practice to manage BPH which is less effective and hazardous for ecosystem. Moreover, application of pesticide often leads to a resurgence of the pest population and affects natural BPH predators. Hence inbuilt host-plant resistance which is found to be workable is adopted for effective management of destructive pest, BPH.

OBJECTIVES

1. Molecular characterization and bioassay analysis of parental line and assessment of gene action.

2. Molecular marker aided BPH resistant gene introgression in parentage of hybrid Rajalaxmi.

3. Genome recovery analysis and assessment of suitability of improved lines.

METHODOLOGY

The parents of medium duration popular rice hybrid Rajalaxmi (CRMS 32A/B and IR 42266-23-3R) is stacked with BPH resistant gene 'BPH31' from the donor CR 2711-76 utilizing MABB strategy. The population is advanced to BC_2F_2 generation. Linked SSR marker 'RM251' was utilized for hybridity and foreground selection (FS) whereas 72 hypervariable informative SSR markers distributed uniformly throughout indica rice genome were utilized RP genome recovery in BC and segregating generation. The BC2F2 and advance segregating generation will be fixed under speed breeding strategies (Field RGA) which accommodates three generations in a year.

RESULT

The F1s of donor (CR 2711-76) and recurrent parent (CRMS 32B and IR42266-23-3R) were sown in staggered and true hybrids were advanced in BC1 generation. Total 160 and 208 BC1F1 seeds of both maintainer and restorer population, respectively were generated and evaluated. In BC1F1, 11 and 27 plants of maintainer and restorer, respectively were found with hetero-alleliec of target QTL (BPH31) where 3 and 7 progenies (both population) recovered with substantial RP genome (73.24% and 71.81%) were advanced in BC2F1. In BC2F1, total 131 and 167 plant progenies of maintainer and restorer were evaluated, where 17 and 08 plant of maintainers and restorer, respectively found positive for target trait, of those 04 and 02 plant were recovered with >85% RP genome were subjected to selfing for development of BC_2F_2 population.

CONCLUSION



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Fig. Severe damage by the brown plant hopper (BPH) Source: https://www.bighaat.com/blogs/kb/management-of-brownplant-hopper-in-paddy-crop

Inbuilt host-plant resistant is found to be workable in enhancement of rice sustainability against biotic and abiotic stresses; several desirable traits have been stacked successfully in popular rice varieties/ hybrids. Genomics approach coupled with speed breeding strategies provides more accuracy and gain to this strategy. Application of molecular markers and simultaneous RP genome recovery analysis in each BC generation has resulted substantial RP genome recovery in early BC with enhanced accuracy. Derivative lines would be of great use in development of BPH resistant rice hybrids and management of most destructive rice insect 'BPH'.

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Indian Rice

BIOFORTIFICATION IN RICE: ACHIEVEMENTS AND WAY FORWARD TO CONTRIBUTE IN THE NUTRITIONAL SECURITY IN INDIA

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Biofortification is the biological process by which the nutritional quality of the food crops is improved. This refers to the genetic enhancement of major food crops with for grain nutrients such as micronutrients (Fe, Zn, etc.), protein, essential amino acids, vitamins, etc. Rice is the major caloric supplement for two thirds of Indian population with a consumption of around 220gm per day. But it is deficient in protein (7-8%) and micronutrients such as Zn (10-15 ppm) and Fe (2-3 ppm) in polished rice. The genetic diversity in cultivated rice crops were observed for grain protein and micronutrients indicating the scope of their improvement. ICAR-NRRI initiated programme to improve major crops including rice for nutritional traits such as protein and zinc. The objectives are to genetically enhance protein and zinc content in high yielding popular varieties and subsequently improve biofortified genotypes for tolerance to biotic and abiotic stresses for better adaptation to climate change.

METHODOLOGY

Low-yielding landraces such as ARC 10075, ARC 10063, Chittimitiyalu, Bindli, etc were identified for higher grain protein and zinc content in milled rice. These genotypes have been used as donors to improve high yielding varieties such as Naveen, Swarna, MTU 1010, etc. for nutritional traits through backcross and bulk-pedigree breeding approaches. Calibrated NIR spectroscopy (at NRRI) and XRF (at IIRR) were used to estimate grain protein and zinc content, respectively. Mapping population derived from ARC10075/Naveen was employed to detect QTLs for grain protein content (Chattopadhyay et al. 2019a) Elite lines with high grain protein and zinc content have been identified for release through multilocational testing (Chattopadhyay et al. 2019b). The nutrient rich elite lines are used in further improvement for bacterial blight resistance and abiotic stresses through molecular marker assisted selection.

RESULTS

ICAR-National Rice Research Institute, Cuttack has released two high protein (10%) rice varieties, CR Dhan 310 and CR Dhan 311 (Mukul). First high protein (10.2%) rice variety, CR Dhan 310 was released in 2016 for cultivation in Odisha, Uttar Pradesh and Madhya Pradesh (Fig. 1a). Subsequently Mukul (CR Dhan 311) with high protein (10.1%) and moderately high level of zinc content (20 ppm) also was released in Odisha and notified in 2019 as nutrientrich rice variety. Both of them are in the genetic background of cv. Naveen, a well adopted popular rice variety of Odisha and eastern India as a whole for irrigated ecosystem. The high protein varieties have been well accepted by the farmers due to their resemblance for grain and plant type to recurrent parent, Naveen. They are the valid replacement of more than 10 years old variety, Naveen for irrigated ecosystem. The rapid detection technique has been standardized for differentiating Naveen with its high-protein counterpart.Higher content of glutelin and some of the essential amino acids such as Lysine was found in high protein lines with quantitative trait loci (QTL) for grain protein content, qGPC1.1 (Chattopadhyay et al. 2019a). High protein lines (CR 2830-PLS-17, CR 2830-PLS-156) in the background of the high yielding variety, Swarna (MTU 7029) were found promising in national and state level multilocational testing. CR Dhan 315 (IET 27179: CR 2826-1-1-2-4B-2-1) was



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Fig. 1. Biofortified rice varieties a. CR Dhan 310 (IET 24780) with high protein (10.2%) and b. CR Dhan 315 (IET 27179) with high zinc (25 ppm) developed at ICAR-NRRI, Cuttack

identified for release by VIC in 2020 for the states of Gujarat and Maharastra as biofortifiedhigh zinc rice variety (Fig. 1b). It contains average 24.9 ppm zinc in milled rice in zone VI. It has medium duration (125-135 days), semi-dwarf plant type (110 cm) with medium slender grain and good grain quality. It is suitable for irrigated and favorable shallow rainfed ecology. National average of grain yield of this variety is 5054 kg/ha.

For further improvement of high protein Swarna lines (CR 2830-PLS-17, CR 2830-PLS-156) crosses have been generated using donor for bacterial blight resistance genes (CR Dhan 800) and submergence and drought tolerant donors (CR Dhan 802). The population are genotyped using gene based molecular markers and phenotyped for grain protein content. Phenotyping for all other traits will be done.

CONCLUSION

Rice based food and feed industry is growing very fast. High protein and high zinc rice varieties can significantly contribute in this industry. Higher support price for growers and subsidy for mid-day meal rice are required to give benefits both the poor rice-farmers and our underprivileged children in villages of India. High yielding rice varieties with high nutritional values developed through biofortication breeding intervention have significant potentiality to contribute towards the better nourishment of millions of poor who depend mainly on rice for their nutrition and also in improving the economic level of the farming community. Improved biofortifed elite lines for biotic and abiotic stress tolerance developed through combination of classical and molecular breeding approaches have potentiality to contribute in stabilizing the sustainable growth and development in rice based rural economy.

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IRC/TM-1/PP-106

Indian Rice

GENE ACTION STUDIES FOR ANAEROBIC GERMINATION TRAITS IN RICE (ORYZA SATIVA L.)

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Flooding during germination or submergence of rice seed during germination is commonly observed in regions where direct seeding is practiced leading to tremendous loss, as rice is extremely sensitive to anaerobic (anoxia / hypoxia) conditions during germination and early growth of embryo. Anaerobic germination tolerance is a quantitative trait which is controlled by multiple genes. Prior knowledge about the relative magnitude of different kinds of genes and an understanding of the mode of inheritance of this complex quantitative character enables the breeder to design the breeding strategies for developing anaerobic germination tolerant varieties.

OBJECTIVES

To understand the additive, dominance and epistatic gene actions involved in the expression of anaerobic germination tolerance traits.

METHODOLOGY

Four anaerobic germination susceptible and high yielding genotypes were selected as female parents (MTU 1010, MTU 1156, SM 10 and SM 14) and one anaerobic germination tolerant line, MTU 1140 was selected as male parent and hybridization was performed to generate four crosses during kharif 2017 at Regional Agricultural Research Station, Maruteru. Six populations $(P_1, P_2, F_1, F_2, BC_1 and BC_2)$ of these four crosses were evaluated for anaerobic germination tolerance as detailed by Reddy et al. (2015) using protray method during 2019. Three days pre-germinated seeds at pigeon breast stage of the six generations (P_1, P_2) P_2 , F_1 , F_2 , BC_1 and BC_2) of the four crosses, were sown in pro-trays (35.5 x 10 x 4.5cm) at about 1cm soil depth and submerged in concrete water tanks by filling water upto 10cm above the trays. Water level in the tanks was maintained at that depth for 14 days

(Figure 1 and 2). The trays were removed from the concrete tanks after 14 days of submergence and data on anaerobic germination tolerance traits was collected for all the generations of each cross in each replication. The experiment was conducted in completely randomized design (CRD) with two replications. For each replication, 5 seeds were sown for P_1 , P_2 and F_1 of each cross, while 10 seeds were sown for BC₁ and BC₂ generations of each cross per replication. However, 40 seeds were sown for F_2 generation of each cross per replication. Observations were recorded for five anaerobic germination tolerance traits namely germination (%), shoot length (cm), root length (%), seedling dry weight (mg) and seedling vigour index. The means and variance of means for five quantitative traits were computed for each generation of the four crosses. To confirm the adequacy of simple additivedominance model and also to detect the presence of epistasis Mather's scaling test (1949) was applied.

RESULTS AND CONCLUSIONS

A perusal of the results indicated that dominance effects (h), had exceeded the corresponding additive effects in almost all the crosses, for all the anaerobic germination tolerance traits studied. Presence of duplicate type of epistasis, as inferred from the opposite signs noticed for dominance (h) and dominance x dominance (l) effects in most of the crosses for most of the traits confirmed the prevalence of dominance (h) effects. This indicated a predominant role of non-additive gene effects in the inheritance of various anaerobic germination tolerance traits and hence, the need for their exploitation through heterosis breeding. Pre-ponderant dominance (h) effects for root length and seedling dry weight were reported. Further, pre-ponderance of non-additive gene action for



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Table 1 Type of epistasis exhibited by four crosses for various anaerobic germination traits

Cross combination	Epistasis			
Germination per cent				
C ₁ = MTU 1010/ MTU 1140	Duplicate			
$C_{2} = MTU 1156/MTU 1140$	Duplicate			
$\tilde{C_{3}} = SM 10/MTU 1140$	Duplicate			
C4=SM 14/MTU 1140	Duplicate			
Shoot length				
C1 = MTU 1010/ MTU 1140	Duplicate			
C2 = MTU 1156/ MTU 1140	Duplicate			
C3 = SM 10/ MTU 1140	Duplicate			
C4=SM 14/MTU 1140	Duplicate			
Root length				
C ₁ =MTU 1010/MTU 1140	Duplicate			
C ₂ =MTU 1156/MTU 1140	Duplicate			
$C_3 = SM 10/MTU 1140$	Duplicate			
C4=SM 14/MTU 1140	Duplicate			
Seedling dry weight				
C ₁ =MTU 1010/MTU 1140	Duplicate			
C ₂ = MTU 1156/ MTU 1140	Duplicate			
$C_3 = SM 10/MTU 1140$	Duplicate			
C4=SM 14/MTU 1140	Complementary			
Seedling vigour index				
C ₁ =MTU 1010/MTU 1140	Duplicate			
C ₂ = MTU 1156/ MTU 1140	Duplicate			
$C_3 = SM 10/MTU 1140$	Duplicate			
C4=SM 14/MTU 1140	Duplicate			
Anaerobic response index				
C ₁ =MTU 1010/MTU 1140	—			
C ₂ = MTU 1156/ MTU 1140	Duplicate			
$C_3 = SM 10/MTU 1140$	Complementary			
C4=SM 14/MTU 1140	Complementary			



Fig:1 Pro-trays used in the study.



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Fig: 2 Submerged pro trays in concrete tanks filled with water.

germination percentage, shoot length and seedlingvigour index was also reported. These results are in conformity with Srilakshmi (2017). The opposite sign of (h) and (l) noticed for most of the anaerobic germination tolerance traits in majority of the crosses indicated the role of duplicate type of epistasis (Table 1), which can be effectively utilized in pedigree method by delaying the selections to later generations, when the dominance effect is dissipated and also by emphasis on multiple crosses rather than simple crosses to make better use of the duplicate epistasis. The information on genetics of anaerobic germination tolerance contributing traits will further aid plant breeders in the selection of breeding programme for improvement of AG tolerance traits in rice.

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IRC/TM-1/PP-107

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TEMPERATURE INDUCTION RESPONSE: A HIGH THROUGHPUT SCREENING TECHNIQUE TO DISSECT THE GENETIC VARIABILITY IN ACQUIRED THERMOTOLERANCE OF RICE GENOTYPES

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World agriculture is facing major challenges to ensure global food security, posed by several abiotic stresses under the changing climate scenario. Extreme climatic changes like drought, high temperature, flooding, or rising sea levels constrain rice production, affecting about one third of the 700 million poor in Asia alone who live in rainfed rice-growing areas. In the face of these challenges, rice production needs to be maintained and improved using fewer input resources. Rice cultivation has to be intensified in rainfed-lowland, dry land (upland) cropping systems and marginal lands, many of which are prone to drought and high temperature stresses. Climate change may aggravate this problem in the future due to a higher probability of higher growing-season temperatures (Battisti and Naylor 2009). Under future climatic scenarios, rice will be exposed more frequently to episodes of drought and high temperature, as well as increasing mean temperatures. To alleviate this threat, it is necessary to improve the adaptability of rice genetically to cope with the warming climates. Association between adaptability of crop plants to high temperature stress and heat acclimation has been reported (Chen et al. 1982). However, the genetic basis for heat tolerance or adaptability to heat stress in rice is poorly understood (Lin et al. 2014). Heat acclimation is a physiological response manifested in the acquired thermo-tolerance of organisms or cells to lethal high temperatures following exposure to a moderate heat stress condition. One of the approaches to improve thermo-tolerance is to transfer superior alleles from intrinsically thermotolerant wild relatives. A large number of genetic variations exist for intrinsic tolerance among the varieties and landraces of rice. It is important to develop a rapid and reliable lab protocol that allows simultaneous screening of large number of genotypes. Temperature induction response (TIR) has been used as a screening technique to identify high temperature tolerant cotton lines (Khier et al. 2012). The present study, therefore, was planned to assess the genetic variability of the widely grown rice genotypes and land races using temperature induction response (TIR) to identify more sources for tolerance at cellular level (TCL).

METHODOLOGY:

The present research work was conducted in the Crop Physiology and Biochemistry Division, ICAR-National Rice Research Institute, Cuttack, during 2019-20.96 NRRI released varieties were used in the study. A novel technique of TIR that was to screen rice genotypes for tolerance at cellular level (Fig 1). The young seedlings were initially exposed to a mild temperature (sub lethal stress) following which, the seedlings were exposed to relatively a high temperature for a specific period of time. The per cent survival of seedlings and recovery growth of seedlings when transferred back to normal temperature was determined as a measure of tolerance. Based on the absolute growth of control as well as treated seedlings, the per cent reduction in recovery growth (% RRG) was determined.

 $RRG(\%) = {AGC-RGI}/AGC$

Where,

AGC=Absolute growth of control seedlings RGI=Recovery Growth of Induced seedlings



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Fig 1. Screening of two day old rice germplasm lines for tolerance at cellular level (TCL) using TIR technique

RESULTS:

The genotypes showed significant genetic variability in parameters linked with intrinsic tolerance. The per cent reduction in recovery growth varied from 45 per cent in N22 to 100 per cent in Moroberekan and other nineteen genotypes, with a mean of 78.9 per cent (Table 1). Genotypes such as Padmini, Sahbhagidhan, N22, Luna Barial, CR DHAN 201 And Luna Sankhi recorded the highest intrinsic tolerance in terms of lowest reduction in recovery growth. On the other hand, Rajalaxmi and other fifteen genotypes recorded the lowest intrinsic tolerance. Similarly, the per cent mortality which is an indication of survivability of seedlings under lethal temperature exhibited large variability ranging from 0.0 to 100 per cent. The results therefore clearly indicated the existence of wide and significant genetic variability for cellular level tolerance in rice genotypes. When the seedlings were not induced (non-acclimatized), the seedling mortality was almost 100 per cent. However, when induction was given, the

 Table 1: Variability in intrinsic tolerance among rice genotypes

Parameters	Mean	Minimum	Maximum
AGC	7.23	3.56	13.31
RGI	1.27	0.57	2.16
% RRG	78.9	45	100
% Survival of the seedlings	50.48	0	100

AGC- absolute growth of control, RGI- Recovery growth of induced and % RRG Percent reduction in recovery growth

majority of the genotypes exhibited more than 75 per cent survival. This again reiterates the importance of induction for survival of seedlings before their exposure to lethal stress. The results clearly indicated the existence of wide genetic variability in various parameters associated with TCL. Based on the %RRG, Padmini, Sattari, CR DHAN 501, N22, Luna barial, Pooja, CR DHAN 201, and Luna Sankhi were identified as the tolerant genotypes for high temperature stress. It is expected that the genotypes which have higher intrinsic tolerance register better growth during recovery. The actual recovery growth of the seedlings after exposure to lethal temperature was also assessed. The actual growth of seedling was arrived by computing the difference between final and initial growth of the seedling in both induced and absolute control treatments. The genotypes with superior intrinsic tolerance can be expected to actively respond to the induction treatment and grow during recovery period. Therefore, the difference in actual growth in the seedling between induced and absolute control treatment is a good measure of thermotolerance.

CONCLUSION:

From the study it can be concluded that TIR technique is an easy and rapid screening protocol to identify genetic variability under high temperature stress in rice within a short time period. This is a high-throughput screening technique that is suitable for screening large number of genotypes within short period of time.

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PHENOTYPIC AND MOLECULAR ANALYSIS OF BACTERIAL BLIGHT RESISTANCE IN RICE CULTIVARS FROM EASTERN AND NORTHEASTERN INDIA

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Bacterial blight (BB) of rice, caused by Xanthomonas oryzae pv. oryzae (Xoo), is found worldwide and is particularly destructive in Asia during monsoon season. Development of resistant cultivars by incorporating major resistance (R) genes(s) has been proved to be the most effective strategy to control BB. The knowledge of the Xoo pathotype diversity is essential for the selection of R genes that could be deployed in future breeding programmes. With the everevolving pathogens and changing climate patterns, it is now essential to know the status of the resistance gene(s), to expand genetic resources with novel BB resistance genes, to deploy and pyramid them in breeding programs for durable resistance to Xoo. Therefore, the present study was carried out to identify BB resistance genes deployed/selected through systematic rice breeding programmes and by natural selection in rice germplasm of eastern and northeastern (NE) India.

METHODOLOGY

Two hundred and thirty-five rice germplasm including 95 NRRI released varieties, 115 landraces from eastern and NE India, 24 Xa/xa differential lines (IRBBs) and the susceptible check (IR24) were grown in the NRRI field during the wet season (July– November 2016). For evaluation against BB-Cuttack (Odisha) isolate, the plants were inoculated with pathogen inoculum through leaf clipping method. Five fully expanded uppermost leaves from five plants of each entry were clip inoculated at around six weeks after transplanting (i.e. at the maximum tillering stage). The lesion lengths were recorded after three weeks on a single leaf from each of the five inoculated plants. Based on the lesions on the inoculated leaves, the germplasms were scored on a scale of 0-9 (SES, 2013) and were categorized as resistant (0-3), moderately resistant (3.01-6) and susceptible (6.01-9). A subset of 70 rice accessions (released variety: 40; landrace: 30) comprising resistant (35), moderately resistant (21) and susceptible (14) genotypes were surveyed for ten major R genes (*Xa1, Xa3, Xa4, xa5, Xa7, xa8, Xa10, Xa11, xa13* and *Xa21*) using a total of 14 reported molecular markers. Microsoft Excel was used to work out the averages and standard deviations of disease scores and to prepare the graphs.

RESULTS

Pathotyping :

The pathotyping of BB-Cuttack was done based on the disease reaction pattern on twelve monogenic differentials. The near-isogenic lines (NILs) possessing Xa7, xa8, Xa11, and Xa21 showed resistance against BB-Cuttack, while Xa3 and the susceptible check IR24 showed susceptible reaction. However, the present isolate exhibited a moderate level of incompatibility with Xa4, xa5, Xa10, xa13, Xa14, and Xa23. The pyramided lines harbouring Xa21 and Xa7 showed resistant reactions. Interestingly, IRBB52 (Xa4+Xa21) exhibited moderate resistance response, while the NIL (IRBB21) carrying Xa21 was resistant.

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Fig. 1. Screening of rice germplasm for resistance to bacterial blight. a, Percentage of bacterial blight resistant, moderately resistant and susceptible genotypes under 95 varieties and 115 landraces; b, Frequency of released varieties and landraces under each category of R genes

IRBB53 carrying xa5 and xa13 was resistant even though the NILs carrying xa5 and xa13 were moderately resistant to the pathogen. The present isolate somewhat matches with the race 1 of previously reported Cuttack isolate (Mondal et al., 2014) showing similar disease reaction for xa5, xa8, Xa10, Xa11, and Xa21. However, its reaction to Xa1, Xa3, Xa4, Xa7, xa13, and Xa14 was different. In another study, ten different pathotypes have been reported within 152 BB isolates collected from Odisha (Mishra et al., 2013). The present BB isolate largely matches the pathotype X in incompatible reaction with Xa7, xa8, Xa11 and Xa21 and partially incompatible reaction with Xa1, xa5, and xa13. But it differs from the pathotype X in the reaction with Xa3 and Xa4 which were categorized as incompatible (Mishra et al., 2013). xa5 and xa13 alone were moderately resistant to the present isolate. However, when combined, these genes showed quantitative complementation and were resistant to the pathogen.

Phenotyping :

The released varieties were phenotypically categorized into resistant (29), moderately resistant (42) and susceptible (24) (Fig.1a). Varieties such as IR64-Sub1, CR Dhan 601, Satyakrishna, Swarna-Sub1, CR DHan 505, Kalyani II, Moti, Nua Chinikamini, Improved Tapaswini, Varshadhan, CR Dhan 300, Jalamani, Khitish, Pyari, CR Dhan 701, Gayatri, Kalinga-III, Nua Dhusara, Nua Kalajeera, Prrona bhog, Naveen, Neela, etc. were found to be resistant to BB-Cuttack (Score: 1-3). Out of 155 rice landraces, only 8 (7%) cultivars were resistant, while 60% of the landraces were susceptible to BB-Cuttack (Fig. 1a). Resistant landraces were 'Kalajeera', 'Kasalath' (ARC6000), 'Rudra ahu' (ARC5801), ARC5774, ARC5791, 'Pani Kekoa' and 'Murgi Badam'.

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Genotyping:

Based on marker assay, *Xa1* was detected in 27 out of 70 rice accessions, followed by *Xa7* (19 acc.), *Xa4* (14 acc.), *Xa10* (13 acc.), *Xa3* (11 acc.) and *Xa11* (10 acc) (Fig. 1b). *xa5*, *xa13* and *Xa21* were not recorded in any of the rice accessions except, IR64-Sub1 and Improved Tapaswini. Although CR Dhan 505 found negative for all the surveyed resistance genes, it showed resistance to BB. The resistance gene xa8 has been reported to be effective against east Indian BB pathotypes (Mishra et al., 2013; Mondal et al., 2014). We also found that xa8 is completely resistant to the present BB isolate. However, none of the used markers were polymorphic between xa8-positive and negative controls.

CONCLUSION

The current findings and the available information on the distribution of BB races in eastern





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and NE India indicated that Xa1, Xa7, and Xa11 have frequently been selected in breeding programmes, and the frequency of xa5, xa8, xa13 and Xa21 should be increased in the released varieties in different combinations to achieve durable resistance.

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COMBINING ABILITY AND HETEROSIS STUDIES FOR GRAIN YIELD AND ITS COMPONENTS IN RICE (ORYZA SATIVA L.)

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Rice is one of the most important food crops in the world, especially in Asian countries. It is estimated that by 2035, global demand for rice will increase to 852 million tons; however, records show that annual yield growth was near to 1% in the past decade. Given the limited resources currently identified, along with various environmental constraints, such as pest, diseases and unfavorable farming conditions, demand for sustainable ways to increase rice production remains an enormous challenge (Gramaje 2020). Hybrid rice technology offers the most effective solution to enhance yield for sustainable rice cultivation. The technology revolutionized the rice farming through boosting the yield from 35 to 40 g/ha from straight varieties of rice to the tune of 65 to 70 q/ha in rice hybrids. For generating promising hybrids, selection of desirable parents and studying the combining ability of them to derive heterotic crosses is very much desired. Keeping the importance of the aspect, present study was carried out to know the combining ability of parental lines and magnitude of heterosis obtained for grain yield and important yield attributes.

METHODOLOGY

The experiment was conducted at Rice Research Center of Agricultural Research Institute, Hyderabad, Telangana, India. During *rabi*, 2018-19, 10 restorer lines and 3 stable CMS lines were sown and planted in three different staggered sowings and affected crosses in line x tester mating design to obtain 30 hybrids. These 30 hybrids along with their 13 parents and two checks (27P63 and MTU 1001) were grown in a single row of 4 m length with 2 replications in RBD by adopting a spacing of 20×15 cm during *kharif*, 2019. Observations were recorded on five randomly selected plants for estimation of different traits *viz.*, plant height (cm), effective bearing tillers, panicle length (cm), spikelet fertility (%) and number of grains per panicle. However, days to 50% flowering and grain yield (kg/ plot) was recorded on a whole plot basis (plot size 5.67 sq. m), whereas, test weight (g) were recorded on a random sample taken in each plot. The character means of each replication was subjected for analysis of variance, combining ability and estimated the heterosis using standard statistical methods.

RESULTS

Analysis of variance revealed significant difference among lines, testers and hybrids for majority of the traits indicating sufficient variability in the material studied. The per se performance of the hybrids for most of the traits was higher than that of parents. The hybrids CMS 59A x HHZ 5-Y3-Y1-Y2, CMS 59A x WGL 14, JMS 13A x HHZ 5-Y3-Y1-Y2, CMS 59A x IR 10 N 230, JMS 13A x RP 5980-109-12-9-27, CMS 59A x RP 5980-109-12-9-27, JMS 13A x RNR 19361, CMS 46A x WGL 347 and CMS 59A x WGL 347 had recorded better per se performance for most of the yield attributing traits. In the present investigation, the degree of dominance was more than unity for the traits viz., effective bearing tillers and spikelet fertility indicating the predominance of non-additive gene action, while days to 50 per cent flowering, plant height, panicle length, test weight number of grains per panicle and grain yield per plant were found to be governed by additive gene action. Two lines, HHZ 5-Y3-Y1-



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Y2 and RP 5980-109-12-9-27 and a tester CMS 59Arecorded significant positive gca effect for grain yield per plant. The gcaeffects revealed that among the lines, HHZ 5-Y3-Y1-Y2 had significant gca effects in the desired direction for important traits viz., grain yield per plant, panicle length and test weight, whereas the line RP 5980-109-12-9-27 was found good for grain yield per plant and spikelet fertility. Among the testers, CMS 59A was identified as good general combiners for the traits viz., grain yield per plant and earliness. In the present study, the effectiveness of choice of parents based on mean performance alone was not appropriate for predicting the combining ability of the parents, hence it was clearly observed in some cases that the lines and testers with good mean performance have not been good general combiners and vice versa, thus the association between mean performance and GCA effects was evident. Similar findings were earlier reported by Manjunath et al. (2020).

The *sca* effects revealed that among thirty hybrids, JMS 13A x RNR 19361 was recorded highest significant positive sca effect for grain yield per plant followed by CMS 59A x SYE 503-78-34-2, CMS 46A x WGL 347 and JMS 13A x RP 5980-109-12-9-27 and found to be desirable. Two hybrids exhibited significant and negative sca effects for days to flowering CMS 59A x WGL 32100and JMS 13A x MTU 1001and were considered to be highly desirable for earliness.JMS 13A x RNR 19361 was found to be good specific combiner for grain yield per plant and spikelet fertility.Further three hybrids viz.,CMS 59A x SYE 503-78-34-2, CMS 46A x WGL 347 and JMS 13A x RP 5980-109-12-9-27 were found to be good specific combiner for grain yield and majority of yield attributing traits.

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Heterosis studies showed that the heterobeltiosis over better parent ranged from 1.87 to 69.63 % for grain yield. Twenty two hybrids showed



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significant positive heterosis for this trait. Highest significant positive heterobeltiosis was recorded by CMS 59A x IR 10 N 230, CMS 59A x RP 5980-109-12-9-27, CMS 59A x WGL 14, CMS 59A x WGL 823, CMS 59A x HHZ 5-Y3-Y1-Y2, CMS 59A x SYE 503-78-34-2, CMS 46A x WGL 32100, CMS 46A x RP 5980-109-12-9-27, CMS 59A x MTU 1001 and CMS 59A x WGL 32100. For standard heterosis, over variety (MTU 1001) ten hybrids were recorded positive significant heterosis. Highest significant positive standard heterosis was recorded for CMS 59A x HHZ 5-Y3-Y1-Y2 followed by CMS 59A x WGL 14, JMS 13A x HHZ 5-Y3-Y1-Y2, CMS 59A x IR 10 N 230, JMS 13A x RP 5980-109-12-9-27, CMS 59A x RP 5980-109-12-9-27, JMS 13A x RNR 19361, CMS 46A x WGL 347, CMS 59A x WGL 347 and CMS 46A x WGL 32100.

CONCLUSIONS

This study concluded that two lines, HHZ 5-Y3-Y1-Y2 and RP 5980-109-12-9-27 and a tester CMS 59Arecorded significant positive *gca* effect for grain yield per plant. Three hybrids *viz.*, CMS 59A x SYE 503-78-34-2, CMS 46A x WGL 347 and JMS 13A x RP 5980-109-12-9-27were found to be good specific combiner for grain yield and majority of yield attributing traits. Two hybrids, CMS 59A x HHZ 5-Y3-Y1-Y2 and CMS 59A x WGL 14 were recorded positive significant heterosis over the standard hybrid check (27 P63). Among the test hybrids, CMS 59A x HHZ 5-Y3-Y1-Y2and CMS 59A x WGL 14were identified as potential hybrids for most of the traits studied based on their *per se* performance and heterosis estimates.

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BIOCHEMICAL RESPONSE OF RICE (ORYZA SATIVA L.) TOWARDS SALT STRESS

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Amongst all abiotic stresses, soil salinity is one of the main factors limiting the crop production throughout the rice growing countries. In this study we evaluated the effects of different levels of salt stress at various growth stages in contrasting rice varieties on enzymatic antioxidant defence system. Rice varieties, CSR 43 (salt tolerant) and Pusa 44 (salt sensitive) were evaluated at three stages (seedling, 50% flowering and milky) of plant development under four levels of salt stress (0, 4, 812 dS/m). The basal level of antioxidant enzymes SOD, POX and GR was found to be higher in tolerant variety as compared to sensitive variety. Increase in salinity from 0 to 12 dS/m led to 2.25- and 1.86-fold increase in SOD activity during the seedling stage of CSR 43 and Pusa 44, respectively. Maximum activity of POX was observed at seedling stage,

followed by 50% flowering and milky stage. The activity of catalase (CAT) and ascorbate peroxidase (APX) was found to be significantly affected by the stage of development of the plant. GR activity increased 1.85-, 2.09- and 2.37-fold at seedling, 50% flowering and milky stage with increase in salinity level from 0 to 12 dS/m in CSR 43. While a decrease of 1.60-, 1.76and 3.23-fold was observed in Pusa 44. The upregulation of APX during seedling stage, CAT at 50% flowering stage and SOD at milky stage of plant development were observed. Thus, the activity of antioxidant enzymes varied with variety, developmental stage and level of salt stress. The higher activity of antioxidant enzymes in tolerant variety as opposed to sensitive variety enabled it to overcome the damage caused by salinity at all developmental stages.



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RESTRICTING SODIUM OR ENHANCING POTASSIUM UPTAKE IS VITAL FOR SURVIVAL UNDER SALT-STRESS AND IMPACT OF OTHER TOLERANCE MECHANISMS IN RICE CULTIVARS WHICH DIFFER IN SALT-SENSITIVITY

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Rice implies several techniques to encounter salt stress. Cultivars possessing various skills i.e. better Na⁺ exclusion with greater Na⁺ sequestration ion ability in older tissues and moderately tissue tolerance capacity could be useful in developing superior salt tolerant varieties. Diverse cultivars possessing more than one tolerance mechanisms are highly valuable in crop improvement.

The objectives of the present study were to check the existence of different salt tolerance mechanisms in twenty four rice cultivars and characterization of physiological parameters in imparting salt-stress in rice.

METHODOLOGY

The study was conducted in two consecutive years of 2014 and 2015 at different rice growing seasons at National Rice Research Institute, Cuttack, India. Twenty four rice cultivars comprising Pokkali (Accession No. AC39416A) and FL478-highly tolerant to salinity (Singh & Sarkar 2014), IR29susceptible to salinity and twenty one other cultivars collected from coastal saline belt of eastern India were included in the present study.

Rapid screening technique for evaluation of responses of the cultivars to salinity stress at seedling stage was followed (Gregorio *et al.* 1997; Sarkar *et al.* 2013).

Leaf to leaf compartmentation: The plant was grown up to 22 days in normal Yoshida's culture solution, thereafter salinity treatment was imposed with NaCl (EC 12 dS m⁻¹). Leaf samples were collected after 1, 2, 3 and 4 days after saline treatment. At each harvest, the 2^{nd} , 3^{rd} and 4^{th} leaf of each individual plant was excised, oven dried @ 70°C for 3 days and estimated for Na⁺ and K⁺ content. The parameter evaluated was the increase in Na⁺ quantity in leaf 4 between two harvests divided by the increase in Na⁺ quantity in leaf 3 during the same period as per the following formulae.

Sodium compartmentation $(C_{Na}) = \{(Sodium content in leaf 4 at day 4 Sodium content in leaf 4 day 3) / (Sodium content in leaf 3 at day 4 Sodium content in leaf 3 day 3) \}$

Tissue tolerance: After 14 days of growth in normal Yoshida's culture solution, the seedlings were treated under different concentrations of salt. All together four different levels of salinity treatments were applied (i.e. EC 0, 6, 12 and 18 dS m¹). Samplings were done when a particular variety at EC 18 dS m¹ exhibited the score of 7 (i.e. complete cessation of growth; most leaves dry; some plants dying). Youngest fully grown leaf from top (2nd from top) were harvested, and used for Tissue tolerance analysis.

To estimate the Na⁺ concentration associated with differing degrees of chlorophyll loss, the following procedure was adapted.

I. For each variety, the leaf data were segregated into class interval according to their chlorophyll content.



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II. Then the Na⁺ concentrations of all leaves falling in that chlorophyll class were then averaged.

III. The LC₅₀ for Na⁺, a paraphrase of the LD₅₀ of toxicology, is defined as the mean Na⁺ concentration in individual leaves falling into the 40-60 % class. The correlation coefficients and regression equations were drawn for each variety, which helped in calculating the LC₅₀ values.

The chlorophyll was measured spectrophotometrically (Model SL 159, Elico, Hyderabad) by taking O.D at 663.6 and 646.6 nm following Sarkar *et al.* (2013).

For Na and K estimation, 50 mg of dried plant materials were placed in 25mL test tubes and tissue extraction was done with 1.0N HCl. Plant tissues with 5 mL 1N HCl was heated in a water bath at 90 °C for two hours. The extract was kept at 30 °C for 48 h. The extracted tissue was then diluted with distilled water and left overnight. The extract was filtered by using Whatman #40 filter paper (Wipro GE Healthcare, Mumbai, India). Sodium and potassium contents in the tissue extracts were determined by using Flame Photometer (Model 130, Systronics India Ltd, Ahmedabad, India).

RESULTS

• Na-compartmentation (cna) was less than 1 in a few tolerant rice cultivars such as AC





39416A (0.48), Kalaputia (0.58), FL 478 (0.65), Nangalmutha (0.78) Ravana (0.86) And Paloi (0.95). Some medium tolerant and susceptible *cvs* also had leaf to leaf partitioning values less than 1 *such as* IR 84649-260-28-1 B (0.76), IR 84645-312-11-1 B (0.78), Marisal (0.86), AC 847A (0.69), AC 813 (0.86). Few tolerant cultivars *like* Kamini (1.09), Rupsal (1.14), Talmugra (1.19) Rashpanjor (1.27) and AC 1472 (1.25) had leaf to leaf partitioning values less than 1.5.

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The concentrations of Na⁺ in respect of 50% reduction of chlorophyll levels i.e. LC_{50} were significantly greater in susceptible cultivar IR29 (26.5 mg g¹ dry weight of leaf), followed AC1996 (24.5 mg g¹ dry weight), AC847A (24.2 mg g¹ dry weight), AC813 (22.8 mg g¹ dry weight) and Marisal (20.9 mg g¹ dry weight). LC_{50} varied between 12.5 and 17.5 mg g¹ dry weight among the rest of the medium tolerant



Fig 2: Tissue tolerance level of different tolerant genotypes, medium tolerant genotypes and susceptible genotypes.



Fig 3: Standard evaluation score (SES) after 7 days of salt stress





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cultivars. On an average, 50% chlorophyll reduction occurred at 14.1, 17.4 and 21.5 mg Na⁺ level in tolerant, medium tolerant and susceptible cultivars.

Salt tolerance score varied from 1 to 9 among the tested cultivars. Injury symptom was almost absent in certain cultivars such FL478, AC39416A, AC1151, Kalaputia, Ravana and were termed as highly tolerant whereas score 9 was given to IR29. The injury symptom of a few other cultivars such as Paloi, Rupshal, Kalaputia, AC1472 and Kamini were also lesser compared to the rest of the cultivars and are termed as tolerant (score 3). The other cultivars either received score 5 or 7 or 9 depending on their sensitivity to salt stress.

CONCLUSION

The tolerant cultivars even differed in terms of Na⁺ transportation and sequestration of Na⁺ in older tissues. Restricting Na⁺ transportation from old tissues to young tissues imparted tolerance to salt stress in rice.

 $\label{eq:cultivars} Cultivars with multiple tolerance mechanisms \\ such as better Na^+ exclusion capacity and greater Na^+ \\$

sequestration ability in older tissues with medium tissue tolerance could help in developing superior salt tolerant varieties.

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Rice Research and Development for Achieving Sustainable Development Goals

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IRC/TM-1/PP-112

Indian Rice

PHENOTYPIC, MOLECULAR CHARACTERIZATION AND ASSESSMENT OF GENETIC DIVERSITY OF RICE (ORYZA SATIVA L.) CULTIVARS FOR BLB RESISTANCE AND SUBMERGENCE TOLERANCE USING TRAIT SPECIFIC STS MARKERS.

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Rice productivity is constrained by climatic adversities, pests, diseases (bacterial, viral and fungal origin) and many other threats. Developing cultivars that are high yielding as well as stress resilient seems a better solution to tackle global food security issues. This study investigates potentiality of 24 rice cultivars against *Xanthomonas oryzae pv. Oryzae (Xoo)* infection causing Bacterial leaf blight disease and submergence stress at both genotypic and phenotypic level, along with assessment of their genetic diversity.

METHODOLOGY

Twenty four rice genotypes, including checks for BLB (two resistant: IRBB60 and Improved PR114 ; one susceptible: IR24) and Submergence (two tolerant : FR13A and Swarna-Sub1; one susceptible : Swarna) were genotyped. DNA was extracted from young leaves of 3 weeks old seedlings using a simplified mini scale DNA isolation protocol (Dellaporta et al. 2002) with requisite modifications. DNA amplification was carried out using previously reported STS and SSR markers to analyze the allelic status of BLB resistance (*Xa4*, *xa5*, *xa13*, *Xa21*, *Xa38*) and Submergence tolerance (*Sub1*) genes.

Xanthomonas oryzae pv. *Oryzae* (*Xoo*) inoculums were prepared for bioassay evaluation. Clip inoculation method was adopted to inoculate bacterial suspension into the leaves of 45 days old rice plant. Then 14 days and 28 days post inoculation, the extent of disease progression on the leaf surface, in form of bacterial lesions were recorded to evaluate the disease

severity as per IRRI scoring standards. Submergence screening on the other hand was performed with twenty-one days old seedlings in a set of 3 replications in submergence tanks at National Rice Research Institute, Cuttack, Odisha, India. After 14 days of complete submergence, the treatment was terminated by draining out water from the tank. The trays were kept outside for 7 days, post de-submergence and on 8th day, scoring for survival rate percentage (%) was recorded.

The possible population structure of genotypes was assessed using Bayesian model based cluster analysis available in software STRUCTURE v 2.3.4. A neighbor joining phylogenetic tree was also constructed based on Nei's unbiased pair wise genetic distance using software MEGA 6 to determine the genetic relatedness of the sub populations (Tamura et al. 2007). Moreover, PCoA and AMOVA analyses were also carried out using GenAlExv6.5.

RESULTS

Molecular characterization using gene specific markers for BLB resistance and Submergence tolerance displayed the presence of *Xa4* resistant allele (78.95%), *xa5* (15.79%) but *xa13* and *Sub1* tolerant allele were not found in any test genotypes. However, new alleles for *Xa21* (84.21%) and *Xa38* (10.52%) genes were spotted in several genotypes. Phenotypic evaluation for respective stress situations was performed to record the cultivars response. None of the genotypes showed resistance against *Xoo* isolates



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based on disease severity, except for positive control (IRBB 60), although varieties viz., Tapaswini and Konark carrying *Xa4* and *xa5* gene combination showed moderate susceptibility. Likewise, survival percentage of genotypes under submergence stress varied from 0 to 100%. Tolerant checks FR13A (100%) and Swarna- Sub1 (97.78%) exhibited highest survival rate, whereas, Gayatri (57.78%) recorded high survival along with a few other cultivars that also displayed substantial level of tolerance to flooding stress, even though all these test genotypes lacked *Sub1* tolerant allele in their genetic background.

A successful breeding programme requires assessment of genetic diversity to select promising parental lines for potential crosses. A total of seven trait specific STS and two SSR markers generated an average of 2.38 allele per locus. Polymorphism Information Content value ranged from 0.08 to 0.42 with an average of 0.20. Model based structure analysis categorized 24 genotypes into two sub-population (Fig.1), which was in close correspondence with Nei's genetic distance-based Neighbor Joining tree and PCoA analysis. The analysis of molecular variance (AMOVA) revealed more genetic variation within population and comparatively less among population.

CONCLUSION

Development of durable rice resilient to various biotic and abiotic stresses is the need of the hour vis-



Fig.1 Model based population structure viz., SP1 (Red) & SP2 (Green) of 24 rice Genotypes

à-vis a challenge. The current study suggests the existence of varying degree of BLB resistance and submergence tolerance amongst the popular high yielding rice genotypes investigated at both genotypic and phenotypic level with respect to availability of either single or a cocktail of two or more different stress resistant genes. Our work revealed the allelic status of five BLB resistant genes Xa4, xa5, xa13, Xa21 and Xa38 present in different gene combinations in majority of rice cultivars investigated, displaying varying degree of host response from moderate susceptibility (Tapaswini and Konark carrying gene combination Xa4 and xa5) to highly susceptible (Jaya) on disease scoring index against the Xoo isolate. Likewise, tolerant Sub1 allelic fragments were not reported in any of the genotypes but absence of sub1 tolerant allele did not confirm their susceptibility status during phenotypic screening under submergence stress, indicating the presence of some other submergence tolerant genes and /or minor QTLs or a different escape mechanism. The information generated from this study would increase efficiency in selecting suitable parental pairs that are high yielding, diverse and with certain characterized /untapped inherent abilities to withstand different biotic and abiotic stress adversities, for development of stress resilient durable rice varieties in future breeding programmes for achieving sustainable production of rice.

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IRC/TM-1/PP-113

. Indian Rice

TRANSMISSION ELECTRON MICROSCOPY FOR UNDERSTANDING PHYSIOLOGICAL STRESS RESPONSE IN RICE

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In the recent decades, a plethora of techniques and instrumentation have been employed for understanding physiological stress response in major crops like rice. The advent and advances in transmission electron microscopy (TEM) have given the advantage of elucidating the changes at the level of cellular ultrastructure. The preparation and processing of the sample for transmission electron microscopy is most crucial for accurate analysis of the ultrastructure of cells. We have standardized a unique method for preparation of rice leaf samples and their ultramicrotomy for further analysis through transmission electron microscope. The various steps in the rice leaf sample preparation include sample collection, primary fixation, secondary fixation, dehydration, clearing of dehydrating agent, infiltration and embedding with intermittent steps of washing at regular intervals. Epoxy based spurr resin is used for embedding of the rice leaf samples which further enables proper ultramicrotomy of the embedded samples. Ultrathin section (70-90 nm) of rice leaves embedded in the spurr resin have been obtained by using an ultramicrotome (Leica) and glass knives. The ultrathin section are placed in small copper grids and double stained with uranyl acetate and lead citrate. The time of exposure to these heavy metal stains have been standardized for different types of samples. Rice leaves under various physiological stress like draught and low light have been processed through this method and analyzed using TEM (Jeol).

METHODOLOGY

1. Sample collection and primary fixation: Rice leaf samples were collected from plants under drought and low light stress as well as their respective controls. The samples were then fixed with primary fixative glutaraldehyde (2.5%) overnight.

2. Secondary fixation: The samples were washed thrice with phosphate buffer (pH 7.4) and fixed with secondary fixative osmium tetraoxide under the fumehood. The samples were incubated for six hour for secondary fixation.

3. Dehydration: The samples were washed thrice with phosphate buffer and then treated with various concentration of ethyl alcohol (30%, 50%, 70%, 90% and 100%) for 30 minutes each.

4. Clearing: The dehydrating agent was cleared by treating the sample with propylene oxide for two hours.

5. Infiltration: Three different mixtures of spurr resin and propylene oxide was used for infiltration. These are: (a) Propylene oxide (3): Resin (1), (b) Propylene oxide (2): Resin (2) and (c) Propylene oxide (1): Resin (3). The samples were treated with each mixture for 4-5 hours under vacuum. Finally the samples were treated with pure resin for 4-5 hours under vacuum.

6. Embedding: The samples were embedded in spurr resin using moulds. The samples were incubated at 60° c for 48-72 hours for polymerization of the resin.

7. Ultramicrotomy: Hard blocks of samples embedded in resin were further subjected to ultramicrotomy using glass knives. 70-90 nm thick sections were transferred to copper grids (mesh 300).



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Fig 1 (A) Electron micrograph of a chloroplast inside a rice leaf cell (5000X); (B) Rice leaf tissue (Draught stress) with multiple cells with distinct chloroplasts, nucleus and cell membranes (2000X).

8. Staining: samples placed in copper grids were stained with uranyl acetate for 5-10 minutes a lead citrate for 2-5 minutes.

9. TEM analysis: Properly stained sampled were observed under the transmission electron microscope in different magnifications.

RESULTS

Ultrastructure of the rice leave cells were observed under the transmission electron microscope. The structure of the cells and cellular organs like chloroplast, nucleus, endoplasmic reticulum and mitochondria were identified and compared (Fig 1).

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DEVELOPMENT OF BACTERIAL LEAF BLIGHT RESISTANCE IN HYBRID RICE (ORYZA SATIVA. L)

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ABSTRACT

Rice is known as "grain of life" because it is the most important basic food in the world and nearly 2 billion people depend on it for more than 80% of their calories. Only Asia is a region that produces around 90% of the world's rice: its consumption is very high, which has exceeded 100 kg/capita annually, and it provides more than 50% of the calorie requirement within this area. Despite the significant increase in rice production and productivity witnessed in the last five decades, a significant proportion of rice production is lost every year. Hybrid rice technology is practically feasible technology to increase future rice production. The technology revolutionized the rice farming through boosting the yield from 35 to 40 q/ha from straight varieties of rice to the tune of 65 to 70 g/ha in rice hybrids. Due to slow improvement in HYV and reduction in natural resources along with biotic and abiotic stresses, increasing rice production for the fulfilment of future food demands is quite challenging. Bacterial leaf blight (BLB) is one of the main constraints to the worldwide rice production system. Management of BLB of rice has been always a herculean task. Due to its seed-borne nature, and its survivability in wild rice or other grassy weeds, make this disease very complex and continuous supply of inoculum, especially in low-land rice growing areas is a very challenging issue. Exploitation of host resistance has been always the safest approach. But identification of resistance source and the development of resistant cultivar is the main problem. Conventional breeding strategies are generally used for the development of cultivar. But these are very slow and time consuming as well as labourintensive process. It also requires extensive phenotypic evaluation of breeding material, thus takes several years to release a variety. The recent technological advancement in molecular breeding and functional genomics helps to improvise our resistance breeding system and to shape the plant defence system in new ways through molecular approaches. Nowadays, a combine approach including conventional breeding along with marker-assisted selection becomes very popular in the bacterial blight resistance hybrid rice breeding program. Already some rice cultivars were developed and some elite cultivars were genetically improved by using conventional breeding in combination with marker-assisted backcross breeding (MABB) approach. Various molecular approaches have been adopted to deploy them for getting a longterm durable resistance. Gene pyramiding of several resistance genes through marker assisted selection is found to be the most effective strategy.

Keywords: Hybrid Rice, BLB, MAS and MABB

. Indian Rice

IRC/TM-1/PP-114



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IRC/TM-1/PP-115

Indian Rice

IMPROVING RICE BLAST RESISTANCE OF BPT 5204 THROUGH MOLECULAR MARKER-ASSISTED BACKCROSSING

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Rice blast, caused by the fungus Magnaporthe oryzae, is the most devastating biotic constraints that challenge the rice production in all the ecosystems and causes considerable economic loss worldwide (Imam et al., 2016). Improvement of disease resistance through conventional breeding is relatively slow, while MAB using major resistance genes is considered to be an efficient and technically feasible approach for rice blast resistance improvement to stabilize the production. Blast resistance gene Pi-9 exhibits broad spectrum resistance against different races of rice blast fungus and is hence considered more stable across geographic locations (Variar et. al 2009). Availability of closely linked markers has made rapid and precise selection of the targeted gene possible (Tanksley et al., 1989) through marker-assisted backcross breeding approach. In the current study, BPT 5204, a high yielding mega rice variety with exceptional good grain quality but otherwise susceptible to blast disease was selected as a recurrent parent for incorporation of major blast resistance genes Pi9 and Pib through marker assisted backcrossing (MAB) to improve its blast resistance.

METHODOLOGY

Two near isogenic lines, IRBL9-w and IRBLBb carrying blast resistance genes *Pi-9* and *Pib*, respectively in the background of LTH were used as donors for incorporation of blast resistance gene into susceptible mega variety BPT 5204 using marker assisted backcrossing. For targeted introgression of *Pi9* and *Pib* into BPT 5204, a simultaneous and stepwise marker assisted backcross breeding strategy was adopted. Two separate backcrosses were carried out wherein the blast resistance genes Pi9 from IRBL9-w as well as Pib from IRBLB-b, were introgressed into BPT5204, respectively. The F₁ plants derived were confirmed for their hybridity by using linked codominant markers, AP5930 (specific for Pi9) and RM208 (specific for Pib). In addition to this gene based STS marker 195-1R were used to identify the plants carrying Pi9 gene.DNA isolation, PCR amplification with the markers AP 5930 and RM208, selection of the heterozygous plants followed by hybridization of recurrent parent with the confirmed plants for the linked markers were done upto BC3F1. The BC3F1s were confirmed for the presence of Pi9 with AP 5930 as well as 195-1R and Pib with RM208, the confirmed plants were selfed. In BC3F2 single plants were confirmed for blast resistance with linked markers and also with phenotypic selection in an outdoor blast nursery and carried forward for agronomic selection.

RESULTS

We report here the introgression of blast resistance genes *Pi9* and *Pib* into the genetic background of good grain quality popular rice variety, BPT5204, for enhancing its blast resistance through marker-assisted backcross breeding strategy. Combining marker-assisted and phenotypic selection, 4 near isogenic lines (NILs) with homozygous *Pi9* and 6 NILs with homozygous *Pib* were selected. The evaluation of results under natural uniform blast nursery conditions showed that the selected BPT5204+*Pi9* NILs were highly resistant against leaf blast with SES score '0', while the recurrent parent BPT5204 had a score of '7'. However, the NILs with Pib gene showed





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BPT5204 NILs	Gene present	Days to 50% flw.	Plant height (cm)	# panicles/m2	Grain Yield (kg/ha)	Blast score (SES)
CRR741-13-1-22	Pi9	94	91	278	3494	0
CRR741-13-1-57	Pi9	93	87	266	2820	0
CRR741-22-2-16	Pi9	115	98	254	4940	0
CRR741-38-2-6	Pi9	115	96	228	5504	0
CRR742-2-2-3	Pib	95	96	234	4329	4
CRR742-2-2-6	Pib	112	98	252	4636	4
CRR742-2-2-8-2	Pib	113	100	233	4804	4
CRR742-2-2-16	Pib	103	107	254	4902	4
CRR742-2-2-32	Pib	112	110	239	4092	4
CRR742-2-2-38	Pib	104	100	218	3558	4
BPT 5204 (RP)		114	95	232	3892	7
LSD 5%		1.5	7.7	66.2	635.5	
CV(%)		0.9	4.8	15.8	8.9	

susceptible reaction at Hazaribag, meaning the gene is not effective at this location. Among the 4 NILs with Pi9, 2 NILs (CRR741-22-2-16 & CRR741-38-2-6) were found very similar to the recurrent parent in a number of agronomic traits and grain yield. The lines were selected for further evaluation in multilocation trials under All India Coordinated Rice Improvement Project (AICRIP) for their possible release as variety for the benefit of the farming community.

CONCLUSIONS

Marker assisted foreground selection was successfully combined with phenotypic selection to develop broad-spectrum blast resistant version of popular rice variety BPT5204 for stabilizing production in the blast endemic areas. This study also confirmed that STS marker 195-1R could be reliably used for MAB even without phenotypic selection for detection of *Pi9* gene. The developed NILs with Pi9 gene have performed better under natural uniform blast nursery and showed resistance. These NILs can be used as a blast resistant version to replace the popular variety or used in future breeding programme for incorporation of blast resistance.

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IRC/TM-1/PP-116

. Indian Rice

ANDROGENESIS IN DEVELOPMENT OF DOUBLED HAPLOIDS FROM RICE HYBRID, CRHR32: YIELD AND QUALITY ASSESSMENT IN IDENTIFICATION OF PROMISING DH LINES

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Rice is one of the world's most important staple cereal food crop. Since world population is increasing rapidly, rice production needs to be increased to meet its demand in coming years to keep pace with increasing population. Due to green revolution technologies, rice production has improved to a great extent in past five decades. The dramatic increase (18%) in world food production was due to development of diversely adaptable, high yielding, insect and disease resistant rice cultivars. Though the production of rice has increased almost three fold over the last decades, the continued increase in sustaining yield for development of high yielding varieties is needed to meet the increasing demand of global population. Rice hybrids have shown significant yield advantages of more than 30% over inbred varieties However, frequent occurrence of hybrid sterility, continuous segregation, high seed cost in the progeny lines has discouraged the popularity of hybrid rice. These constraints in hybrid rice attract attention to adopt DH technology as there is a possibility to produce F1 performing high yielding DH lines from the heterotic F1s of rice by fixing hybrid performance exerting the partial to complete dominance in homozygous lines. Anther culture shows its effectiveness and applicability in the production of homogenous pure lines in rice. Conversely, the development of pure lines or inbred lines by conventional methods takes 6-8 years. Doubled haploid approach can effectively addresses the problems associated with hybrid rice through production of high yielding doubled haploids with uniform grain quality rice varieties (Tariq et al., 2008).

Grain quality, along with crop yield is an important criteria in most rice breeding programs especially in rice variety selection and development (Dela and Khush, 2000). Therefore, this approach was adopted to generate DHs from an elite rice hybrid, CRHR32 for development of high yielding rice lines along with acceptable grain quality.

METHODOLOGY

The present study was conducted at the National Rice Research Institute, Cuttack during 2012-2014 to develop a procedure for high frequency androgenesis in an elite indica rice hybrid CRHR32 for agronomic characters, yield and grain quality of the fertile doubled haploids respectively. The green plants were generated from CRHR32 by manipulating physical and chemical factors through anther culture which were assessed for their ploidy status on the basis of morphological characters.150 DH lines generated through androgenesis were evaluated under irrigated conditions using an augmented design. Based on these agronomic characters in the field trial, 20 DHs were selected and evaluated for promising yield and grain quality characteristics.

RESULTS

A total of 150 DHs from an elite indica rice hybrid CRHR32 were produced following androgenic protocol (Rout et al., 2016). Subsequently, these 150 DHs were assessed based on agronomic characters in the field for two consecutive seasons. Uniformity was maintained between and among the150 DH populations. Subsequently, 20 DHs showing the best



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Figure-1: Androgenesis to Field evaluation and Quality analysis

agronomic performances were selected for further evaluation. Out of 20 DHs, 6 selected DHs were found to be promising based on higher grain yield (2-5.16%) as compared to the parent. Besides, the rice cooking qualities characterized for 20 DHs included water uptake, grain length during cooking and volume expansion ratio. A number of DHs demonstrated superior grain quality characteristics such as head rice recovery, alkali spreading values, grain length, volume expansion ratio and amylose content. In addition, protein, iron, zinc and phytic acid were found in the range of (9.23-11.59), (1.7-3.1), (14.3-23.5), (0.71-1.48), respectively. Out of 6 DHs, a single DH showed considerable amount of zinc, iron, protein and phytate with yield of 6 t/ha. The amount of micronutrients along with quality and yield in DHs could prove the power of DH technology in development of promising lines (figure-1).

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CONCLUSION

DH technology could be taken as an efficient method among all the developed speed breeding techniques for development of promising rice lines to feed the increasing population. Besides, this method could be utilized for production of biofortified rice in a short period of time.

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. Indian Rice

DOUBLED HAPLOID TECHNOLOGY IN DEVELOPMENT OF ENHANCED PROTEIN CONTENT IN INDICA RICE (ORYZA SATIVA L.)

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Rice is one of the most consumed staple foods worldwide. In developing countries, people often rely on rice as their sole source of nutrition. Since, most of the global population depends on rice based diet and sole source of carbohydrates, bio fortification of rice through genetic strategies is essential to address the nutritional requirements of people world-wide. In general, polished grain or white rice contains nutritionally insufficient concentration of micronutrients and need to be improved for nutritional security. Further, undernutrition and micronutrient deficiencies contribute substantially to the global burden of disease (Ezzati and others 2002). Thus, novel breeding approaches such as doubled haploids could rapidly assist in development of bio fortified rice from various donors. In this work, doubled haploid population was developed through a cross between the Geetanjali (aromatic property) and Bindli high Zn and high protein.

MATERIALS AND METHODS

A DH rice population comprising 77 lines was developed from a cross between Geetanjali, an indica cultivar with aroma, and Bindli, an indica cultivar with high grain zinc and protein content. All the 77 DHs were evaluated for their morpho-agronomic characters in Rabi, 2019-20. Further, all the DHs were also assessed for grain protein content. Out of 77 DHs, 25 promising DHs were selected based on grain size, spikelet fertility and high protein content.

The harvested paddy was stored for three months at room temperature and cleaned thoroughly from dirt or inert matter. Paddy was de-hulled (Mini lab rice huller), grains were ground to a fine powder using mortar and pestle and protein content in each ground sample was determined by the Kjeldahl method. The Kjeldahl method was chosen as an example of this analytical principle in this study as it is still recognized as the official method for food protein determination by the AOAC International.

RESULT

The protein content of 25 DHs quantified using the Kjeldahl method ranged from 5 g/100 g to 13 g/ 100 g. (Table 1). Bindli and Geetanjali showed the protein content 9.23% and 6.46%, respectively. Further, among 25 DHs, seven DHs showed high protein content in grains (Mean GPC:9.06%) while the grain protein content in the analysis ranged from 6.46 – 10.35%. Specifically, one DH namely GB-52 showed 10.35% protein content higher than the donor cultivar Bindli. (Table 1, Figure 1). Additionally, the spikelet fertility of the developed DH lines ranged from 64.06 – 92.38%. Further, one of the DH line namely GB-23 showed spikelet fertility of 92.38% as compared to other DHs and parents.

Table 1.GPC and Spikelet Fertility%

DH lines	Protein content	Fertile Spikelet(%)
GB-23	8.64	92.38
GB-34	8.53	89.02
GB-52	10.35	57.04
GB-58	8.69	87.90
GB-61	8.85	77.61
GB-65	9.39	53.87
GB-66	8.98	64.06
Avg.	9.06	74.55
Geetanjali	6.46	78.36
Bindli	9.23	79.53



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Fig.1 : Protein content and spikelet fertility of developed doubled haploid lines

CONCLUSION

Bio fortification is a promising strategy for sustainable long-term approach in combating micronutrient deficiency. Molecular breeding techniques integrated with doubled haploid technology can be considered as a powerful tool in production of bio fortified crops within shortest span of time. A wide variation in grain protein content within DHs population indicates several QTLs will be governing the grain protein content. Besides, the developed high protein DHs could be used for bio fortified varietal improvement.

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. Indian Rice

BIOFORTIFICATION OF RICE

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ABSTRACT

Biofortification is considered to be an effective process to increase the micronutirents in rice. It is also a sustainable and feasible strategy to alleviate micronutrient deficiencies for people who mainly consume rice. Imbalanced supply of micronutrients and vitamins leads to deficiency and affecting human metabolism. Rice endosperm is deficient in many nutrients including vitamins, proteins and micronutrients. The aleurone layer of dehusked rice grain is nutrient rich but is lost during milling and polishing, so biofortification in rice is necessary. Earlier methods used for biofortification in rice viz Argobacterium mediated gene transfer and particle gene gun method but they integrate transgenes at random locations in the plant genome. This can disrupt gene function, resulting in reduced yield. Different micronutrients (Iron, Zinc) and

vitamins (Vitamin A, Vitamin B9) are biofortified in to rice. CRISPR-Cas9 genome editing is the new approach which offers a promising strategy for making genetic improvements in rice a staple food for more than half the world's population. CRISPR-Cas9 can be successfully used to biofortify rice with carotenoid, a precursor to the essential nutrient vitamin A. This study also suggests that targeted gene insertion could facilitate stacking multiple genes with desired traits in a specific location in the genome. Rice biofortification has several advantages which helps in increase in nutritional value, increase in yield (Rice biofortified with Glycine betaine for enhanced abiotic stress tolerance) reduced dietary deficiency diseases (Blindness in children, anemia, diarrohea) and reduced adult and child micronutrient caused mortality and healthier population with strong and quick immune responses to infections



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MORPHOLOGICAL CHARACTERS: A DEPENDABLE INDICATOR FOR DISCRIMINATION OF HAPLOIDS FROM DIPLOIDS IN *INDICA* RICE

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Doubled haploid (DHs) is an important resource for breeding and genetic research, helps in shortening the breeding cycle and production of homozygous lines from the segregating population. For genetic studies, DH lines are excellent materials particularly on quantitative traits because of their homozygosity and uniformity. They are additionally viewed as a permanent mapping population since they can be multiplied and reproduced without genetic change happening over the long haul (Semagn et al., 2006). These features enable the accurate measurement of quantitative traits by repeated trials and the reduction in the environmental component of the total phenotypic variance. Anther culture (AC) proved to be an efficient approach to produce desiarable amount of DHs. This study was the first of its kind to report about the morphological charatceristics that helps to discriminate the haploids from the diploids in *indica* rice.

In rice, the characterization of AC-derived DH lines are limited and based mostly on cytological, molecular and morphological observations. Besides, characters such as plant height, leaf length, and spikeletfertility are mostly considered as basic parameters to discriminate the haploids from doubled haploids(Naik et al. 2017). However, physiological characters like the position of the anther in the spikelets, shape and size of anther and florets are closely linked to the ploidy level of the plant. Additionally, discriminating diploids from DHs using morphological character is not possible due to similar ploidy levels. With the progress made in the development of polymerase chain reaction (PCR)-based markers, evaluation of genetic variation at the DNA level is possible. Molecular markers such as simple sequence repeats (SSR) have proven to be a powerful tool in the assessment of gametoclonal variation in AC-derived DH lines and their homozygosity (Afza et al., 2001).

MATERIALS AND METHODS

The study was carried out at ICAR-National Rice Research Institute (NRRI), Cuttack using 198 DHs derived from F_1 s IR-20 and Mahulata. The characters namely no. of leaves, no. of tillers, plant height, leaf length, leaf width was recorded. Also, panicle exertion from flag leaf seath, floret size, anther position inside the spikelets and anther length were recorded and visualized under the microscope at the reproductive stage.Genomic DNA was extracted from the leaf sample using CTAB method with some modification. A total of 1010 sequence-tagged microsatellite site (STMS) markers distributed throughout the rice genome were assessed for parental polymorphism survey.

RESULTS

Based on the morphological assessment, out of 159 regenerants tested 41(20.70%) plants were haploids and 118 were diploids. Microscopic examination showed that the haploid florets were smaller, and anther positioned towards the tip of the floret while the anther length was also very small as compare to the diploids/DHs.



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Figure 1: Frequency distribution of polymorphic SSR markers based on their repeat motif. The SSR motif, di, tri and tetra nucleotide repeats containing various SSR markers were depicted on X axis and numbers of polymorphic markers were represented in Y axis.

The molecular studies using 1010 SSR marker resulted in the identification of 109 polymorphic SSR (10.8%) markers. It was also found that the dinucleotide and trinucleotide repeat microsatellite markers were found to be more polymorphic than tetranucleotide repeats. For instance, (GA) repeats containing markers were the highest (21 nos.) followed by STMS markers having CTT repeats (14 nos.) among all the studied polymorphic markers (Figure 1). Similarly, 12 polymorphic STMS markers had AG repeats, 7 polymorphic markers had TCT repeats and 6 polymorphic markers had AT repeats, whereas 4 polymorphic markers of each contained CGG and GAA repeat motifs. All these markers were further utilized for selective genotyping to identify putative markers linked to drought tolerance at the vegetative stage in rice.

CONCLUSION

Androgenes is results in development of plants with different ploidy levels. Hence, discriminating the androgenesis derived plants is one of the major factors in its utilization. The traditional morphological characters may not always be relible to the ploidy as most of them are influenced by environments, where as the anther position and size along with the floret size is completely ploidy dependent and independent of environmental influences. The study highlighted the uniqueness of the anther characters for the identification of haploids. Further, screening of 1010 SSR markers revealed 109 polymorphic markers which will be evaluated in the developed doubled haploids for QTL mapping and gene characterization.

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. Indian Rice

PARENTAL LINE IMPROVEMENT IN HYBRID RICE (ORYZA SATIVA L.) THROUGH MULTIPLE TRAIT INTROGRESSION USING CONVERGENT DOUBLED HAPLOID BREEDING APPROACH

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Climate changes have significant impact on food security and livelihoods of millions of rice farmers especially in the coming decades. Rice production and productivity need to be sustained and secured under harsh climatic conditions across all ecosystems. There is an urgent need to develop multiple stress tolerant varieties along with rice hybrids by exploiting the existing genomic resources especially from the primary genetic pools. Hybrid rice is one of the most viable technologies that ensure >20% increased productivity over the conventional inbred varieties both under favorable and unfavorable conditions (Yao et al., 1997). Despite its yield advantage over inbreds, the hybrid rice technology has not found favors with the farmers of India. The advent of various biotechnological techniques like anther culture in the recent years has offered vital breakthrough to improve crop varieties in terms of yield and quality in a sustainable manner. Further, the problems associated with hybrid rice technology can also be circumvented through doubled haploid approaches.

Doubled haploid (DH) breeding through anther culture has emerged as an exciting and powerful tool, and a convenient alternative to conventional techniques for crop improvement (Purwoko et al, 2010), like shortening the breeding cycle by immediate fixation of homozygosity, offers high selection efficiency, widen genetic variability through the production of gametoclonal variants, and earlier expression of desirable recessive genes suitable for breeding (Devaux and Pickering, 2005). Therefore, combining the genomics and DH breeding technologies innovatively will help us to breed several climate-smart inbred rice varieties and a considerable number of parental lines for their exploitation of heterosis.

METHODOLOGY

The most important aspect of the research is marker-guided foreground and background selection for selecting and advancing those genotypes which have the functional trait (genes) major fertility restoration genes Rf3 and Rf4 along with maximum recurrent parental genome.Donorswerescreened for the presence of desired gene and major fertility restoration genes Rf3 and Rf4 using SSR and the gene specific markers. F1s were developed using selected donors and trueness of the crosses were assessed through hybridity test in F1 by using linked/specific markers. The, true hybrids were advanced for intercross F1 generation (IC1F1).

The validated IC1F1s seeds were grown in net house/field. The spikeletswere collected at booting stage and necessary pre-incubation temperature and duration was established. After proper incubation of the spikes and examination of the appropriate stage of the microspores, the anthers were inoculated in suitable media for callusing followed by shoot regeneration using suitable culture medium.Further, the regenerants will be transferred to the rooting media for root induction.After the development of the green regenerants the plantlets will be acclimatized and transferred to net-house.The ploidy level of the *in-vitro* regenerated plants will be assessed morphologically.

All the DHs developed along with the parents will be raised in the field in augmented design following



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Fig.1. Strategy for DH production for multiple gene introgression in rice

standard agriculture practices to screen the promising characters. Subsequentlypromising DHs will be evaluated for their promising DHs will be evaluated for stress tolerance in the field conditions and yield related traits such as number of panicles per plant, number of grains per panicle, grain weight, heading dates, number of tillers and plant height with their respective parents along with the combining ability with A-lines. The best promising DHs will also be identified on the basis of morpho-agronomic characters.

RESULTS

In order to combine the multiple traits *Bacterial Blight (Xa21, xa13),PsTol, Sub-1, Tac1, Hd3a and HTSF*) through convergent breeding approach, six lines (3 B-lines and 3 R-lines) were selected and F_1s/IC_1F_1 swere developed accordingly (Fig. 1). Healthy boots of the IC_1F_1 swere harvested and followed by proper pre-treatment, the boots were subjected to two-step androgenesis. Trueness of DHs and introgression of genes will be confirmed using molecular markers. The validated carriers will be carried forward for next assessment. Physical evaluation of the confirmed DHs of B and R lines for

their stress tolerance in the field conditions taking yield, physical architecture, and other important parameters into consideration along with the combining ability with other A-lines and B-lines via crossing will be tested

CONCLUSION

The present study showed the significance of DH technology in accumulating multiple gene for improvement of B and R lines within a short period of time as compared to 7-8 years of conventional breeding. Utilization of B and R line in development of hybrid rice could circumvent the yield loss due to the biotic and abiotic stresses, which could sustain the evergrowing human population in future.

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. Indian Rice

GENE STACKING FOR MULTI-TRAIT IMPROVEMETN IN ELITE, HIGH YIELDING, FINE-GRAIN TYPE, BACTERIAL BLIGHT RESISTANT, LOW GLYCAEMIC INDEX RICE VARIETY, IMPROVED SAMBA MAHSURI

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The emergence of new diseases, pests and a rapdily changing climate are the major issues that threaten rice production and productivity in the future (Hasan et al., 2015). Biotic stresses like bacterial blight (BB), Blast, gall midge and BPH are serious production constraints leading to rigorous yield loss affecting the rice cultivation throughout the world. For the development of suitable cultivars possessing multiple biotic stress resistance, development of cultivars possessing two or more genes/QTLs conferring resistance/tolerance to various stresses is the most effective and economical approach. In recent years, molecular-markers have accelerated the process of resistance breeding in rice and use of markers has become imperative in gene-pyramiding programmes. The objective of the present study is to stack genes conferring resistance to blast (Pi2, Pi54), gall midge (Gm4, Gm8), BPH (Bph33t) in an elite, high yielding, fine-grain type, bacterial blight resistant and low glycaemic index rice variety, Improved Samba Mahsuri (possessing the BB resistance genes, *Xa21*, *xa5*, *xa13*; Sundaram et al. 2008).

METHODOLOGY

Improved Samba Mahsuri (ISM), fine grain, BB resistant, highly popular rice variety with low GI content (50.99) was used as recurrent parent. The donor parents, RP Biopatho-1, RP Biopatho-2, RP2068-18-3-5, which pre breeding lines of Samba Mahsuri possessing the target resistance genes (*Pi2*, *Pi54, Bph33t, Gm4 and Gm8*) were utilized. In order to introgress these genes into the genetic background of ISM, initially, independent crosses were performed between the respective donor parents and the recurrent parent, ISM. True F_{1s} were identified using gene specific markers, pTA248 (for *Xa21*), xa13prom (for *xa13*), xa5FM (for *xa5*), Pi2pro9 (for *Pi2*), Pi54MAS (for *Pi54*), Gm4 LRR (for *Gm4*), Gm8PRP (for *Gm8*) and HSP (for *Bph33t*), respectively and backcrossed with the recurrent parent, ISM till BC₂ generation. Simultaneously, parental polymorphism survey was carried out between recurrent parent and donor parents which were further used in the background analysis of introgression lines.

The homozygous BC_2F_2 lines possessing the respective target resistance genes along with maximum recurrent parent genome recovery from each cross were identified and intercrossed to develop improved lines possessing two or more resistance genes with different combinations. These intercrossed lines were screened for the presence of target resistant genes (foreground selection) and advanced further through selfing by pedigree method. Phenotypic screening was done at BC_2F_6 and ICF_4 generation against various biotic stresses viz., bacterial blight, blast, Gall midge and BPH. The agromorphological data was collected among advance backcross and intercross generation lines for key traits. The resistant lines identified were



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also nominated for AICRIP trails (DSN, PHSS and GMSS) for multi-location screening against the target stresses.

RESULTS AND DISCUSSION

At BC_2F_1 , generation foreground selection was done to identify the plants possessing resistant alleles of the targeted genes; these selected positive plants were backcrossed to generate BC_2F_1 generation. At BC_2F_2 generation, intercrosses were initiated with different gene combinations, so as to stack two or more targeted genes into the genetic background of ISM. The intercross combinations developed from the current study include BB + Blast (nine plants); BB+ Blast+ BPH (seven plants); BB+ Blast+ Gall midge (six plants); BB + BPH + Gall midge (Four plants). Background selection revealed 92-95% recovery of the recurrent parent genome for each individual backcross derived lines.

Phenotypic screening for the target stresses indicated that all the introgression lines show resistance reaction for BB (with lesion length 3.0cm) and blast (Score 3), while the resistant parents showed lesion length of 1 (for BB reaction) and score 0 (for Blast reaction). The pyramid lines when screened against gall midge and BPH; the donor parents showed 100% resistance while the recurrent parents showed high susceptibility and the pyramided lines showed resistance to gall midge and BPH, ranging from 60-80%. All the homozygous selected lines were advanced further for agromorphological characterization and the selected lines were on par with the recurrent parent in terms of grain type and some of them were superior in terms of yield paramaters and most of them showed complete panicle exsertion (which is not the case in Improved Samba Mahsuri).

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Based on the above observations, it can be inferred that the combination of genes is most effective than single gene and significant genetic enhancement was observed with respect to the the recurrent parent, for all the target traits. The present study has demonstrated that gene stacking in Improved Samba Mahsuri (ISM) with multiple resistant genes through limited number of backcrosses is possible through a stringent marker-assisted backcross breeding strategy coupled with phenotypic selection in later stages.

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DEVELOPMENT OF HAPLOID INDUCER LINES IN *INDICA* RICE USING CRISPR-CAS9 APPROACH

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Doubled haploid, a novel approach, provides a leading edge over traditional plant breeding techniques which hastens the development of homozygosity and maintains the developed genotypes as pure lines. Since, there are number of established doubled haploid (DH) production technologies available, androgenesis shows its potentiality in production of doubled haploids within a short period of time. Utilization of androgenesis resulted in development of number of rice varieties in japonica rice. However, indica rice is recalcitrant to anther culture with frequent appearance of albino shoots along with requirement of expertise, which hinders the wide-spread use of DH technology through anther culture. Therefore, there is a need to identify an alternative DH production technique that can be user friendly especially for the breeders. A 4-bp insertion in MATRILINEAL (MATL) gene, which codes for pollen specific phospholipase caused haploid induction in maize (Kelliher et al. 2017). Since, rice and maize share a synteny of genes, editing of MATL in rice also caused haploid induction but the rate was less than 6% (Yao et al. 2018). This could be enhanced by combining other related genes associated with pollen maturity for which the cutting-edge technology like CRISPR-Cas9 approach was employed to generate haploid inducer (HI) line in rice.

METHODOLOGY

Seed-based haploid induction based on edited HI genes would allow routine, germplasm-independent DHs production. Demonstration of knockouts of *OsMATL* in rice for 2-6% HI (Yao et al. 2018) has generated immense hope indicating that modifiers in genetic background are playing an important role. Similarly, rice (*Oryza sativa* L.) is exceptionally rich in intraspecific diversity with presence of many ecotypes. The *OsMATL* and *OsDMP* (orthologue of *ZmDMP*) might behave differently in diverse ecotypes that could be exploited for gaining higher haploid induction frequency.

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Keeping in view, *OsMATL* gene-based marker was developed which was utilized to screen a number of *indica* rice genotypes namely Swarna, N22, and DHs of 27P63 (M129-1), BS6444G (PA27-1, PA139) and CRHR32 (Y2-1, Y2-5, Y9-1), and amplicons were subjected to Sanger's dideoxysequencing.

RESULTS

The developed marker related to *OsMATL* showed a ~400bp amplicon size in all the samples. Further, sequencing showed highly conserved sequences which was used as target for CRISPR-Cas guide (Fig. 1). Further, the guide sequence for *DUF679* and *DMP* would be identified in-combiation with *MATL*. Meanwhile the embryogenic tissue culture protocol was standardized for establishing the callus induction and green shoot regeneration using the developed callus for *indica* rice, which served as the ground work for *Agrobacterium* mediated genome editing protocol for generation of edited lines.

CONCLUSIONS

Developing an HI line by exploiting CRISPR/ Cas9 genome editing technology for the genes *OsMATL*, *DMP* and *DUF679* in different genetic background will enable us to compare the HI frequency in different genetic backgrounds and find a suitable



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Fig. 1.a: Development of CRISPR-Cas9 mediated Haploid Inducer Lines. b: Production of doubled haploids using Haploid Inducer Lines.

system for DH production in rice. Besides, combination of both the genes (MATL and DMP) could increase the HI frequency. This study will also help us to develop a high-throughput pipeline for doubled haploid induction in rice which would be immensely beneficial to breeders and molecular biologist for mapping of genes, speed breeding, varietal development and gene characterization. Moreover, like maize, pigmented rice genotype can be a suitable candidate system for early detection of haploids in the matured panicles. Utilization of tissue culture method could circumvent the uses of antimitotic agents, producing DHs from haploid seeds since the methods developed for androgenesis produces ~99% spontaneous doubling. Further, using the sequencing data, Cas9 guide would be generated for developing DUF679, DMP knock-out lines using CRISPR-Cas9 approach.

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INTROGRESSION OF QTLS GOVERNING ROOT MORPHOLOGY AND YIELD UNDER DROUGHT STRESS INTO POPULAR RICE VARIETY ADT 43 THROUGH MABB

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Rice is stable food for one-third of world population. Rice is cultivated under varying ecosystems and it can withstand waterlogged and poorly drained to well drained soils under varying climates (Singh, 2009). Green revolution has increased the rice production by 2.5 times since 1961, but mainly focused on irrigated ecosystems. In the Indian state of Tamil Nadu rice is grown in an area of 18 lakh hectares and most rice growing areas are prone to drought stress at one or more growth stages. Drought is major limiting factor in rice production ecosystem and impacts world food security. According to climate change prediction models, impact of drought on rice production will be more in coming years and depends on severity of drought prevails during that year (Guo et al. 2021). Therefore, breeding for drought tolerance in rice becomes an important task to sustain the food security. In the present study, QTLs governing root morphology and yield under drought stress have been introgressed into ADT 43 a high yielding fine grain popular rice variety of Tamil Nadu through marker assisted back-cross breeding.

METHODOLOGY

Initially the recurrent parent ADT 43 was hybridized with the donor parent to synthesis F_1 plants. The F_1 s were then genotyped using the markers RM 252 and RM 348, based on the genotyping the F_1 s carrying both the marker alleles were identified. The F_1 s with both marker alleles were then back crossed with the recurrent parent ADT 43 to synthesize BC₁F₁ population. BC₁F₁ population was again genotyped with the foreground markers and thereby plants with marker alleles were identified. In similar fashion BC₂F₁ to BC_4F_1 plants were synthesized and in each back cross generation foreground selection was done using the trait specific markers. The positive plants identified in BC_4F_1 were advanced to four generation based on phenotype and yield potential of plants. In BC_4F_4 the selected plants were again genotyped to shortlist the phenotypically superior plants with targeted marker alleles. Finally, the selected plants were phenotyped for root traits and yield under artificial drought stress (Fig 1). For which, one and half feet tall and one feet width pots were filled with the mixture of sand, soil and compost and all the four progenies and their parents were sown in the pots with three replications. All the pots were watered regularly up to 70 days to ensure the good growth and establishment of the plants. Drought was imposed for a period of 15 days from 70 to 85 days after sowing. The plants were rewatered on 86th day and thereafter normally irrigated up to harvest. At the time of harvesting the biometric observations viz., days to flowering, plant height (cm), number of productive tillers, panicle length (cm), spikelet fertility percentage and single plant yield (g) were recorded. After harvesting the pots with root portions were immersed in to the tubs with water for three days to loosen the soil, then the root portions were slowly separated to record the observations viz.,

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Best plants phenotyped for root traits & yield under stress

Figure 1. MABB for introgression of QTLs in ADT 43 from CT 9993

root length (cm) and root volume (ml).

RESULTS

A total of 27 F_1 hybrids were synthesized by hybridizing the drought-susceptible recipient variety ADT 43 with donor parent CT 9993 and 11 true F₁s were fixed with polymorphic SSR markers. These true F₁s were backcrossed with recurrent parent and 79 BC₁F₁ plants were produced. These backcrossed plants were genotyped with specific markers viz., RM 252 and RM 348 for basal root thickness and yield under drought stress respectively. Based on the genotyping, 17 plants carrying both QTLs were again hybridized with ADT43 and 66 BC₂F₁ plants were synthesized. Based on foreground selection with the specific markers, $13 BC_{2}F_{1}$ plants were identified for further round of back crossing. The cycle was repeated for two more generations to produce BC_4F_1 . In BC_4F_1 eight plants were identified with both marker alleles and were advanced to three more generations based on phenotypic, visual selection, In BC_4F_4 four single plant progenies viz., 13-3, 26-5, 48-1 and 111-2 harboring both QTLs viz., basal root thickness and yield under drought stress were identified using trait specific SSR markers. Selected four entries along with parent were raised in pots to study the yield under drought stress and phenotyped for root length and volume. Among the four progenies 13-3 possessed long roots when compared to both recurrent and donor parents with a length of 49.4 cm. However, all the four plants were phenotypically similar to ADT 43 and possessed with root traits similar to donor parent CT 9993. Successful introgression of drought yield QTLs into rice variety MR 219 was demonstrated by Shamsudin et al., 2016.

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CONCLUSION

This study was aimed to develop drought tolerant ADT 43 through MABB. Four BC_4F_4 plants harboring QTLs for root traits and yield under drought stress were identified in ADT 43 background. Performance of all the four genotypes were found to be superior under artificial drought stress and among the four 13-3 was top ranked. All the four entries and their parents are being assess their performance under direct sown natural drought prone environment.

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Indian Rice

CORRELATION AND PATH COEFFICIENT ANALYSIS IN RICE GENOTYPES UNDER AEROBIC CONDITION

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Aerobic system of cultivation has gained momentum in irrigated lowlands where rainfall is not sufficient and pumping water from deep well is expensive and upland system with supplemental irrigation. The lack of stable yielding and dry direct seeded adapted varieties for aerobic system is a major limitation in achieving the maximum yield potential under water and resource limited conditions (Sandhu et al., 2019). To combat this situation, it is essential to focus the research priority towards development of water efficient 'aerobic rice'. Since yield is a complex trait associated with the other yield attributing characters and is much influenced by the environment, the selection based on yield alone will often result in retrograde or less optimum progress in isolating superior genotypes (Manjunatha et al. 2017). Correlation studies helps the breeders to ascertain the nature of relationship between important traits. The present investigation was undertaken to find out the nature of the relationship of grain yield with its yield components, direct and indirect contribution of these components towards grain yield and to identify better combinations of such yield components as selection criteria for developing high yielding aerobic rice genotypes.

MATERIALS AND METHODS:

The present experiment was conducted with 65 rice genotypes including popular rice varieties, drought tolerant rice varieties, aerobic rice genotypes and land races at Rice Research Station, Tirur, Tiruvallur during Kharif, 2015 which is located at about 13°N latitude and 79°E longitude at an altitude of 40 meters above MSL. The genotypes were raised in Randomized

Block Design with three replications under aerobic condition and irrigated at weekly intervals. The plot size was 3 x 3 m² with the spacing of 20 x 10 cm. Observations were recorded on five randomly selected plants per replication for the characters *viz.*, Plant height, No. of productive tillers /plant, Panicle length, No. of grains / panicle, Hundred seed weight and Panicle Harvest Index whereas, the characters like plot yield and days to 50 % flowering were recorded on plot basis. Then the data were subjected to statistical analysis by following Singh and Chaudhary (1995) for correlation coefficient and Dewey and Lu (1959) for path analysis.

RESULTS AND DISCUSSION

Genotypic Correlation coefficient is generally of higher magnitude than the corresponding Phenotypic Correlation coefficient level indicating that the environmental causes of correlation had affected the genetic cause, thereby reducing the reliability of utilizing the phenotypic correlation for the crop improvement programme. As Genotypic Correlation coefficient would give the realistic picture of relationships existing among the characters in the absence of environmental influence, the genotypic correlation coefficient were utilized in the present study. Significant and positive associations with plot yield were exhibited by the yield contributing traits viz., no. of productive tillers/plant (0.455), panicle length (0.243) and hundred seed weight (0.219) (Table 1). Significant and positive association of these traits indicates that selection based on these traits would ultimately improve grain yield under aerobic conditions. The characters plant height, no. of grains per panicle



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	DFF	PH	NPT	PL	NGP	HSW	PHI	PY
DFF	1.000	0.110	-0.056	0.272*	0.272*	-0.125	0.063	-0.063
PH		1.000	0.081	0.219*	0.132	0.186	-0.278	0.033
NPT			1.000	0.020	0.114	0.183	0.401*	0.455*
PL				1.000	0.454*	0.065	-0.251	0.243*
NGP					1.000	-0.015	- 0.201	0.069
HSW						1.000	0.279*	0.219*
PHI							1.000	0.088
PY								1-000

Table 1. Genotypic correlation coefficients of yield and yield attributing traits

* Significance at 0.05 % probability

and panicle harvest index showed positive but non significant association with plot yield whereas the trait days to fifty per cent flowering registered negative and non significant correlation with plot yield.

The intercorrelation among the important component traits is also important in order to decide upon which traits to be given due weightage in exercising selection. The inter correlation between the yield contributing traits *viz.*, days to fifty per cent flowering with panicle length (0.272) and no. of grains per panicle (0.272): plant height with panicle length (0.219); no. of productive tillers/plant with panicle harvest index (0.401); panicle length with no. of grains per panicle

(0.454) and hundred seed weight with panicle harvest index (0.279) were positive and significant indicating the possibility of simultaneous improvement of these traits by concentrating on any one or two of these traits (Table 1).

Path analysis

Information obtained from correlation study could not indicate whether the association of the yieldrelated traits with yield is due to their direct effect on yield or is a consequence of their indirect effect via some other traits. As the correlation coefficient is not sufficient to explain true relationship for an effective manipulation of the character, path coefficient was

Table 2	Direct and	Indirect	of vield	and via	eld attri	huting	traite
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	DFF	PH	NPT	PL	NGP	HSW	PHI	PY
DFF	-0.036	-0.013	- 0.028	0.074	-0.030	-0.021	-0.009	-0.063
PH	-0.004	0.118	0.040	0.060	-0.015	-0.031	0.040	0.033
NPT	0.002	-0.010	0.496	0.006	-0.013	0.030	-0.057	0.455*
PL	-0.010	-0.026	0.010	0.274	-0.051	-0.011	0.036	0.243*
NGP	-0.010	-0.016	0.056	0.124	-0.112	- 0.002	0.029	0.069
HSW	0.004	-0.022	0.091	0.018	0.002	0.166	-0.040	0.219*
PHI	-0.002	0.033	0.198	-0.069	0.023	0.046	-0.142	0.088

* Significance at 0.05 % probability*

Characters - DFF (Days to 50 % flowering), PH (Plant height), NPT (No. of branches per plant), PL (Panicle length), NGP (No. of grains per panicle), HSW (100 Seed Weight), PHI (Panicle Harvest Index), PY (Plot yield) Residual effect - 0.815

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worked out. Path coefficient analysis is useful to understand the direct and indirect effects of each character on grain yield and the application of selection pressure in a better way for yield improvement, partitioning of correlation coefficient into direct and indirect effects. In the present study, Path analysis showed that the maximum positive direct effect contributing to plot yield was exhibited by no. of productive tillers / plant (0.455) followed by panicle length (0.243) and Hundred Seed weight (0.219) which implies that selection for these traits would improve seed yield per plant (Table 2.). Panicle Harvest Index exhibited highest indirect effect on yield via no. of productive tillers per plant (0.198) followed by no. of grains per panicle via panicle length (0.124). This shows that selection for the traits no. of productive tillers per plant and panicle length would indirectly help in increasing the grain yield. Low residual effect of 0.815 depicts that number of observed traits in the present study is sufficient for the study.

The traits no. of productive tillers/plant, panicle

length and Hundred Seed weight had positive association with higher direct effect on plot yield which could be used as selection criteria for developing new rice varieties with high productivity under aerobic condition.

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INFLUENCE OF LONG-TERM USE OF MANURES AND FERTILIZERS ON YIELD TREND, NUTRIENT CHANGE AND SUSTAINABLE YIELD INDEX IN RICE-RICE CROPPING SEQUENCE OF ASSAM

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Long-term fertilizer experiments were conducted across the country at fixed site in different agro-ecological zones (AEZ) and on important cropping system to monitor the changes in yield responses in soil environments which are influenced by continuous use of organic and inorganic sources of nutrients. This is a classical experiment which intends to formulate the rational use of fertilizers (Janzen, 1995). Further, this type of experiments also studies the dynamics of soil and crop productivity in different cropping system and relates to management for identifying the constraints that affect the sustainability of a given production system.

This paper intends to focus on the crop yield in different years of cultivation as influenced by continuous use of manures and fertilizers and its sustainability issue reflected by change in soil fertility parameters.

METHOLOGY

This long-term experiment was initiated during the year 1989 at RARS, AAU, Titabor (26°352 E and 96°102 N) and is being continued till date. There are 14 treatments in total which are as follows: T1 (Control), T2 (100%PK), T3 (100%NK), T4 (100%NP), T5 (100% NPK + Zn),T6 (100%NPK+Zn+FYM @ 5t/ha), T7 (100%NPK-Zn), T8 (100% NPK-S), T9 (100% N+50% PK), T10 (50% NPK), T11 (50% NPK+50% GM-N), T12 (50%NPK+50% FYM-N), T13 (50% NPK+25% GM-N+25% FYM-N), T14 (FYM@10t/ha). Here, 100% NPK implies the fertilizer dose of 40kg N: 20 kg P₂O₅ and 20 kg K₂O /ha. The plot size of individual treatment was 10m x10m with 4

replication using RBD. All the standard package of practices was followed during experimentation. Some of the selective treatments were considered for their study namely: T1 (Control), T5 (100% NPK+Zn), T6 (100% NPK+Zn+FYM @ 5t/ha), T13 (50% NPK+25% GM-N+25% FYM-N), T14 (FYM@10t/ha).

Further, the available yield data in terms of sustainable yield index (SYI) and its relationship with some of the important soil fertility parameters like organic-C, available P_2O_5 and available K_2O status of the soil were done. The data in terms of sustainable yield index (SYI) was worked out by using the following formula (Singh *et.al*, 1990)

 $SYI=(A-Y) \times 100/Ymax$

Where,

A= Mean yield of a particular treatment

Y=Standard deviation of the treatment and

Ymax= The maximum yield recorded in different years and treatments.

RESULTS

Crop productivity in different years of cultivation as depicted in the Fig 1 showed variation over the years both in Rabi and Kharif season. The range of yield between the years varies significantly. Regarding grain yield during 2019, it ranged from 2.02 (control) to 4.94 t/ha (RDF+FYM) with an average increase of 14%. Linear trends of productivity over the years with current RDF indicated positive growth

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Fig 1: Crop productivity in different years of cultivation

rate in this acid alluvial soils (35 kg/ha/yr). Additional dose of FYM @ 5 t/ha along with RDF improved the growth rate substantially with 79 kg/ha/yr. During rabi also, RDF+5 t/ha FYM recorded maximum mean grain yield (4.34 t/ha) and this treatment recorded growth rate of 54kg/ha/yr. Higher growth rate was observed in Kharif season compared to rabi season. The trends in mean grain yield over 31 years (1989-2019) in kharif and rabi were assessed by filling to linear function using actual yield.

Changes in soil fertility compared to initial values:

The organic carbon content increased in all the aforesaid treatments compared to initial values. The organic carbon content at Titabor decreased in control but increased in RDF, RDF+FYM and in other integrated treatments. Maximum increase was in sole application of FYM. In case of the available P, there was a buildup of P content in all treatments except on initial control plots. In case of available K, there was decrease in control plot and increase in other treatments.

Sustainability of soil and crop productivity

Sustainability refers to the maintenance or enhancement of productivity on a long term basis through integrated land management. In order to monitor the changes in soil fertility and yield response due to continuous application of plant nutrients from fertilizers and organic manures, an attempt has been made to evaluate the yield data in terms of sustainable yield index (SYI) and its relationship with some of the

Table 1: Influence of continuous use of manures and fertilizer on sustainable yield index (SYI) and percent of nutrient change in selective treatment of rice-rice cropping sequence

Treatments	SYI(%) 2012	Mean yield (kg/ha)	SYI(%) 2019	Mean yield (kg/ha)	% changes SOC	Avg. P	Avg. K
Control	22.0	2156	18.60	2020	-41.1	-14.2	-40.6
100% NPK+Zn	50.4	4161	4235	4320	28.4	16.7.	10.4
100% NPK+Zn+FYM	60.7	4600	6465	4900	60	198	12.5
50%NPK+25%GM-N+25%FYM-N	51.3	3700	56.04	3950	57.9	187	15.10
FYM 10 t/ha	53.5	3750	57.10	4010	65.4	194	16.8
Correlation (r)	0.90		0.94		0.78	0.82	0.78
Regression coefficient (R ²)	0.82		0.88		0.60	0.69	0.62



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important soil fertility parameters like organic carbon, available P_2O_5 and available K_2O (Table 1). In this rice-rice cropping system the SYI for rice range from 20.60- 64.65% during the current year (2019) and during the year of 2012 SYI values varied from 22 to 60.7%. The treatment receiving 100% NPK+Zn+FYM maintained the highest SYI values. Besides there was increase of organic carbon content in treatments receiving organic manures as well as in INM treatments. In case of K, the buildup of available K was marginal.

Correlation of SYI values with available soil data on changes in nutrient status indicated a moderate to high level of relationship between SYI and the soil parameters. Most of the variations in SYI could be related to changes in soil carbon P and K availability in this acid alluvial soil. The percent of change in soil organic carbon varied from 28.4 to 68.4%, for P it ranged between 167 to 194%. While for K the change was marginal ie., 10.4 to 16.8%.

CONCLUSION

From the results of 31st year of study on longterm soil fertility management in rice-rice sequence indicated superior performance of RDF+FYM over the other treatments in both wet and dry season. In general, INM and other organic treatments alone resulted in improvement of soil fertility parameters which reflected positively in rice productivity and SYI as an when compared between the year 2012 and 2019.

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EVALUATION OF THE TOTAL TOCOPHEROL CONTENT IN A SET OF WILD RICE ACCESSIONS

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Rice (Oryza sativa L.) is the most important food crop and a staple food which contributes up to 70% of daily calories for more than half of the world's population. The 27 Oryza species span ~15 million years of evolution, with 11 genome types, 6 of which are diploid (*n* = 12: AA, BB, CC, EE, FF and GG) and 5 of which are polyploid (n = 24: BBCC, CCDD, HHJJ, HHKK and KKLL). Wild relatives of rice are known to harbor untapped reservoir for many useful traits of nutritional importance. Wild rice, like most cereals, is not a complete food. It has been reported to be a health promoting cereal, particularly due to its cholesterol-lowering and antioxidant properties and its ability to participate in the prevention of diabetes type II. Whole rice contains a wide range of bioactive compounds such as vitamin E (tocopherols and tocotrienols), Y-oryzanols, phenolic acids, flavonoids and phytic acid. One of the features in determining the quality of rice is the tocopherol content, which is genetically controlled and highly influenced by prevailing environmental conditions. Tocopherol is one of the antioxidants with diverse functions and benefits for humans and animals. In the present study, a set of 35 wild rice accessions were screened for total tocopherol content. These wild rice accessions were selected on basis of their high protein content in brown rice (e" 12%) as brown rice is nutritionally rich due to the presence of the bran layer, which is removed in case of polished rice. Wild accessions which have high total tocopherol content along with higher protein content in brown rice, could be used as donors in the hybridization programme for nutritional enhancement of elite rice cultivars.

METHODOLOGY:

The experimental material consisted of 35 wild rice accessions, comprising 34 accessions of AA genome species (O glaberrima, O. barthii, O. rufipogon, O. meridonalis) and one accession of CC genome species (O. officinalis) along with 7 nonbasmati cultivars, PR 114, PR 121, PR 123, PAU 201, Pusa 44, PR 128 and PR 129 (widely grown in Punjab state). The crop was raised following the standard agronomic practices and harvested at maturity. Seed of accessions was dehusked with hand dehusker to get brown rice and samples were ground to powder. Total tocopherol was extracted and estimated using the method proposed by Kayden et al 1973. For tocopherol extraction, 500 mg of sample was homogenized with absolute ethanol. Then estimation of total tocopherol content was done using purified xylene, bathophenanthroline reagent (0.4% in absolute ethanol), FeCl₂ reagent (60 mg FeCl₂.6H₂O in 100 ml absolute ethanol), o -- phosphoric acid (0.5 ml of 85 % phosphoric acid in 100 ml of absolute ethanol). Absorbance of the test was read at 536 nm against xylene as reference within 30 seconds. The contact of sample with sunlight was avoided. Amount of tocopherols were calculated from the standard curve prepared with tocopherol (2-10 µg) as standard.

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RESULTS:

The total tocopherol contents of different accessions of wild rice ranged between 8.9 \geta/gm (*O. rufipogon*) to 37.3 \g/gm (*O. rufipogon*). For the non-basmati, it varied from 16.7 \g/gm (PAU 201) to 22.4 \g/gm (PR 128). The total tocopherol content of 19



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wild rice accessions were found to be more than that of non-basmati cultivars. Results from different studies on total tocopherol content were reported by Goufo and Trindade (2014), with overall range from 3.00-105.5ìg/gm in non-basmati brown rice cultivars and wild rice.

CONCLUSION:

This study provides information on total tocopherol content of different rice wild accessions. Results showed that some of the wild accessions have high total tocopherol content along with higher protein content in brown rice. These could be used as donors

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SCREENING OF GERMPLASM ACCESSIONS FOR MULTIPLE DISEASE RESISTANCE IN RICE (ORYZA SATIVA L.)

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India, is the largest rice growing country with nearly 44 million hectares area and the second largest producer after China. Bacterial blight (BB) caused by Xanthomonas oryzae pv. oryzae (Xoo) is one of the most destructive disease of rice, which is prevalent in the major rice growing countries of Asia. False smut (FS) is an important emerging disease caused by Ustilaginoidea virens especially in North West region of India due to wide spread cultivation of highly fertilizer responsive cultivars and increased application of nitrogen fertilizer. It not only greatly reduces grain yield but also deteriorates grain quality. Till date, 45 resistance genes conferring resistance to BB pathogens have been reported from rice, including few genes from wild accessions (Pradhan et al 2020). Resistance genes against U. virens have not been identified yet, but numerous efforts have been undertaken to study the inheritance of the resistance. Exploitation of host plant resistance is the most effective, economic and environmentally safe measure for controlling both diseases. Keeping in view the importance and devastating potential of these diseases the present study was undertaken to identify potential donors for resistance to BB and FS from a set rice germplasm accessions.

METHODOLOGY:

A set 180 germplasm accessions of rice including released varieties, landraces and elite genotypes were cultivated at during *Kharif* 2020, at Punjab Agricultural University, Ludhiana, India. The lines were artificially inoculated against BB pathotype PbXo-7 by Clip Inoculation Technique at maximum tillering stage. In addition, incidence of FS disease was recorded under natural conditions along when the susceptible check PR 116 should high disease incidence. Data was recorded for both diseases using standard scale as given by IRRI, Philippines scale 1 to 9.

RESULTS:

The pathotype PbXo-7 is virulent on BB resistance gene *viz. Xa1*, Xa3, *Xa4*, *Xa5*, *Xa7*, *Xa8*, *Xa10* and *Xa11* (Lore *et al* 2011). Results showed that out of 180 lines, 65 (36.11%) lines showed resistant reaction, 46 (25.56%) lines showed moderately resistant reaction and rest of 69 (38.33%) lines were susceptible to BB (Fig. 1). On the other hand, 53 lines showed less than 1% incidence, 71 lines showed 1 to 5% incidence, 41 lines showed moderately susceptible reaction and 15 lines showed higher susceptible reaction against FS (Fig. 1). Relatively higher number of lines with lower incidence of FS was observed due to non-coinciding of lines with the favorable environment for FS disease development.



Fig. 1. Reaction of germplasm lines against BB and FS



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CONCLUSION:

Thirty five (19.44%) lines showed resistance/ moderate resistance reaction against both BB and FS diseases. These promising resistant lines can be further evaluated for presence of known BB genes using molecular markers and the resistant FS lines can further be evaluated under natural hot spot conditions. The potential donors these identified can be used in breeding programme to develop high yielding cultivars with resistance against both the diseases.

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VARIABILITY STUDIES ON YIELD AND GRAIN QUALITY TRAITS IN ADVANCE GENERATION OF RICE (ORYZA SATIVA L.)

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Rice is the staple food crop in India and is grown in diverse ecological conditions ranging from rainfed upland to deep water conditions of which 56% comes under rainfed ecosystem. Development of high yielding varieties combined with drought tolerance had been the major objective of researchers working on drought tolerance. However, the consumer acceptance and popularity of any new variety is decided by its physical appearance, milling and cooking quality characters apart from its high yield and drought tolerance. The quality traits assume prime importance in order to identify genotypes with superior grain quality in any variety release programme. Hence the present investigation was undertaken to study the extent of genetic variability and heritability among some important yield contributing and quality characters in an advanced generation of a cross IR 20/Nootripathu mainly developed for rainfed uplands.

METHODOLOGY

The present investigation was carried out in the Research Farm of the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai using 140 Recombinant inbred lines of F_9 generation of a cross IR 20 / Nootripathu advanced to evolve high yielding drought tolerant genotype. The genotypes were raised in a randomized block design with two replications in rows of 3m length with spacing of 20cm between rows and 15cm between plants. Observation on yield and grain quality characters viz., days to 50% flowering, plant height, No. of productive tillers/plant, Panicle length, No. of grains/panicle, Spikelet fertility, 100 grain weight, grain weight,

grain length, L/B ratio, Milling percentage, head rice recovery, linear elongation ratio, Breadthwise elongation ratio and Single plant yield were recorded on ten plants selected at random per replication.

Hulling and milling were done using 20 g representative sample using Satake Grain Testing Mill and Polisher (Type TM05) for 90 seconds to obtain uniform 5% polishing. Milling percentage and Head Rice Recovery, Linear elongation ratio and breadthwise elongation ratio were calculated.

Phenotypic and genotypic coefficients of variation were estimated as given by Burton (1952). Heritability in broad sense and genetic advance were estimated as per Singh and Chaudhary (1977) and Allard (1960) respectively and were categorized into various classes as suggested by Johnson *et al.* (1955).

RESULTS

The analysis of variance revealed significant differences among the genotypes for all the 14 characters studied. The maximum range of variation in mean was observed for number of grains/panicle followed by plant height, spikelet fertility, milling percentage, head rice recovery and single plant yield while the range of variation was minimum for the traits like grain length, linear elongation ratio and breadthwise expansion ratio (Illustration 1).

Knowledge on genetic variability is important for selection of superior genotypes. In the present study, the GCV was high for single plant yield (33.3%) followed by no. of grains/panicle, no. of productive tillers/plant, plant height and head rice recovery. High level of variability observed for these traits indicated



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Characters	Mean	Range	PCV (%)	GCV(%)	h ² (%)	GA (as % of mean)
DFF	86.40	78.50-106.50	5.98	5.94	98.6	12.15
PH	113.96	73.50-167.35	20.58	20.44	98.6	41.83
NPT	12.30	6.70-18.75	23.78	22.83	92.2	45.20
PL	22.14	14.65-28.10	10.63	9.99	88.4	19.33
NGP	92.07	37.35-168.20	25.86	25.53	97.5	51.92
SF	84.32	26.20-96.65	10.41	10.13	94.8	20.33
100GW	2.48	2.03-3.07	8.89	8.83	98.8	18.15
Œ	0.59	0.52-0.65	4.45	4.36	96.1	8.48
L/B	2.27	1.81-3.00	8.60	8.46	96.8	17.18
MP	68.47	35.2-86.35	13.76	13.44	95.5	27.06
HRR	54.60	26.10-74.05	21.13	21.01	98.9	43.06
LER	1.28	1.04-1.59	10.13	9.88	95.1	19.53
BER	1.38	1.21-1.64	7.47	7.23	93.5	14.49
SPY	15.28	6.06-30.29	34.34	33.33	94.2	66.62

Illustration 1. Estimates of Variability, heritability on yield and grain quality parameters in Rice

the broad genetic base of the genotypes under study. The difference between the estimates of PCV and GCV were very less for all the characters indicating the least environmental influence.

The less influence of environmental factors on the observed characters was also supported by the high heritability observed for all the traits. High h² estimates for no. of fertile grains/panicle, grain length, L/B ratio and Single plant yield was reported earlier by Singh et al. (2000). The characters Single plant yield, no. of grains/panicle, no. of productive tillers/ plant, head rice recovery, plant height, milling percentage and spikelet fertility registered high GA as per cent of mean coupled with high h². This was in accordance with the findings of Umadevi et al. (2010) for milling percentage and Linear elongation ratio. Higher estimates of GA indicated the preponderance of additive gene action. Hence improvement of these traits could be brought about by simple selection procedures. Lower estimates of GA observed for the traits like grain length, days to 50% flowering and linear elongation ratio indicated the predominance of non additive gene action which requires advancement of generations for exercising selection.

CONCLUSION

Grain quality characters in Rice highly influence the consumer preference and acceptability of a variety in long run and need to be given due importance while framing any breeding programme. The present study shows high level of variability for grain quality traits which indicates the broad genetic base of the genotypes. High heritability and Genetic Advance as per cent of mean observed for the characters like plant height, no. of productive tillers/plant, no. of grains/panicle, milling percentage, head rice recovery and Single plant yield indicated the preponderance of additive gene action and genetic improvement through simple selection procedures. As the study was conducted in advanced generation, it is easy to exercise selection of genotypes based on their performance.

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IMPROVEMENT OF THE INDIAN MEGA-RICE VARIETY, MTU1010 FOR RESISTANCE AGAINST BACTERIAL BLIGHT, BLAST AND TOLERANCE TO LOW SOIL PHOSPHORUS THROUGH MARKER ASSISTED PEDIGREE BREEDING

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To cope up with the steadily increasing population, it's important to enhance the rice production, which is adversely affected by several biotic and abiotic stresses. There is an imminent need to develop improved varieties tolerant to stresses via genetic improvement. The present study focused on improvement of the mega-rice variety, adaptable to multiple rice growing ecosystems, MTU1010 (IET 15644; also known as Cottondora Sannalu). Despite of its desirable features like medium-duration and medium-slender grain type, MTU1010 is highly susceptible to bacterial blight (BB) disease, has only moderate level of tolerance to blast disease and highly sensitive to low soil P levels which can cause significant yield losses in the variety. The main objective of the study was to combine combine resistance against BB (conferred by Xa21) and Blast (Pi54) and low soil phosphorous (Pup1) into the genetic background of MTU1010 using marker-assisted pedigree breeding strategy coupled with stringent phenotypic screening for the target stresses and also for the key agromorphological traits specific for MTU1010.

METHODOLOGY

Initial crosses were carried out between RP 5973-20-9-8-24-12-7, (a NIL of MTU1010) possessing *Pup1* QTL and RP6132 (a NIL of Akshayadhan) (developed by ICAR-Indian Institute of Rice Research (ICAR-IIRR). The F₁s generated

were confirmed for their heterozygosity using target resistant gene specific markers viz., K-20-2_{Bspel} (specific for Pup1; Chin et al. 2011), Pi54MAS (specific for Pi54; Ramkumar et al. 2011) and pTA248 (specific for Xa21; Ronald et al. 1992) and the true F_1 plants (i.e. heterozygous F₁ plants) were selfed to develop F₂s. Homozygous positive F₂ plants identified through foreground selection using the target QTLs/gene specific markers and advanced further by selfing through Pedigree breeding till F₅ generation. Phenotypic screening was done at F₅ generation against biotic stresses viz., Bacterial blight, blast and abiotic stress i.e, low P tolerance along with the parents and check lines in the normal field and low soil P plot respectively, at ICAR-IIRR, Hyderabad during Wet season (i.e. Kharif season), 2018. Fifteen promising homozygous positive F₅ lines, which closely resembled MTU1010 in terms of plant type and grain type were selected and further evaluated for their resistance/tolerance to target stresses (viz., BB and blast diseases and low soil phosphorous tolerance) and also for key agromorphological traits. Data was recorded for all the parameters in both normal soil P and low soil P plots and statistically analyzed.

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RESULTS AND DISCUSSION

At F_1 generation foreground selection was done using the co-dominant markers, specific for *Xa21*, *Pi54* and *Pup1*. A total number of 76 plants were



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heterozygous with the marker(s) specific for the target gene and were forwarded to F_5 generation through selfing. At each generation foreground selection was done to identify the plants possessing resistant alleles of the targeted genes using the co-dominant markers specific for the three target genes. At F_5 generation, phenotypic screening for the target stresses identified that all the fifteen improved breeding lines have shown resistant reaction for BB with mean lesion length ranging from 1 ± 0.3 to 3 ± 0.3 ; while four lines showed resistant reaction to blast with score 3 and eleven lines exhibited moderate reaction to blast. When screened for low P tolerance, four lines identified to be low P tolerant. These best four promising lines were assessed for grain yield and other key agromorphological traits which are observed to be equivalent to or better than the MTU1010 NIL. Among which, two breeding lines exhibited good performance with high level of resistance/tolerance to all the three stresses viz., BB, blast and low soil P and performed well under both normal soil P and low soil P possessing desirable long slender grain type like MTU1010 and also were nonshattering (drawback in MTU1010). Gene pyramiding of biotic and abiotic stresses was accomplished using systematic marker assisted breeding program with selected plants possessing targeted genes/QTLs along with morphology similar to that of the MTU1010. In the present study, using the same female parent (MTU1010) in multiple crosses with intensive genotypic-phenotypic selection and agro trait-based selection has helped in selecting plants with MTU1010 plant type and grain type to a great extent, despite of not following backcross breeding strategy.

ILLUSTRATION/INTERPRETATION

Development of broad-spectrum resistance against diseases like blast, BB and climate resilient

varieties in the Indian subcontinent is a foremost challenge due to the multiplicity of the agro-climatic zones where rice is cultivated. In addition, under the climate change scenario, tolerance to low P tolerance assumes great significance to rice. The current study has demonstrated that the deployment of appropriate gene or gene combinations against each biotic and abiotic stress can help develop new introgression lines with durable and broad-spectrum resistance/tolerance. The developed ILs will be of great use in the future rice breeding programs /improve rice cultivation in marginal soils (i.e. problematic soils with low P) and breeders can use them suiting to their needs as varieties or as donors for introgressing multiple genes/QTLs.

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MARKER ASSISTED IDENTIFICATION OF RESTORATION AND BACTERIAL BLIGHT RESISTANCE GENES IN A SET OF TEST CROSS NURSERY

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Rice is an important *Kharif* crop of Punjab occupying an area of about 2.8 lakh ha with a productivity of 6384 Kg/ha during *Kharif* 2019. However, there is a need to increase its productivity to feed the ever increasing population. Hybrid rice technology is one of the most important and practically feasible technology to enhance the rice productivity.

In rice, primarily, three-line system is deployed for commercial hybrid seed production. In indica rice, wild abortive (WA) cytoplasm, derived from Oryza sativa f. sp. spontanea (Li and Yuan 1986) is one of the most widely used cytoplasmic male sterility (CMS) source for hybrid rice production, due to its complete and stable fertility restoration. For developing heterotic hybrid, there is a need to identify/ develop locally adapted restorers with high restoration efficiency in the hybrids. Evaluation for fertility restoration is mainly done through test crossing with CMS lines and evaluating the fertility (both pollen and spikelet) of the F₁ hybrids, which is laborious and time consuming. The use of molecular markers linked to Rf genes can enhance the selection efficiency, save time and avoid the complications associated with phenotype based screening. The objective of this study was to evaluate and identify BB resistance, heterotic combinations and new maintainers with desirable grain quality and a set of promising lines were also characterized for the presence of Rf3 and Rf4 genes along with known BB resistance genes Xa4, xa13 and Xa 21.

METHODOLOGY

A set of 181 test crosses along with checks PR 121 and PR 126 with 17 different CMS lines were evaluated during *kharif* 2019 to identify new restorers and maintainers. The testcrosses and parents were sown in paired rows of 1.5 m each. Data was recorded for days to 50% flowering (DF), bacterial blight (BB) resistance (Pathotype VII) and fertility percentage. These 181 parental lines were also characterized for the presence of *Rf*3 and *Rf*4 genes using the marker DRRM-*Rf*3-10 amplified >200 bp for *Rf*3 allele &

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<200 bp for *rf3* allele and marker DRCG-*Rf4*-14 amplified 845 bp for *Rf4* allele & 875 bp for *rf4* allele. Balaji Suresh P *et al* (2012) identified QTLs and their interactions for fertility restoration in *Rf3* and *Rf4* loci. For BB resistance, gene based markers *viz.* Xa4, xa13 and Xa 21 were applied to these lines.

RESULTS

Days to 50% flowering of the test crosses ranged from 70-114 days. The early maturing test crosses have a great potential especially in the south west districts with salinity and water logging. Forty nine test crosses flowered in less than 90 days. IR 106156-BK-BK, IR 31802-56-4, IR 112777 and PR 126 were found to be maintainer for the corresponding CMS line because test crosses were totally sterile. Out of these, test crosses involving CMS lines: IR 64608A, PCMS 24A, PCMS 11A, IR 80156A, PCMS 12A and IR 58025A and restorers: PRR 815, IR 112750, PAU 5187-RIL-1649-F8, IR 86515-19-1-2-1-1-



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The marker DRRM-*Rf3*-10 amplified >200 bp for *Rf3* allele and <200 bp for *rf3* allele. The marker DRCG-*Rf4*-14 amplified 845 bp for *Rf4* allele and 875 bp for *rf4* allele.

1-1, PR 121 and PR 126 had higher yield and other desirable agronomic characters like height and tillering ability. The Spikelet fertility % ranged from 1.13% to 89.42%. Test crosses with CMS lines: IR 58025A, PCMS 19A & PCMS 24A and restorers: PR 126, HHZ 3-SAL 13 Y2-DT1 and IR 112750

showed higher standard heterosis of 10% to 15%. Among all the TCN, 16 showed resistant to moderately resistant reaction to bacterial blight while most of the test crosses were susceptible, high incidence of false smut was also observed in many test crosses.

Molecular analysis of these lines with SSR markers Rf3 and Rf4 and Xa4, xa13 and Xa 21 were characterized for the presence of Rf3 and Rf4 genes and BB resistance respectively. Results showed that most of the lines (around 104) had Rf4 gene while 17 lines had Rf3 gene. Twenty genotypes had both the genes. Overall frequency and restoration action of Rf4 was higher than Rf3 in our lines which were studied thus suggesting that Rf4 gene located on chromosome 10 is the major restoration gene. It revealed that all

three BB genes *viz*. Xa4, xa13 and Xa 21 were present in 9 lines, Xa4 and xa13 in 7 lines and Xa4 Xa 21 in 5 genotypes.

CONCLUSION

The early maturing hybrid with higher yield and desirable quality characters along with resistance to bacterial leaf blight will be multiplied and further evaluated in replicated yield trials. The promising partial restorers will also be involved in restorer improvement programme.

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MOLECULAR MODELLING AND DOCKING OF NAC TRANSCRIPTION FACTORS IN ORYZA SATIVA

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The NAC family of Transcription factors plays a central role in abiotic stress responses such as drought response, flowering time, pathogen resistance and cold response amongst many more. Crucial in their functioning are 3 conserved domains namely, NAM (No Apical Meristem), ATAF2 and CUC2 (Cup shaped Cotyledon). SPL is involved in early flowering and by binding to NAC Promoters, a link could be established between flowering and Abiotic stress by regulating these interactions.

OBJECTIVES

1. Selection of 2 NAC Transcription factors via Promoter analysis.

2. To understand interactions between NAC41, NAC79 and SPL12 with their respective target DNAs.

METHODOLOGY

ONACs and SPL ASSOCIATION

To link NACs and early flowering owing to *SPL12* and *SPL14*, we randomly selected 11 unanalysed NACs and checked for *SPL12* and *SPL14* binding sites on their promoters. PLANT PAN 3.0 was used to check for these binding sites. The crystal structures of the nearest PDB hit for *OsNAC41*, *OsNAC79* was identified using BLAST against PDB database.

DNA AND PROTEIN MODELING

The Protein and DNA sequences of *NAC41* and *NAC79* were obtained from GBROWSE of RAP DB. The protein sequences of *NAC41 and NAC79* were submitted for homology modelling in RAPTOR X to obtain the 3D models. The DNA models of the Promoter regions of both NACs were obtained from DNA Sequence to Structure Prediction of SCFBio. The obtained models and Docks were visualized using Chimera 1.14.

MOLECULAR DOCKING USING HADDOCK 2.4

Haddock 2.4 was used to dock the NAC transcription factors (*NAC41*,

NAC79) to specific DNA binding regions and *SPL12* Protein to both NAC Promoters.

RESULTS

ONACs AND SPL ASSOCIATION

Binding sites of *SPL12* and *SPL14* were plotted on the 1 Kb promoter region of 11 selected NAC promoters generated. From these genes, 2 NACs with binding sites distributed majorly in the core promoter were selected for further studies.

A. Os01g0925400 - NAC41

B. Os04g0437000 - NAC79

STRUCTURAL ANALYSIS OF NAC41 AND NAC79

BLAST against PDB database using *OsNAC41, OsNAC79* as query identified *AtNAC19* from *Arabidopsis thaliana* as the nearest crystal structure. *AtNAC19* was thus considered a Standard. *AtNAC19* has 6 DNA binding motifs (Welner et.al, 2012). Their corresponding motifs in *NAC41* and *NAC79* were identified via multiple sequence alignment. The evolutionarily conserved residues within these consensus sequences can be considered as most important in DNA-binding. Of these residues, those substituted (not conserved) in OsNACs showed similarity with the original *AtNAC19* residues in terms

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of amino acid biochemical properties, increasing their similarity to *AtNAC19* motifs. It was observed that the Group 2 motif, which is specific for DNA recognition, undergoes a fold in *NAC41* and *NAC79* similar to that of *AtNAC19* in binding to DNA's major groove, suggesting evolutionary relatedness.

MOLECULAR DOCKING OF *NAC79* AND *NAC41* TO TARGET DNA

The obtained PDB model of NAC79 was docked with the DNA of the AtNAC19 crystal structure using HADDOCK 2.4. The Group 2 motif (WKPI) in NAC79, is the DNA recognizing motif and was submitted as the active residues along with CACG repeat in the DNA which is the core DNA binding region for most NAC Transcription factors. All the docks were screened for orientation and atomic distances with AtNAC19 (WKAT) as a reference. The best dock for NAC79 obtained is on the basis of atomic distances, highest binding energy and Haddock Docking score. Coming to deviations, in NAC79 Proline replaces Alanine and Isoleucine replaces Threonine showing slight difference in atomic distances which is thus explained. Similarly, in NAC41, for docking between WRAS and CACG, the best dock was obtained. In NAC41, Arginine replaces Lysine and Serine replaces Threonine giving variations in atomic distances.

MOLECULAR DOCKING OF *SPL12* TF TO PROMOTER REGIONS OF *NAC41* AND *NAC79*

Firstly, we performed BLAST of *SPL12* and *SPL14* Proteins against PDB to find the nearest hit. *SPL12* had a higher identity and was selected for further



FIG 7A, B: SPL12 TF-NAC47 AND SPL12-NAC79 PROMOTER INTERACTIONS 28

studies. This *SPL12* Protein sequence was modelled using Phyre2, which generated a model that had homology with the PDB hit. The Promoter sequences of *NAC41* and *NAC79*, and *SPL12* binding sites on them were obtained and the TF binding site nearest to the Transcription Start Site was selected. They were found to be TTCGTAAGA at -149 in *NAC41* and TGCATACAC at -52 in *NAC79*. Also, these binding sites coincided with the consensus sequence of SPB-DNA binding domains in promoter region of target genes: TNCGTACAA. HADDOCK 2.4 was then used to perform docking of the *SPL12* TF to *NAC41* and *NAC79*. All Docks were screened for their Haddock score and best fits with the selected. In

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both the models, *SPL12* binds to the minor groove of the DNA. In both cases, out of the long stretch of DBD, RRR and RRRK residues were found to be most involved in closely binding to the DNA, showing that they are crucial in this SPL12 and NAC interaction.

CONCLUSION

In our attempt at this thought, we were successful at modelling the TFs and their promoters, docking it with their target DNAs and isolating *NAC41* and *NAC79* in the first attempt at characterizing these NACs. Cloning, Transformation and expression studies would validate our finding and lead to a variety with abiotic stress tolerance and early flowering, which definitely seems far-fetched, but a step closer.

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WILD RICE ORYZA RUFIPOGON- A NEW ACCESSION FROM KARNATAKA

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ABSTRACT

Rice is one of the major cereal of global importance, cultivated in diverse agro-ecological regions. The rice genus *Oryza* is classified into 11 groups bassed on the genome. The AA genome has two cultivated species and six wild species. India is the center of origin and diversity for the Asian Rice, especially the foothills of the Himalayas, Chhattisgarh, Jeypore tract of Odisha, north eastern India. The cultivated *Oryza sativa* has two close relatives, believed to be progenitors, i.e., *O.nivara* and *O.rufipogon*, which seems to have evolved 10000-14000 years ago.

Oryza rufipogon, grows wild in India, China, Southeast Asia and South Asia. It is mentioned in the Red IUCN threatened list, this species is least threatened and found widely distributed across tropical Asia to Australia where subpopulations can be very large. For the improvement of cultivated rice and broadening its genetic base, genes from many landraces and wild species have been identified. One bacterial



Fig.1: *Oryza rufipogon* germplasm collection of the country in NGB

blight resistant gene from *O.rufipogon* has been identified and has been transferred to *O.sativa*. Research is being carried out to use *O. rufipogon* accessions as the potential donor for improving phosphorus uptake efficiency and to increase yield component.

O.rufipogon is a perennial species found in grassland, wetlands(inland), artificial/terrestrial, artificial/ aquatic and marine habitats. Due to rapid change in the natural habitats of the crop wild relatives, collection and conservation of the diverse *O.rufipogon* has gained priority for as potential genetic resource.

The germplasm collections of the National Genebank at ICAR-NBPGR has 364 accessions of indigenous collections of *O.rufipogon* from 10 states of the country (Fig. 1). These germplasm collections are primarily from the states of Odisha, West Bengal, Uttar Pradesh and some parts of Chhattisgarh, which



Fig.2: Potential areas of future exploration for *O.rufipogon* in Southern India



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are nearby regions of the primary and secondary centres of diversity. The 5 % of the marginal accessions belong to the other states such as Assam, Bihar, Jharkhand, Maharashtra, Gujarat and Kerala.

In the present study, an accession of *O.rufipogon* was collected from the north Karnataka region, which was hitherto not collected. As seen from the map (Fig.2), the collections reported along the western peninsular region mainly during 1999 are not present in the National Gene Bank. The accession from Jalibenchi, Raichur almost 20 years later shows the southern region as the potential areas for exploration of wild rice accessions and augment the germplasm collection of *O.rufipogon*.

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IMPROVEMENT OF PR 121 VARIETY OF RICE BY TRANSFERRING DROUGHT YIELD QTLs

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Due to changing climate, the ever-rising incidents of abiotic stresses have become a challenge in varietal development programme. PR121 is the most popular high yielding (7.6 t/ha) and bacterial leaf blight (BB) resistant variety predominantly grown in Punjab. It iswidely accepted by farmers as well as millers of Punjab state occupying about 22% (6.2 lakh hectares) area of the state during *kharif* 2020. This variety possesses three BB resistant genes, *Xa*4, *xa*13 and *Xa*21(Bharaj et al 2014). Keeping in view the deteriorating ground water table of the state, efforts were made to improve its water use efficiency by transferring drought yield QTLs *i.e.*, *qDTY*_{1.1} and *qDTY*_{3.1} from donor IR96321.

METHODOLOGY

PR121 was used as a recurrent parent and IR96321 possessing $qDTY_{1.1}$ and $qDTY_{3.1}$ was used as donor parent. Marker assisted breeding was done and lines possessing either or both QTLs, resemblance to PR121 and BB genes (Xa4, xa13 and Xa21) were selected. Thirty elite lines derived from backcrossalong with recurrent parent were evaluated in replicated randomized block design in multilocation trial. Data were recorded for different agronomic traits like, days to 50% flowering (DF), plant height (cm) (HT), ear bearing tillers per m^2 (EBT/m²), yield per plot (kg/ha) (YLD) and 1000 grain weight (gm). Averages of five plants for each genotype were assessed for ANOVA. For confirmation of BB resistance Xa4, xa13 and Xa21 gene based markers (Brar et al 2017) were applied. For tracking the transfer of drought QTLs from donor parent (IR96321) markers linked to $qDTY_{11}$ and $qDTY_{3,1}$ were applied on all genotypes.

RESULTS

The range of DF varied from 102 days to 121 days with nine genotypes flowering earlier than PR121

(107 days). Theplant height ranged from 94 cm to 106 cm, while the recurrent parent was 101 cm tall. About 50% of the elite lines out yielded PR121 and also possessed significantly higher EBT/m². RYT 3851 and RYT 3874were thehighest yieldinggenotypes among all. The 1000 grain weight ranged from 20.68gm to 27.40 gm. With maximum value of 27.40 gm, RYT 3851 had7% higher1000 grain weightthan recurrent parent PR121. Molecular marker analysisrevealed thatall three BB genes viz. Xa4, xa13 and Xa21 were present in 20 genotypes, while only 2 lines had Xa4 and xa13, and 8 lines carried Xa4 and Xa21. Among 30 elite genotypes, 2 lines showed presence of both drought tolerance QTLs in homozygous form, whereas 4 genotypes had only $qDTY_{31}$ and 6 lines carried only $qDTY_{11}$.

CONCLUSION

In the present study, both drought yield QTLs $viz.qDTY_{1.1}$ and $qDTY_{3.1}$ were successfully transferred in the background of PR 121. Two genotypes had both the QTLs in homozygousform while a total of 10 lines carried either of the two QTLs. The better performing lines in the field trial will be subjected to quality evaluation and will alsobe forwarded to multilocation trials for further evaluation.

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MOLECULAR CHARACTERIZATION OF RICE GENOTYPES FOR TOLERANCE TO PHOSPHORUS STARVATION

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Rice, the most vital crop and holds a unique position among cereals and serves as the staple food for the world population. It provides a total caloric intake of the Asian population where it is a prime source of energy. Phosphorus (P) is referred to as "king-pin" in Indian agriculture and it is one of the important macronutrients required for normal growth and development of all crop plants. The potential yield of rice cultivars is decreasing due to the phosphorus deficiency in problematic soils, thereby increasing the application of P fertilizer throughout the world. About 50% of the rice fields are experiencing a deficiency of P in Asia and about 60% of rainfed rice is grown on soils affected by multiple stresses including the P deficiency. Therefore, an alternative strategy is required to overcome the problem and to address this development of phosphorus starvation tolerant rice varieties holds significant for beneficial rice farming.

A major quantitative trait locus (QTL) phosphorus uptake 1 (*Pup1*) detected on chromosome 12 associated with tolerance to phosphorus deficiency. Fine mapping and candidate gene analysis of *Pup1* locus identified *PSTOL1* (Phosphorus Starvation Tolerance 1), which was very closely associated with tolerance to phosphorus deficiency. Based on the sequence information, the allele-specific insertion-deletion (InDel) and DNA markers for *Pup1* locus have been developed for use in gene identification and marker-assisted selection (Chin *et al.* 2011). With this information, our study was aimed to screen the rice genotypes for phosphorus deficiency tolerance using

Pup1 locus associated markers to identify the P-starvation tolerant genotypes that can be exploited for future rice breeding programme.

MATERIALS AND METHODS

The experiment was carried out at the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Tamil Nadu Agricultural University, Madurai. Thirty rice genotypes including two tolerant checks (IR 64 *Pup1* and Samba Mahsuri *Pup1*) were used in the present study. Genomic DNA was isolated from the young leaves of each genotype using Cetyl Trimethyl Ammonium Bromide (CTAB) method. Five SSR markers comprised of three dominant (K46-1, K52 and K59) markers in INDEL region and two co-dominant markers (K29-2 and K29-3) in *Pup1* genomic region (Chin et al. 2010, 2011) were used for genotyping to screen for the presence or absence of *Pup1* locus in the genotypes.

RESULTS AND DISCUSSION

Five *Pup1* QTL linked markers *viz.*, K29-2, K29-3, K46-1, K52 and K59 were genotyped for all the 30 rice genotypes. Amplified bands were scored from 0 (absence of allele in all the markers) to 5 (presence of the allele in all the markers). Among the 30 genotypes, 80 per cent of the genotypes possessed the probable presence of *Pup1* QTL. The marker K46-1 was observed to be the highest (70%) among the genotypes followed by K52 (66.66%), K59 (60%), K29-2 (36.66%) and K29-3 (30%).

Five genotypes i.e., ADT (R) 48, APO,



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Improved Pusa Basmati 1, PMK (R) 3 and UPLRI 5 have shown the *Pup1* allele for all the five markers. Six genotypes *viz.*, ADT 39, ADT 47, Anna (R) 4, CO 52, CR 1009 *Sub* 1 and TKM 13 did not show any *Pup1* allele amplification. Three genotypes had four amplified bands each, eight genotypes with three bands each, two genotypes with two bands and four genotypes with single amplified band were also observed with respect to all the five *Pup1* specific markers.

Based on the molecular screening, five genotypes *viz.*, ADT (R) 48, APO, Improved Pusa Basmati 1, PMK (R) 3 and UPLRI 5 were classified as tolerant for its response to P deficiency as they possessed the *Pup1* allele for all the five markers. The selected genotypes may be useful for the exploration of novel genes conferring phosphorus deficiency tolerance and used as donor parents in the breeding programs. Absence of this allele in the rice genotypes may be used as recipient parents in future rice breeding program

CONCLUSION

In this study, five genotypes *viz.*, ADT (R) 48, APO, Improved Pusa Basmati 1, PMK (R) 3 and UPLRI 5 were identified as phosphorus-deficient tolerant genotypes which could provide and display the tolerance sources for effective breeding of rice cultivars tolerant to phosphorus deficiency.

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PYRAMIDING OF QTLs FOR DROUGHT TOLERANCE (*qDTY1.1*, *qDTY 2.1*, *qDTY2.2* and *qDTY 3.1*) IN RICE

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Drought is one of the major abiotic stresses drastically affecting rice grown under rainfed low lands and uplands leading to yield loss of 13–35% (Shamsudin *et al.*, 2016). In view of changing climate, the water deficit appears to be the major constraint affecting rice production in near future (Wassman *et al.*, 2009). Hence breeding for improved drought tolerance leading to increased grain yield under drought stress is the most promising approach for managing the drought stress.

Deployment of two yield QTLs under drought (*qDTY2.1 & qDTY3.1*) into the background of Samba mahsuri *sub1* led to the development of DRR Dhan 50, the first drought cum submergence tolerant variety at ICAR-IIRR, Hyderabad through marker assisted back cross breeding approach. In the current study, we attempted to pyramid two additional QTLs for drought tolerance (*qDTY1.1* and *qDTY2.2*) into DRR Dhan 50 (*qDTY2.1, qDTY3.1* and *sub1*) to develop drought tolerant pyramided lines possessing enhanced drought tolerance.

METHODOLOGY

In order to generate drought tolerant pyramided lines with 4 QTLs, DRR Dhan 50 was used as the recurrent parent possessing qDTY2.1 and qDTY3.1 and SAB 4-7-5 as donor possessing qDTY1.1 and qDTY 2.2. The validation of 31 reported foreground SSR markers linked to the respective QTLs was done in the parental genotypes. Samba Mahsuri was used as negative control for this analysis . A cross was made between recurrent and donor parents to obtain F₁ seeds. Five true F₁ plants were backcrossed to DRR Dhan 50 to obtain BC_1F_1 progenies. The parents were screened with genomewide SSR markers unlinked to drought QTLs and identified 84 backgrounds markers. In each back cross generation, six foreground SSR markers were used to select positive plants. Background selection was done in those plants found positive for the targeted QTL combination. Recurrent parent genome recovery was estimated by Graphical Genotyping (GGT 2.0) software. Subsequently heterozygous BC_1F_1 plants having the QTLs under study and similar agronomic traits of recurrent parent were backcrossed with DRR Dhan 50 to obtain BC_2F_1 progenies.

RESULTS

The parental genotypes (DRR Dhan 50 and SAB 4-7-5) were screened for reported SSRs linked to drought tolerance QTLs. DRR Dhan 50 was screened with a set of seven reported SSR markers linked to qDTY 2.1 namely RM5791, RM521, RM3549, RM324, RM6374, RM525 and RM221 and; ten SSR markers linked to *qDTY 3.1* namely RM416, RM16030, RM520, RM55, RM168, RM186, RM293, RM468, RM15935 and RM16 to confirm the presence of qDTY2.1 and qDTY3.1. Three linked SSR markers namely RM521, RM324, and RM6374 (qDTY 2.1) and two linked SSR markers ie., RM168 and RM 186 (qDTY 3.1) showed polymorphism between DRR Dhan 50, positive check and Samba mahsrui, the negative check indicating presence of corresponding QTLs in recurrent parent which were selected for further screening of the crosses and segregating populations.



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Similarly the donor parent, SAB 4-7-5 along with Samba mahsuri, the negative check was screened for eight SSR markers linked to *qDTY 1.1* namely RM 11943, RM 12023, RM 12233, RM 12091, RM 431, RM 12146, RM 212 and RM 486; and six SSR markers linked to *qDTY 2.2* namely RM 236, RM 279, RM555, RM12460, RM154 and RM109. Polymorphism was observed with RM 12091 for *qDTY 1.1* and RM 279 for *qDTY 2.2* between donor and negative check.

DRR Dhan 50 (qDTY 1.1 and qDTY 2.2), the recurrent parent was crossed with a donor SAB 4-7-5 (qDTY2.1 and qDTY3.1) and generated 60 F₁s. They are tested for hybridity and confirmed 56 true F₁ heterozygote plants expressing both the alleles of recipient parent and donor with respect to foreground markers linked to four drought QTLs namely qDTY 1.1 (RM 12091), qDTY 2.2 (RM 279), qDTY 2.1 (RM 521 and RM 6374) and qDTY 3.1 (RM 168 and RM 186).

The recurrent parent was backcrossed with the five out of 56 confirmed heterozygous F_1 plants to generate 200 BC₁ F_1 seed. The marker assisted foreground selection of 200 BC₁ F_1 plants was performed for confirmation of targeted alleles utilizing the linked SSR markers *ie.*, RM 521 and RM 5791 (*qDTY 2.1*), RM 16030 (*qDTY 3.1*), RM 12091 and RM 431 (*qDTY 1.1*) and RM 279 (*qDTY 2.2*) (Fig



Fig 1: Foreground selection of BC_1F_1 plants using RM521 marker linked to *qDTY2.1*

1). Identified seven heterozygous BC_1F_1 plants designated as BC_1F_1 -9 (A), BC_1F_1 -12 (B), BC_1F_1 -25 (C), BC_1F_1 -50 (D), BC_1F_1 -52 (E), BC_1F_1 -72 (F) and BC_1F_1 1-76 (G) harbouring all four QTLs *viz.*, *qDTY 1.1*, *qDTY 2.1*, *qDTY 2.2* and *qDTY 3.1*.

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For background selection, a set of 909 SSR markers unlinked to drought QTLs evenly spaced across the twelve rice chromosomes were selected to find out polymorphic background markers between the parents (RP and donor). Out of 909 SSR markers, 84 were polymorphic between recurrent and donor parents. The number of polymorphic markers per chromosome ranged from 4 (Chromosome # 5) to 13 (chromosome 1).

Background selection of seven BC_1F_1 plants with 84 genome wide SSRs revealed the percentage of recovery of recurrent parent genome from 59.5 to 75% using Graphical Genotyping (GGT 2.0). Two BC_1F_1 plants with 73% (BC_1F_1 -52) and 75% (BC_1F_1 -25) genome recovery and phenotypically similar with recurrent parent were again back crossed with recurrent parent (DRR Dhan 50) for producing BC_2F_1 progenies

CONCLUSIONS

In the present study the pyramiding of 4 yield QTLs under drought (qDTY 1.1, qDTY 2.1, qDTY 2.2 and qDTY 3.1) in the genetic background of DRR Dhan 50 using marker assisted back cross breeding (MABB) is being done for attaining enhanced drought tolerance. In each back cross generation the foreground selection of the targeted QTLs using tightly linked reported SSR markers as well as the background selection of the maximum genome recovery of recurrent parent in BC₁F₁ progenies revealed the potential of MABB in breeding program. Screening of the subsequent BC₂F₁ progenies with foreground and background markers is in progress.





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IRC/TM-1/PP-136

. Indian Rice

APPLICATION OF A NOVEL PHENOTYPING PROTOCOL FOR LEAF FOLDER RESISTANCE IN WILD INTROGRESSION LINES DERIVED FROM ORYZA NIVARA AND QTL MAPPING

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Leaf folder, Cnaphalocrocis medinalis Guenee is one of the major leaf feeding insects damaging rice crop in all the rice ecosystems. The green larva causes damage by folding the leaf margins longitudinally and feeding on the leaves at all the crop growth stages. This folding and feeding results in reduced photosynthesis affecting the plant growth and grain yield. Heavily infested fields have a whitish scorched appearance that is visible from a distance. Padmavathi et al (2013) quantified the yield losses caused by rice leaf folder and found that more than three larvae per plant at maximum tillering stage resulted in 20% unûlled grains while flag leaf damage of above 25% caused more than 50% unûlled grains resulting in direct effect on yield reduction in rice. The highly noticeable damage symptoms in the field triggers the famers to frequently and sometimes indiscriminately apply toxic insecticides leading to adverse effects on natural enemies, human health and environment. Therefore, development and cultivation of a resistant variety as a component of rice pest management can have a major beneficial impact on the farmers especially in low input farming situations of India and South Asia. So far, few cultivars with low leaf folder damage have been identified as resistant/ moderately resistant, however, wild species of Oryza which are important sources of genetic variability can potentially offer options for incorporating resistance in popular varieties. Earlier, resistance screening was done as per the Standard Evaluation System (SES) for rice (IRRI, 2014) taking damaged leaves into consideration. Later, a rapid novel field screening method was developed for the evaluation of resistance to leaf folder (Padmavathi et al., 2017). The present study was carried out with the objective of phenotyping of a population of wild introgression lines derived from Swarna/ *O.nivara* using this novel phenotyping protocol and identifying QTLs governing resistance to rice leaf folder.

METHODOLOGY

Field experiments were conducted at research farm, ICAR- Indian Institute of Rice Research (17°19¹N and 78°29¹E), Hyderabad, Telangana State, India. A set of 92 backcross inbred lines (BILs - $BC_{2}F_{2}$), derived from a cross between an elite cultivar Swarna (O. sativa) as a recurrent parent and a wild accession O. nivara (Acc. NO. 81832) as a donor parent were subjected to leaf folder screening. Phenotyping of BILs along with parents was done by the rapid field screening method for two seasons during Kharif 2018 and 2019. The BILs were grown in the field at 30 x 20 cm spacing in three blocks, each representing a replication. In each block, three plants were randomly selected and leaves of each plant were covered with a nylon mesh bag and tied at the bottom. A single 3rd instar larva was released and allowed to feed for 48 hrs. After 48 hrs of larval the number of damaged leaves were counted, collected and preserved for the measurement of damaged leaf area. The damaged leaves were scanned using Cannon MF 4320-4350 scanner at colour mode with 300dpi image quality. Leaf area damaged was measured using ImageJ software (http://imagej.nih.gov/ij/). The damaged area

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(DA) recorded was converted to adjusted damaged area rating (ADAR) by dividing the damaged area in test entry by the damaged area in susceptible check and multiplying with 100. These percentages were converted to 0 to 9 scale representing the damage score (DS). BILs with mean scale score of 0 to 3 were considered as resistant, 3.1 to 5.0 as moderately resistant and 5.1 to 9 as susceptible. Data on leaf morphological traits like leaf length and leaf width were also recorded from five leaves randomly selected from five hills in each BIL. BILs were genotyped using 140 random polymorphic SSR markers with genome wide distribution. Inclusive Composite Interval Mapping software (IciMapping v4.0.1) was used for linkage mapping and QTL detection.

RESULTS

Phenotypic variation in BIL population-The mean phenotypic variation for damaged area and damage score showed a continuous normal distribution in both seasons. The damaged area during *kharif* 2018 varied from 157.90 to 2580.84 mm² and 140.35 to 1508.64 mm² during *kharif* 2019. Twenty BILs were identified as resistant with a damage score of 3.0 and 31 BILs as moderately resistant with damage score of 3.1 - 5.0. Leaf morphological parameters like leaf length and leaf width showed variation among the BILs. Leaf length ranged between 24.3 and 53.8 cm, while leaf width varied from 0.53 to 1.40 cm. A significant positive correlation was found between damage area and leaf width (r = 0.53) while it was negative with leaf length (r = -0.47).

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QTL mapping – Seven QTLs were identified for damage area during 2018 and six QTLs for 2019 damage area. For mean damage area of two years' data, three QTLs were identified on chromosome 2 and 3. Of these QTLs, QTL identified on chromosome 3, between RM231 – RM517 was found stable across the years with an LOD value of 4.08. This is a candidate region for further investigation into leaf folder resistance. Another major QTL was identified for damage score on chromosome 5 with a LOD value of 3.09 and phenotypic variance of 14.86 between markers

Table. 1 QTLs identified for leaf folder resistance based on phenotyping in two seasons

TraitID	TraitName	Chromosome	Position	Left Marker	Right Marker	LOD	PVE(%)	Add	LeftCI	RightCI
1	DA_2018	1	6	RM283	RM1220	3.7047	2.8666	-1023.17	5.5	6.5
1	DA_2018	2	15	RM290	RM341	5.5917	3.2558	-1012.14	12.5	16.5
1	DA_2018	2	30	RM53	RM250	4.1509	2.423	-1039.88	29.5	30.5
1	DA_2018	3	4.4	RM231	RM517	2.7285	1.8229	-752.367	3.9	6.9
1	DA_2018	3	30.4	RM55	RM1352	2.6598	1.5895	-599.173	27.9	31.9
1	DA_2018	10	17.7	RM271	RM6100	2.6808	1.5553	-1092.08	17.2	18.2
1	DA_2018	11	22.8	RM206	RM224	2.5034	2.9834	-982.897	22.3	24.3
2	DS_2018	5	14.071	RM5140	RM146	3.0947	14.8566	1.2242	13.57	15.57
3	DA_2019	2	9	RM8080	RM290	2.5738	1.7512	-518.925	5.5	10.5
3	DA_2019	3	5.4	RM231	RM517	3.1869	2.8416	-284.236	4.9	6.9
3	DA_2019	4	26.16	RM273	RM241	2.8897	2.2266	-423.695	25.66	26.66
3	DA_2019	7	8.67	RM125	RM5436	3.5939	1.7994	-327.401	7.17	9.17
3	DA_2019	9	7.02	RM316	RM434	3.3541	2.359	-401.001	1.02	11.52
3	DA_2019	12	19	RM277	RM519	4.2639	1.7418	-529.041	18.5	19.5
4	DA_M	2	15	RM290	RM341	3.7427	4.3433	-495.092	12.5	16.5
4	DA_M	2	30	RM53	RM250	2.8698	2.8648	-514.276	29.5	30.5
4	DA_M	3	5.4	RM231	RM517	4.0836	3.2438	-431.463	3.9	6.9



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RM5140 and RM146 (Table 1).

Introgression of major and stable QTLs identified in this study, into popular susceptible high yielding rice varieties may help in building resistance to the damage by rice leaf folder. The genomic region in these QTLs may be further explored to identify the causative candidate genes for leaf folder resistance. The identified introgression lines with both leaf folder resistance and high yield can be tested through multilocation trials for development of improved varieties.

CONCLUSIONS

A recently developed novel phenotyping protocol was validated in the present study. This protocol is field based and considers damage area for scoring.

Phenotyping of 91 BILs identified 20 BILs with a damage score of 3.0 as resistant to rice leaf folder

qDS5.1 identified on chromosome 5 for damage score and qDA_M 3.1. on chromosome 3 for mean damage area were considered as major QTLs in the present study based on LOD and PV values. These QTLs need to be validated and fine mapped.

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. Indian Rice

CALLUS INDUCTION EFFICIENCY OF TRADITIONAL RICE VARIETIES

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Rice (Oryza sativa) is a monocotyledonous cereal crop which is the world's most important food crop after wheat and maize and is the primary food source for more than one third of the world's population. Today rice production has been increasing worldwide by large scale adoption of modern high yielding rice varieties and through various improved cultural practices. Rice consumers are increasing at the rate of 1.8% every year. Plant tissue culture is commonly used to describe the in vitro and aseptic cultivation of any plant part whether a single cell, a tissue, or an organ, on a nutrient medium. Plant regeneration is better on traditional rice varieties when compared to rice cultivars. Traditional rice varieties have better grain quality profile with sweet aroma. Traditional varieties provide several health benefits to human beings. These serve as better choice for consumers suffering from diabetes and obesity. These are rich in fibre, vitamins, antioxidants and micro nutrients. These varieties show high level of resistance to pest and diseases and tolerant to environmental stresses. Grains of traditional rice varieties have their unique features such as nutritive, cooking and eating qualities.

OBJECTIVES:

To find out the callus induction efficiency of traditional rice varieties

MATERIALS AND METHODS:

The materials subjected in this study include healthy seeds of ten traditional rice varieties *viz.*, Chandikar, Mattaikar, Kallurundaikar, Kattanur, Kuliyadichan, Poongar, Kuruvaikalangiyam, Norungan, Nootripathu and Chittiraikar received from Agricultural Research Station, Paramakudi, Tamil Nadu. Murashige and Skoog medium (MS) was selected as a basal medium for callus induction and plant regeneration. Sterilized dried seeds were inoculated onto MS media supplemented with 2,4-D for callus induction. The MS medium (Murashige and Skoog, 1962) was prepared with 0.8% (8g/l) agar (the gelling agent) and it is fortified with 20 g sucrose. The pH of the medium was adjusted to 5.8. The sterilization of the medium was carried out at 121p C for 20 minutes at 15 psi in an autoclave. Mature rice seeds were dehusked manually and washed with distilled water for 2 times. Dehusked seeds were taken as a source of explants. Thereafter, seeds were surface sterilized with Mercuric chloride (0.1% w/v) for 3 minutes and finally rinsed 3 times with sterile distilled water in the laminar air flow cabinet to remove all the traces of Mercuric chloride.

Embryo portion of 2-3 undamaged seeds of each variety were aseptically transferred into the test tube containing MS basal medium with different concentrations *viz.*, 1mg/l, 2mg/l, 3mg/l, 4mg/l of plant growth regulator 2,4-D (2,4-Dichlorophenoxyacetic acid) for studying the callus response of seed embryo explants. Cultured test tubes were kept for incubation inside the culture room in dark condition which was maintained at $25\pm1p$ C and 85% humidity. Each treatment was conducted in 40 test tubes. Frequency (%) of callus induction was counted in each tube after six weeks of inoculation.

After the incubation period of three weeks (21-24 days), embryogenic calli were obtained. After the induction of callus, it was identified and sub cultured in different test tubes containing same media with growth



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regulator of same concentration. Then, the cultures were kept in growth chamber under 16 hrs light and 8 hrs dark photoperiod at 25p C for about 3 weeks. The response of ten varieties of traditional rice varieties was determined in terms of callus induction and callus growth. Callus induction was noticed within ten days



(a) Callus induction in Poongar at 3mg/l + 2,4-D (b) Callus induction in Poongar at 4mg/l + 2,4-D (c) Callus induction in Chandikar at 4mg/l + 2,4-D (d) Callus induction in Chandikar at 2mg/l + 2,4-D (e) Callus induction in Chithiraikar at 3mg/l + 2,4-D (f) Callus induction in Kallurundaikar at 3mg/l + 2,4-D (g) Callus induction in Kuruvaikalangiyam at 4mg/l + 2,4-D (h) Callus induction in Kattanur at 3mg/l + 2,4-D (i) Callus induction in kuliyadichan at 3mg/l of 2,4-D.

of inoculation. The frequency of callus induction was measured using the following formula:

Frequency of callus induction =

No. of explants inducing callus No. of cultured explants

RESULTS:

Callus induction of dehusked rice seeds of traditional rice varieties was carried out on MS medium with four different concentrations of growth regulator 2,4-D *viz.*, 1mg/2mg/3mg/4mg/1. Calli were developed within ten days after inoculation. MS medium was found to be superior in its callus induction ability in all genotypes of traditional rice varieties.

DISCUSSION:

The result from the study revealed that all the ten traditional rice varieties gave better callus induction response on MS media. These results were in agreement with the findings of Gouranga Upadhyaya *et al.*, 2015. MS medium supplemented with 4mg /l 2,4- D gave more frequency of callus induction (60%) and had the most desired calli features. Results of the present study were in agreement with those of Libin *et al.*, 2012 which showed that 4.0 mg/l 2,4-D was the most optimum concentration for callus induction from mature rice seeds. Moreover, Based on the response of the ten traditional rice variety used, callus induction

Variety	Conc.of.2,4-d at	% of callus	
	which maximum	induction	
	callus induction (mg/i)		
Chandikar	3	70	
Mattaikar	3	50	
Poongar	3&4	50	
Kuruvaikalangiyam	3	70	
Norungan	3	50	
Nootripathu	4	60	
Kattanur	1	40	
Kuliyadichan	4	60	
Chittiraikar	4	40	
Kallurundaikar	3	50	



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efficiency was achieved in MS medium supplemented with 3.0 mf/l and 4.0 mg/l 2,4-D

CONCLUSION:

The findings of the study provided *in vitro* protocol for generating high frequency callus formation and its subsequent growth potentiality in traditional rice varieties. Chandikar (70%), Poongar (50%), Mattaikar (50%), Kuruvaikalangiyam (70%), Kallurundaikar (50%) and Norungan (50%) showed maximum callus induction frequency on MS medium

supplemented with 3mg/l 2,4-D. Kattanur (40%) recorded maximum callus induction efficiency on MS medium supplemented with 1mg/L 2,4-D. Kuliyadichan (60%) and Nootripathu (60%) showed maximum callus induction frequency on MS medium supplemented with 4mg/l 2,4-D. These findings could also be utilized for further tissue culture based biotechnological experiments viz., transformation experiment for disease and pest resistant, enhanced nutritive value, stress and salt tolerance through gene transfer techniques.

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ENHANCEMENT OF NUTRITIONAL QUALITY ATTRIBUTES OF SELECTED RICE LANDRACES OF SOUTHERN ODISHA THROUGH OMICS BASED APPROACHES

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Rice landraces are ecotypes which are grown in pristine habitats by tribal farmers of a region who serve as custodians for these races and adopt traditional methods for cultivating them. The landraces of rice harbor dominant genes for biotic, abiotic stresses, aroma and palatability being nutritionally rich and therefore hold considerable promise for their utilization in plant breeding and biotechnology programs. The rice landraces represent a wide range of genetic variability particularly for more useful characteristics in terms of their growth in various land types (upland, medium land, lowlands etc.), possession of strong aroma, drought tolerance nature, stable yield (without the use of chemical fertilizers), weed competitiveness, moderate tolerance to pests/diseases, good cooking quality/taste, higher grain number, suitability for various fast-food preparations etc. The landraces of rice have particularly found a place in various occasions like festivals, ancestral ceremonies, family functions and rituals and hence given top priority for conservation by the tribal farmers. But the adoption of modern agricultural practices, increased usage of chemical fertilizers, rising global temperature coupled with changing weather patterns, increased pressure on land for higher production and the advent of biotic intruders have substantially reduced the overall productivity and nutritional milieu of rice landraces. These factors have necessitated to seek for alternative approaches to

maintain the nutritional quality traits of these races to fulfil the dietary needs of the growing population.

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The present work is an attempt to explore the tools of omics for enhancing the nutritional quality traits of rice landraces highlighting the essentiality of genomics, transcriptomics and proteomics to elucidate the cellular intricacies and regulatory mechanisms in understanding this important food crop.

Genomics, proteomics, transcriptomics and metabolomics in rice research provide new dimensions for the improvement of qualitative and quantitative traits in rice. The integration of data science with the current rice-omics scenario is increasing its potential across the scientific community to study the roles of potential genes in enhancing its nutritional quality attributes. Due to the availability of its complete genome sequence, rice has evolved as a model crop among monocotyledons and tremendous progress has been observed in the techniques relevant to all tissues, organs and organelles of rice. This provides a means for several omics studies like genome-wide transcriptome, proteome and metabolome analyses (Agrawal & Rakwal 2011; Kyndt et al. 2012; Chen et al. 2014). The advent of Next generation sequencing has greatly accelerated the rice genomics study and genomic approaches has opened new vistas in rice research including gene mapping, mutant analysis for agronomic



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traits, study of evolutionary relationships and gene pyramiding. NGS has also provided fresh perspectives on the impact of transposable elements in the genome dynamics of the species and molecular spectrum of somaclonal variation in regenerated rice and identification of rare and spontaneous mutations with high confidence within the genomes. Thus, NGS provides an opportunity to expedite the genotyping operation for effective genetic mapping and genome analysis over tedious traditional breeding approach. Genome wide association studies has recently appeared as a method for dissecting agronomic traits in different rice landraces. Genotyping by sequencing is one of the recent applications of next generation sequencing for generating high density SNP markers useful for mapping inbreeding populations. Similarly, rice transcriptomics involves the study of the different functions of the genome during different stages of the life cycle under different physiological conditions in response to various

Databases in the field of rice omics

Rice genome databases



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Fig.1 Rice landraces selected for the study

environmental stresses. Transcriptomics serves as a reliable tool to study gene expression profiles of developing embryos of rice using RNA-sequence, study of different developmental stages of rice anther, effects of abiotic and biotic stress in rice, identification and characterization of novel genes related to metal homeostasis using microarray studies and study of RNA sequence of drought resistant rice to tolerate other unrelated stresses. The study of the rice proteome has unveiled many critical biological processes using tools like one dimensional and two dimensionsal SDS PAGE electrophoresis, mass spectrometry, multidimensional

S.N.	Name of database	Role played	URL
1.	Oryza sativa genome DB	Provides a convinience sequence centred genome view for Oryza sativa	http:// www.plant gdb.org
2.	Rice DB: An Oryza information portal	A database on genome identifiers, functional and proteomic annotations, subcellular localization phenotypes and upstream transcription motifs	http://ricedb.plantenergy.ewa.edu.au/index
Rice	transcriptome databases		
1.	Rice genome annotation	Provides high quality annotation for genes found in rice	http://rice.plantbiology.msu.edu/ expression.shtml
2.	Rice expression profile database (RiceXPro)	It is a repository of gene expression profiles derived from microarray analysis of tissues/organs encompassing the entire growth of the rice plant under different conditions	http:// ricexpro.dna.affrc.go.jp/
Rice	proteome databases		
1.	Oryza PG-DB	Rice proteome database based on shotgun proteogenomic	http://Oryzapg.iab.keio.ac.jp/
2.	Rice proteome database	First detailed database to describe the proteome of rice	Gene64.dna.affrc.go.jp/RPD/
Rice	metabolome databases		
1. 2.	MassBank METLIN	Metabolite annotation, MS/MS databases Repository of metabolite information and tandem mass spectrometry data designed to facilitate metabolite identification in metabolomics	http://www.massbank.jp/index.html http://metlin.scripps.edu



Rice Research and Development for Achieving Sustainable Development Goals

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Fig.2 Schematic representation showing multiomics based strategy for the enhancement of nutritional quality attributes in rice

protein identification technology or a combination of both. Recent developments in high-thoroughput protein identification approaches like ICAT and SILAC have facilitated the identification of rice proteins having enhanced nutritional value. A number of metabolic compounds influence the developmental activity and quality traits in rice. These compounds are mostly the secondary metabolites associated with diverse traits like yield, nutritional value, taste, colour, fragrances, defense against biotic and abiotic stresses. Molecular detection techniques like gas chromatography-mass spectrometry (GC-MS), liquid chromatography-mass spectrometry (LC-MS), capillary electrophoresismass spectrometry (CE-MS) and nuclear magnetic resonance (NMR) are the commonly used methods in metabolic profiling.

METHODOLOGY:

The methodology involved the collection of seed grains from the tribal pockets of South Odisha followed by their morphometric characterization. The biochemical and nutritional quality evaluation was carried out further following standard procedures to screen the potential races in terms of their nutritional quality traits. The data analysis and visualization was done using iResearch and a database was made using the tools of bioinformatics. Further, approaches were carried out to include these rice landraces in food fortification and biotechnology programs with an effort to conserve the gene pool of these fading races.

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RESULTS:

Screening and establishment of some potential races on the basis of their nutritional quality attributes. Recommend the best races for cultivation suiting to varied agro-climatic conditions. Conservation of gene pool of the fading races

CONCLUSION:

Conventional research on rice has its limitation but omics study has opened new vistas to explore the lesser known biological processes at molecular level. This is likely to pave ways for the enhancement of both qualitative and quantitative characteristics in rice. Further, the omics driven rice research would serve to ensure food security offering great promises for the future.

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Rice Research and Development for Achieving Sustainable Development Goals

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IRC/TM-1/PP-139

. Indian Rice

AROMATIC SHORTGRAINED RICE LANDRACE GOBINDABHOG PURIFIED INTO FOUR SORTS

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Gobindabhog is a popular non-basmati, short grained aromatic landrace of West Bengal. The landrace wasprocured from the NRRI Genebank with IC No 257238. It was subjected to several cycles of purification since Kharif-2015. The landrace was purified into four different sorts. The purified sorts were characterized for the physical properties of grains and were genotyped. The sorts varied for their graintypes, aroma and maturity duration.

INTRODUCTION

Gobindabhog is one of the most popular aromatic landraces of West Bengal.Ithas been traditionally grown in eight districts of the state including Bardhaman,Bankura, Hooghly, Nadia, Birbhum, Murshidabad, North 24 Parganasand Howrah (1). It is cultivated over an area of more than 40, 000 ha in the state. Due to its premium quality and better market returns, its cultivation spread to other adjoining districts like Bankura and Purulia in the state and Kaimur and Naugachia in Bihar. Tosave the interest of the farmers in the traditional growing areas of West Bengal who have been cultivating and preserving this premium quality, traditional variety over 400 years, *Gobindabhog* has been GI tagged by IPO for being grown in the eight demarcated traditionally growing districts of West Bengal (1).

Gobindabhog rice owes its premium quality due to its unique buttery aroma, small grains, intermediate stickiness, and excellent taste. It is a rice of choice for preparation of *Khichdi*, *Pulao*, *Payas* and poorman's *Biryani*.

Since *Gobindabhog* is a landrace, and landraces are mixtures of several genotypes and therefore are considered as the reservoir of allelic diversity, it needs to be purified before undertaking any improvement program. Otherwise the original genotype may get lost in due course of genetic improvement program of the landrace. Therefore, a purification program for the popular landrace was undertaken at the Institute to initiate further improvement program utilizing the superior purified genotypes.

MATERIALS AND METHODS

Gobindabhog accession collected from Burdwan with IC No 257238 was collected (50g) from the Genebank at ICAR- National Rice Research Institute, Cuttack and grown in the research field of the institute during Kharif-2015. Selection bypanicle progeny method was followed for purification of the



Fig. 1: Paddy of the four sorts derived from *Gobindabhog* (IC No 257238)



Fig.2. Milled rice of the four sorts derived from *Gobindabhog*(IC No 257238)



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Table1: Characterization of the four sorts derived fromGobindabhogIC257238basedonthe physicalcharacteristics of their grain types

Si No.	Genotype	Planth eig ht (cm)	Duration (Days)	Husk Calor	i, L/B (Paddy)	L, L/B (Rice)
1.	GB-1	130	142	Darker	6.26, 3.26	4.36, 2.6
2.	GB-2	135	140	Lighter	5.88,3.12	4.31, 2.67
З.	GB-3	135	140	Lighter	6.21, 3.26	4.46, 2.67
4.	GB-4	125	130	Darkest	6.30, 2.85	4.38, 2.36

landrace displaying sufficient diversity for grain type, panicle architecture and maturity duration. The purification process was undertaken for the next four years. Thepurified sorts were characterized for the physical properties of grains and were genotyped using thirty microsatellite markers. The results of the same are presented here.

RESULTS

Based on the morphological features, plants in the population were sorted out into two types. The panicles were harvested from the two types and were separately bulked for planting in next season, Kharif-2016. Again, variation was observed in the first sort and it was differentiated into three sorts based on their grain type and maturity duration. Panicles were harvested from the four different sorts and bulked for planting separately during the Kharif 2017. Panicle progeny row method was practiced duringKharif 2018 and Kharif 2019 for purification of the sorts. The sorts have been maintained as bulks as well. Variation is still observed in the bulked harvest of two sorts suggesting the scope of identification of other types in the population. The four sorts identified from the original population were characterized for their plant height, duration and grain type as described in Table1. Figure 1 and 2 represent the morphological features of the paddy and milled rice of the four sorts. The sorts were found to vary for their plant height which varied from 125 cm in Type4 to 135cm in Type2 and Type3. Type3 recorded a plant height of 130cm. Type2 and Type3 recorded crop duration of 140 days while Type 4 recorded the shortest duration of 130 days. Type4 was characterized with the darkest husk color among the four while Type2 and Type3 have lighter husk color. Based on their length and l/b ratio of the milled kernel, the grains of all sorts were characterized under short and bold category. Variation in grain type was also recorded among the four sorts which is depicted in Table 1. The variation in grain type identified in the sorts is in accordance with the range of variation reported for Gobindabhog in the description of the landrace in the GI application document (1). Little longer kernel types were also identified. The sorts were genotyped using thirtySimple Sequence Repeat (SSR) markers. Out of these, tenwere found to be polymorphic. At least one primer to distinguish each sort from the other three was identified. This led to the conclusion that each of the purified sorts was genetically

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Representative gel photograph for the amplicons of SSR markers polymorphic between the four sorts derived from *Gobindabhog*(IC No 257238)

Note: Pr-267:RM22143; Pr-202:AUT17337; Pr-271: RM22674; Pr-30:RM17363;



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distinct from each other and the original population borne sufficient genetic variation.

CONCLUSIONS

Sufficient genetic diversity existed in the original sample of *Gobindabhog* collected and stored in the Rice Genebankof ICAR- National Rice Research Institute, Cuttack as IC No 257238. Since landraces are populations of individuals which are similar in phenotype due to selection by farmers for superior types over ages, but they are genetically not uniform. Therefore, landraces are correctly categorized as homozygous but heterogeneous group of individuals making the populations. The purification of this accession of *Gobindabhog* landrace into four different sorts, their characterization on basis of morphological features and microsatellite markersbased genotyping could clearly reinforce the fact that landraces hold a huge genetic diversity which can be utilized in different genetic improvement programs [2]. Landraces must be purified for identification of superior genotypes in the breeding programs for further improvement [2]. This is critical in breeding where landraces are involved.

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. Indian Rice

CORRELATION AND PATH COEFFICIENT ANALYSIS FOR YIELD AND ITS TRAITS IN MID EARLY HYBRIDS OF RICE

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Rice (*Oryza sativa* L.) is one of the staple cereal crops which feed more than half of the world population. Correlation studies among yield and its component traits give a better view towards the relationship between yield and its components. Path analysis also helps in determining the direct and indirect causes of association and formulation of effective breeding strategies for development of better genotypes. Hence, the present study was undertaken to know the inter-relation among different yield contributing characters and their association with grain yield.

METHODOLOGY

The experimental materials consisting of 30 mid early rice hybrids along with 4 different checks supplied by Hybrid Rice section, Indian Institute of Rice Research, Hyderabad under All India Coordinated Rice Improvement Project (AICRIP). The test hybrids were evaluated under irrigated situations in AICRP on Rice Scheme, Regional Agricultural Research Station, PJTSAU, Warangal, Telangana during Kharif, 2018. These experimental materials were evaluated in a randomized complete block designs with three replications. The rice hybrids along with checks were transplanted in eleven row plots of 4.05m length with a row to row spacing of 20 cm and 15cm between plants. The recommended agronomic practices were followed to raise healthy crop. Observations were recorded on nine characters viz., days to 50 percent flowering, plant height, panicle length, panicle number per metre square, number of filled grains per panicle,

number of unfilled seeds per panicle, Spikelet fertility %, 1000-grain weight and grain yield per plot, which converted in to kg/ha. Statistical analysis for the above characters were done following Singh and Chaudhary (1979) for correlation coefficients and Dewey and Lu (1959) for path analysis.

RESULTS AND DISCUSSION

The results revealed that the estimates of genotypic coefficients were higher than phenotypic correlation coefficients for most of the characters under study which indicated strong inherent association between the characters which might be due to masking or modifying effects of environment. Grain yield was positively correlated with 1000 grain weight and spikelet fertility. It was observed that days to 50 per cent flowering was recorded non-significant positive association with single plant yield means early maturing variety produced lower yield. Similar results were reported by Swapnil et al. (2018). Days to 50 per cent flowering had significant positive association with plant height (0.7116), panicles per metre square (0.3762) and panicle length (0.3057). Plant height (-0.2129) was recorded significant negative association with grain yield per hectare at genotypic level. Therefore, selection of semi dwarf genotypes/lines will be preferred to increase the grain yield in rice. Plant height had significant positive correlations with number of panicles per square meter (0.3762), Panicle length (0.3057) and number of unfilled seeds per panicle (0.2927). Number of panicles per sq.m had a positive



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association with 1000 grain weight (0.1480), panicle length (0.1908), spikelet fertility (0.0949) and number of unfilled grains per panicle (0.0995), whereas it exhibited a significant negative association with number of filled grains per panicle (-0.0882). Panicle length had negative and significant association with grain yield per plant (-0.2563) while positive and significant association with number of filled grains per panicle (0.2377). Number of filled grains per panicle had negative correlation with number of unfilled grains per panicle (-0.137) and negative significant correlation with spikelet fertility (-0.2388). Number of unfilled grains per panicle (-0.1452) had negative and non-significant correlation with grain yield kg per ha and negative and significant correlation with 1000 grain weight (-0.2762) and positive association with spikelet fertility (0.536). Character association spikelet fertility (0.3135) revealed significantly positive association with grain yield kg per ha and positive association with 1000 grain weight (0.1347). 1000 grain weight (0.3481) had positive and significant correlation with grain yield kg

per ha. Hence, selection for these traits can improve yield.

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Path coefficient analysis revealed that spikelet fertility and thousand grain weight possessed the highest positive direct effect on grain yield followed by days to 50 per cent flowering and number of filled grains per panicle. This indicates that more filled grain in panicle is the highly reliable component of grain yield. Another important character with high direct effect on seed yield is 1000 grain weight which showed positive direct effect on seed yield. Hence, spikelet fertility and 1000 grain weight should be given prior attention in rice improvement program because of their major influence on yield. These findings were in accordance with Swapnil et al. (2018) and Dhavaleshwer et al. (2019). Days to 50% flowering had negative association with yield. Negative direct effect was observed for plant height, number of panicles per meter square, panicle length and number of unfilled grains.

Indirect effects of days to fifty percent flowering was found to be positive through plant height (0.1537),



Fig 1: Graphical representation of Direct and indirect effects of different characters on grain yield per plant at genotypic level in rice (*Oryza sativa* L.)



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no.of unfilled seeds per panicle, no.of panicles per metre square, panicle length, spikelet fertility and 1000 grain weight and panicle per metre square (-0.045). Indirect effects of spikelet fertility were found to be positive through number of unfilled seeds per panicle (0.3032), plant height (0.1136), 1000 grain weight (0.0762), days to fifty per cent flowering (0.066), panicle per metre square (0.0537) and negative through panicle length (-0.1099) and number of filled grains per panicle (-0.568). Indirect effects of test weight were found to be positive through plant height (0.0544), panicles per metre square (0.0402), spikelet fertility (0.0365), days to fifty per cent flowering (0.026), panicle length (0.018) and negative through number filled seeds per panicle (-0.0648). Indirect effects of number filled seeds per panicle were found to be positive through panicle length (0.0156), days to 50 percent flowering (0.0023) and negative through test weight (-0.157) and plant height (-0.0075). These results are in agreement with previous reports of Swapnil et al. (2018). The residual effect of the present study was 0.653, indicating that 34.7 % of the variability in grain yield was contributed by nine characters studied in the path analysis. This result gives an impression that some other major characters than those involved in the present study might also contribute to yield.

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CONCLUSION

Partitioning of correlation values showed that some of the characters could not produce significant correlation with grain yield kg per ha which might be either due to very high negative direct effects. Critical analysis of results obtained from character association and path analysis indicated that the spikelet fertility and thousand grain weight possessed both positive significant association and high positive direct effects. Hence, selection for these traits could bring improvement in yield and yield components.

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. Indian Rice

IMPROVING RICE BLAST RESISTANCE OF BPT 5204 THROUGH MOLECULAR MARKER-ASSISTED BACKCROSSING

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Rice blast, caused by the fungus Magnaporthe oryzae, is the most devastating biotic constraints that challenge the rice production in all the ecosystems and causes considerable economic loss worldwide (Imam et al., 2016). Improvement of disease resistance through conventional breeding is relatively slow, while MAB using major resistance genes is considered to be an efficient and technically feasible approach for rice blast resistance improvement to stabilize the production. Blast resistance gene Pi-9 exhibits broad spectrum resistance against different races of rice blast fungus and is hence considered more stable across geographic locations (Variar et. al 2009). Availability of closely linked markers has made rapid and precise selection of the targeted gene possible (Tanksley et al., 1989) through marker-assisted backcross breeding approach. In the current study, BPT 5204, a high yielding mega rice variety with exceptional good grain quality but otherwise susceptible to blast disease was selected as a recurrent parent for incorporation of major blast resistance genes Pi9 and Pib through marker assisted backcrossing (MAB) to improve its blast resistance.

METHODOLOGY

Two near isogenic lines, IRBL9-w and IRBLBb carrying blast resistance genes *Pi-9* and *Pib*, respectively in the background of LTH were used as donors for incorporation of blast resistance gene into susceptible mega variety BPT 5204 using marker assisted backcrossing. For targeted introgression of *Pi9* and *Pib* into BPT 5204, a simultaneous and stepwise marker assisted backcross breeding strategy was adopted. Two separate backcrosses were carried out wherein the blast resistance genes Pi9 from IRBL9-w as well as Pib from IRBLB-b, were introgressed into BPT5204, respectively. The F₁ plants derived were confirmed for their hybridity by using linked codominant markers, AP5930 (specific for Pi9) and RM208 (specific for Pib). In addition to this gene based STS marker 195-1R were used to identify the plants carrying Pi9 gene.DNA isolation, PCR amplification with the markers AP 5930 and RM208, selection of the heterozygous plants followed by hybridization of recurrent parent with the confirmed plants for the linked markers were done upto BC3F1. The BC3F1s were confirmed for the presence of Pi9 with AP 5930 as well as 195-1R and Pib with RM208, the confirmed plants were selfed. In BC3F2 single plants were confirmed for blast resistance with linked markers and also with phenotypic selection in an outdoor blast nursery and carried forward for agronomic selection.

RESULTS

We report here the introgression of blast resistance genes *Pi9* and *Pib* into the genetic background of good grain quality popular rice variety, BPT5204, for enhancing its blast resistance through marker-assisted backcross breeding strategy. Combining marker-assisted and phenotypic selection, 4 near isogenic lines (NILs) with homozygous *Pi9* and 6 NILs with homozygous *Pib* were selected. The evaluation of results under natural uniform blast nursery conditions showed that the selected BPT5204+*Pi9* NILs were highly resistant against leaf blast with SES score '0', while the recurrent parent BPT5204 had a score of '7'. However, the NILs with Pib gene showed



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BPT5204 NILs	Gene present	Days to 50% flw.	Plant height (cm)	# panicles/m2	Grain Yield (kg/ha)	Blast score (SES)
CRR741-13-1-22	Pi9	94	91	278	3494	0
CRR741-13-1-57	Pi9	93	87	266	2820	0
CRR741-22-2-16	Pi9	115	98	254	4940	0
CRR741-38-2-6	Pi9	115	96	228	5504	0
CRR742-2-2-3	Pib	95	96	234	4329	4
CRR742-2-2-6	Pib	112	98	252	4636	4
CRR742-2-2-8-2	Pib	113	100	233	4804	4
CRR742-2-2-16	Pib	103	107	254	4902	4
CRR742-2-2-32	Pib	112	110	239	4092	4
CRR742-2-2-38	Pib	104	100	218	3558	4
BPT 5204 (RP)		114	95	232	3892	7
LSD 5%		1.5	7.7	66.2	635.5	
CV(%)		0.9	4.8	15.8	8.9	

susceptible reaction at Hazaribag, meaning the gene is not effective at this location. Among the 4 NILs with Pi9, 2 NILs (CRR741-22-2-16 & CRR741-38-2-6) were found very similar to the recurrent parent in a number of agronomic traits and grain yield. The lines were selected for further evaluation in multilocation trials under All India Coordinated Rice Improvement Project (AICRIP) for their possible release as variety for the benefit of the farming community.

CONCLUSIONS

Marker assisted foreground selection was successfully combined with phenotypic selection to develop broad-spectrum blast resistant version of popular rice variety BPT5204 for stabilizing production in the blast endemic areas. This study also confirmed that STS marker 195-1R could be reliably used for MAB even without phenotypic selection for detection of *Pi9* gene. The developed NILs with Pi9 gene have performed better under natural uniform blast nursery and showed resistance. These NILs can be used as a blast resistant version to replace the popular variety or used in future breeding programme for incorporation of blast resistance.

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SALT-STRESS RESPONSIVENESS IN RICE GENOTYPES OF EASTERN PART OF ODISHA

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Rice (Oryza sativa L.) is the main staple food for the world's population. Major constraint that limits the production of rice cultivation is salinity in the eastern part of India. Salt stress conditions limit the rice plant growth and development at seedling stage. Such conditions reinforce the selection of high-yielding varieties, adoption and cultivation that further strengthens the seedling vigor. The high-yielding rice varieties like MTU-1001, Sarala, Govinda Bhog, Kudrat-4 and RNR were selected for the present study. For instance, MTU-1001 was developed and released in India based on its best performance to yield ranging from 40-45 quintals/ha and resistant for various biotic stresses (DRR technical Bulletin, 2011 and Munns, 2005). However, salinity-stress responsiveness associated with physiological and molecular responses is far from elucidation at tribal dominated part of the country.

The rice varieties used in the present study are cultivated amongst tribal farmers in eastern part of India. Despite high-yielding and multigenic properties, these rice varieties possess high potential for crop improvement and they are to be further explored for various other physiological and molecular traits. Thus, to explore high-yielding and salt-stress tolerant rice varieties and make this staple crop reach tribal society would be a significant milestone in scientific community. The present study with an objective of scientific explorations to reach the tribal community in the country would be an attempt to reach the demand of coastal tribal people through this study that includes physiological, biochemical and molecular traits responsiveness for salt tolerance.

METHOD:

Plant Material

Rice seeds of five different varieties of Eastern part of India (MTU-1001, Sarala, Govinda Bhog, Kudrat-4 and RNR) were used in the study.

Physiological trait analysis

1. Fresh/Dry weight and Relative Water Content

After recording the germination rate, the seedlings of all genotypes were continued to grow till 14th day under 0 mM, 150 mM salt stress conditions. Further, the values of fresh weight (FW), turgor weight (TW) and dry weight (DW) were used to calculate relative water content (RWC) as follows,

RWC = (Fresh Weight - Dry Weight)/(Turgid Weight - Dry Weight)*100

Biochemical parameters and analysis

2. Chlorophyll and Carotenoids estimation

The 14th day harvested seedlings (0.5 g) of all genotypes (control and salt-stressed) were homogenized in mortar and pestle separately by using 80 % acetone. The homogenized solution was centrifuged at 1500 - 2000 rpm for 8 - 10 min and the supernatant was collected. The total chlorophyll was measured at 663 nm and 645 nm and carotenoids at 520 nm. It was further calculated for content of



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chlorophyll a, chlorophyll b and total chlorophyll as follows, Chl a = 12.7*(the value of 663 nm) - 2.69*(the value of 645 nm)

Chl b = 22.9*(the value of 645 nm) - 4.68*(the value of 663 nm)

Total Chl = 20.2*(the value of 645 nm) + 8.02*(the value of 663 nm)

The chlorophyll stability index (CSI) was analyzed and is expressed as a percentage.

3. Leaf proline estimation

The control and NaCl treated 14th day old seedling samples of each variety were used to study the proline content. The samples were weighed uniformly to 0.5 g and homogenized in 1 ml of 3 % aqueous sulfo-salicylic acid. It was centrifuged at 8000 rpm for 12 min to remove the debris. A ratio of 1;1 (acid Ninhydrin and glacial acetic acid) was mixed with the supernatent and the mixture was heated to 100°C in water bath for 1 hr and then the tubes were immediately transferred to ice bath. An equal aliquot of toluene was added to the mixture and vortexed for 15 to 20 sec. Further, the chromophore phase was used to measure the absorbance at 520 nm. The readings obtained were analyzed with a basic standard curve of L-Proline

Molecular analysis

The varieties MTU1001 (salt-tolerant) and



Validation of MTU1001 and Sarala for *OsHKT1:5 and OsNHX1* for salt tolerance

Sarala (salt-sensitive) were selected for the gene validation. The seedlings grown for 14 days were used to extract RNA by Promega RNA extraction kit and quantified using nano-drop. The salt-specific gene primers *OsHKT*1;5 and *OsNHX*1 were used to run and validate varieties for the above mentioned genes in real-time polymerase chain reaction (rtPCR).

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RESULTS:

Physiological response of rice varieties

A. Rate of Germination under salt stress conditions : The germination percentage was measured in all the genotypes (MTU-1001, Sarala, Govinda Bhog, Kudrat-4 and RNR), under different concentrations of salt (0, 50 mM, 100 mM and 150 mM), to select one optimum level of stress conditions. The pattern of germination rate was consistent under 50 mM salt stress among MTU1001 (96 %) and 150 mM NaCl conditions exhibited 5 to 10 % difference reduction over 100 mM salt stress.

B. Shoot fresh weight (FW) and dry weight (DW) to relate with relative water content (RWC) : The shoot fresh weight among these genotypes against different salinity levels was significantly different. MTU1001 and RNR showed the highest SFW under control conditions and reduction over control (ROC) among these genotypes remained similar under high salt concentrations.

Biochemical estimations

A. Chlorophyll content variations under salt stress conditions

A minimum reduction over control (ROC) was significant in MTU1001 with 1.3 folds under 150 mM NaCl stress conditions. The traces of chlorophyll were slightly significant among Sarala and RNR with ROC of 6.6 and 8.3 folds respectively under 150 mM stress conditions.

B. Proline accumulations and its variations



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The proline content increased with increasing salt concentrations in all the genotypes except for Sarala and MTU1001. These varieties exhibited a trend of increased proline at 150 mM NaCl over control and decreased trend at 250 mM salt stress conditions. The varieties including Govinda Bhog and Kudrat-4 showed a noticeable increase in proline content with increasing salt concentrations.

Validation by rtPCR:

The rtPCR-based validation showed up- and down- regulation between the two-contrasting rice genotypes MTU1001 (salt-tolerant) and Sarala (saltsensitive) using the salt-specific homologous primers *OsNHX*1 and *OsHKT*1;5 with two distinct variations. **CONCLUSION:**

The present study aims towards understanding physiological, biochemical and molecular traits in the high-yielding varieties cultivated by tribal community at germination and seedling stage for low-to-moderate salinity stress tolerance. Although, MTU1001 performed very well with 96 % germination rate at 150 mM salt stress conditions, higher levels of salinity exhibited detrimental effects on other varieties. Hence, the salt concentration 150 mM was optimally selected to screen the varieties for biochemical and physiological traits. The high-yielding varieties MTU1001, RNR and Sarala exhibited reduction over control (ROC) with relative water content (RWC) for 150 mM salt concentrations. The level of proline, increased with increasing concentrations of NaCl among most of the varieties and significantly high content was found in MTU1001. The chlorophyll content was remained consistently same in Sarala under 150 mM salt concentrations. Interestingly, MTU1001 emerged as the most salt-tolerant landrace for physiological and biochemical traits. Further, expression analysis of saltspecific genes OsHKT1;5 resulted in up-regulation of salt-stress responsiveness in MTU1001 and OsNHX1 showed significant down-regulation in Sarala. Further, the study revealed a major difference at gene expression level among high-yielding varieties and made a pathway for exploration of transcriptional gene regulation for saltstress tolerance.

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GENOME-WIDE ASSOCIATION STUDY UNRAVELS NOVEL MARKER-TRAIT ASSOCIATIONS FOR REPRODUCTIVE STAGE HEAT STRESS TOLERANCE IN RICE

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Rice is an important staple crop in India occupying an area of 43.79 m ha with 116.42 m tons during 2018-19. It is highly sensitive to heat stress particularly at anthesis stage followed by booting. Developing heat stress tolerant rice varieties can help manage the predicted temperature spikes in near future. Rice is endowed with enormous genetic variability, large scale screening of which will help in identifying useful donors as well as mapping the genomic regions governing high temperature stress tolerance is an important prerequisite. Genome-wide association study (GWAS) is one of the popular mapping methods which exploits historic recombination and linkage disequilibrium analysis between the marker and target trait to identify statistically robust marker trait associations (MTAs). In the present study, a set of 192 rice genotypes were phenotyped for reproductive stage heat stress tolerance (RSHT) based on spikelet fertility and grain yield per plant, and genotyped with 50K SNP array. For GWAS, three models, one single locus model - mixed linear model (MLM) and two multi-locus models, FarmCPU and BLINK were used.

METHODOLOGY

The present study consisted of a set of 192 diverse rice germplasm assembled from a collection maintained at the Division of Genetics, ICAR-Indian Agricultural Research Institute (ICAR-IARI), New Delhi. Phenotyping was conducted at Rice Genetics and Breeding Research Centre (RGBRC)-IARI, Aduthurai, Tamil Nadu (11Ú 00'N; 79Ú 28'E, 19.5 m) during off-season, 2018-19. Two staggered sowing with a gap of 30 days were done so as to adjust the flowering time of the germplasm to the targeted seasonal temperatures. First sowing done in the second fortnight of December was treated as control where the peak anthesis of the genotypes coincided with optimum (maximum) temperatures, 33-35°C. Second staggering was taken up in second fortnight of January, which was considered as heat stress treatment where peak anthesis of genotypes overlapped with higher ambient temperatures, *i.e.*, 39-41°C. Observations were recorded on grain yield plant⁻¹ (g) and spikelet fertility (%) under heat stress and stress tolerance index (STI) derived from them (STIGY and STISF, respectively) was utilized for association analysis. Genotyping was done using 50k Affymetrix SNP GeneChip (Singh et al. 2015). Briefly, the chip houses 50,051 SNPs selected from 18,980 genes covering 12 rice chromosomes with an interval of 1 kb between two adjacent SNPs. After filtering for SNP with minor alleles (>5%) and for missing values (>20% missing reads), final number of markers utilized for GWAS analysis reduced to 32,712 SNPs. Principal component analysis (PCA), inbuilt in R platform for association analysis, Genome Association and Prediction Integrated Tool (GAPIT), was conducted to check the sub-population structure (Lipka et al. 2012). Linkage disequilibrium was estimated based on squared allele frequency

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correlations (r^2) with significant p values (<0.05) for each pair of loci. The association analysis was done in GAPIT by executing different models – MLM, FarmCPU and BLINK models. The genomic locations of significant MTAs were compared with previously reported QTLs for RSHT.

RESULTS

The two staggered sowing windows showed a clear difference in the diurnal mean temperatures during peak anthesis stage of the rice germplasm. Significant reduction was observed in grain yield and spikelet fertility observed for late sown set of rice germplasm which experienced heat stress at reproductive stage. The mean reduction was higher for grain yield (26%) relative to spikelet fertility (19%) in the late sown rice germplasm set exposed to heat stress. Wide variation was observed for grain yield and spikelet fertility under both control and heat stress in the germplasm. Both grain yield and spikelet fertility showed quantitative inheritance. PCA analysis based on SNP data showed three sub-populations in the panel of which one subpopulation captured majority of cultivated varieties and advanced breeding lines, while the remaining shared land races. Later, GWAS was carried out using three models as mentioned above. For grain yield plant¹, 10 Marker Trait Associations (MTAs) were identified for grain yield plant⁻¹, seven through FarmCPU and three through BLINK. Considering Bonferroni cuff-off (6 log10 P>7, for á=0.05), one highly significant MTAs (qHTGY10.1) was found on chromosome 10 by FarmCPU, while a significant MTA, qHTGY8.1 was identified on chromosome 8 using BLINK. A total of 22 MTAs was identified for spikelet fertility through three GWAS models, 7 through MLM, 7 through FarmCPU and 8 by BLINK. Among these, two MTAs, qHTSF5.1 at 20.54 Mb on chromosome 5 and gHTST6.1 at 28.02 Mb on chromosome 6, were shared by all the three models. Considering Bonferroni cuff-off, four MTAs each for FarmCPU and BLINK were high significant were found highly significant. In

general, the number of MTAs identified using stress tolerance index was lesser compared to the respective trait values under heat stress. Moreover, most of the MTAs identified through STI were same as those found for the original traits. Only one MTA, *qSTIGY8.1* was identified by both FarmCPU and BLINK models for STIGY. For STISF, two under FarmCPU, *qSTISF1.1* and *qSTISF2.1* were different from those identified for spikelet fertility, while one MTA, *qSTISF2.1*, under BLINK was found different. Two MTAs for grain yield per plant, five MTAs for spikelet fertility and two MTAs for STISF were found to co-localize with previously reported QTLs. Thus, majority of the MTAs identified in the present study were novel.

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CONCLUSION

GWAS was successfully employed to identify novel genomic regions associated with RSHT in rice. FarmCPU and BLINK were found equally efficient and better than the routinely used MLM in resolving MTAs. Majority of the genomic regions identified in the present study are novel and promising genotypes identified in the present study can be valuable donors for incorporating RSHT rice through molecular marker assisted breeding.

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MOLECULAR CHARACTERIZATION FOR ALLELIC STATUS OF 55 LOCUS IN RICE GERMPLASM

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Rice is a major food crop grown and consumed all over the world. Nearly 87% of rice production comes from Asia and India has major share in the total output of production and revenue. Rice occupies an area of 44 mha in India while hybrid rice occupies merely 3.1 mha. The magnitude of heterosis exploited from different crosses can be summarized as: indica x japonica > indica x javanica> japonica x javanica> indica x *indica* > *japonica* x *japonica*. The hybrid productivity is less than maximum exploitable as India exploits mainly indica x indica heterosis. Hence the productivity of rice could be increased by utilizing the high heterosis from indica x japonica crosses. The major problem in inter-subspecific cross between indica and japonica is hybrid semi sterility. The sterility is governed by nearly 50 genes among them S5 locus is major locus and well characterized governing embryo sac sterility in inter subspecific crosses. There are some varieties which give fertile hybrids when crossed with either indica or japonica called as wide compatible varieties (WCVs). Indica possess S5-i, japonica has S5-*j* and WCV has neutral allele S5-*n* at S5 locus. Only two varieties Nagina 22 and Dular are being used as promising WCVs over the world. Therefore, it is necessary to characterize the rice germplasm through molecular screening using PCR based functional markers of S5 locus to identify wide compatible varieties carrying neutral allele S5-n.

METHODOLOGY

The present study conducted at Division of Genetics, ICAR-Indian Agricultural Research Institute

(ICAR-IARI), New Delhi. It includes a total of 967 rice genotypes which includes 297 IRG lines, 180 tropical japonica lines and 490 germplasm lines for molecular screening using functional markers. The plants were grown in propots. After 7 days each entry was cut and DNA was extracted using CTAB method. The DNA extracted was subjected to PCR amplification by using functional markers for indica (S5-i), japonica (S5-j) and neutral (S5-n) alleles. The markers being used are namely: S5-InDel for neutral allele, S5-ELSP (F), S5-IASP (R) for indica allele and S5-JASP (F), S5-ELSP (R) for *japonica* allele. Annealing temperature for indica specific primers was kept at 59.1 °C, japonica specific primers at 57.4 °C and neutral specific primers was kept at 61.2 °C. Indica specific markers amplified a band size of 527 bp in indica lines and no amplification in japonica whereas japonica specific markers amplified a band size of 325 bp in japonica and no amplification in indica and genotypes which carried neutral alleles amplified band size of 417 bp using neutral specific allele.

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RESULTS

After molecular screening it was found that 166 lines having neutral allele (*S5-n*), whereas 220 lines carried *japonica* allele (*S5-j*) and 581 lines carried *indica* allele (*S5-i*). It is necessary to evaluate the phenotypic performance of WCVs and F_{1s} derived from crosses of WCV with *indica/japonica* in order to identify best performing WCVs.

CONCLUSION



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The PCR based marker system could be successfully utilised for characterization of the rice germplasm for identification of *indica*, *japonica* and wide compatible varieties. These WCVs identified could be well utilized to obtain fertile hybrids in crosses between *indica/japonica* and combine and transfer beneficial genes between the two ecotypes of rice.

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GENETIC MAPPING FOR HIGH GRAIN NUMBER IN *TROPICAL JAPONICA* DERIVED PUSA NPT34 USING BULKED SEGREGANT ANALYSIS

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Rice is widely grown and consumed food crop in the world and also in India. Rice occupies an area of 44 mha in India. But the per hectare productivity is less to meet the food requirement of the Indian population. Therefore, it is necessary to increase the productivity of the rice. The grain yield of rice is mainly contributed by grain number per panicle, total number of panicles per plant and 1000 grain weight. Grain number per panicle is major contributor towards increase in rice productivity and it is a quantitative trait shows continuous variation. Mapping of gene/QTL governing the high grain number and its utilization in breeding program is an important step to enhance the yield potential of rice.

METHODOLOGY

The present study was carried out with an objective of mapping gene/QTL for grain number using bulked segregant analysis (BSA). New Plant Type lines were developed by making crosses between indica and japonica lines. The tropical japonica line was crossed with Pusa 44 and advanced to F_{e} and based on phenotypic performance for grain number, Pusa NPT34 was selected to attempt cross with the PR126, a low grain parent. The NPT34 parent was high grain number parent with an average of 393 grains per panicle where as PR126 is low grain parent with an average grain number of 159 per panicle. The cross was attempted in ICAR-IARI, New Delhi during kharif-2017 and developed sufficient F_1 seeds. The F_1 seeds were sown in RBGRC, Aduthurai, Tanil Nadu during rabi-2017-18. The F₂ population was grown subsequently at ICAR-IARI during *kharif* 2018 along with parents for further phenotyping and QTL mapping using BSA. Parental polymorphism survey was carried out using a total of 663 SSR markers which includes RM, HvSSR, nksssr. The identified polymorphic markers were used for bulked segregant analysis (BSA) to identify putatively liked marker(s). The bulking was carried out by pooling DNA of 10 low grain F_2 plants and 10 high grain F_2 plants. The identified putatively liked marker was used to genotype all the plants of F_2 population to know the marker trait association.

RESULTS

The phenotyping was carried out by collecting 3 panicles per plant from F₂ population. 10 plants having low grain number and 10 plants having high grain number were selected to make the bulk. The samples DNA was quantified using nanodrop before bulking and equal amount of DNA was taken from all the samples to make the bulk. Based on parental polymorphism survey, 58 markers were identified as polymorphic between Pusa NPT34 and PR126 and these polymorphic markers were further used for BSA to identify putatively linked marker to the target trait. The genotyping of bulks along with parents using polymorphic markers showed that RM424 is polymorphic between parents as well as bulks. RM424 marker was further used to genotype all plants of F₂ population. RM424 marker showed significant association with the trait (p = 0.008) and a QTL for

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high grain number was mapped on chromosome-2 at a mapping distance of 27.3cM. The phenotypic effect associated with the QTL was observed to be 22.58.

CONCLUSION

In the present study RM424 was identified as linked marker to the high grain number using BSA. As the marker present at a genetic distance of 27.3 cM away from the QTL, it is necessary to identify marker present close to the *QTL*. Therefore, these F_2 plants can be advanced to RILs to identify the tightly linked marker to the trait and its further use in breeding program.

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CHLOROPHYLL FLUORESCENCE AS A TOOL FOR IDENTIFICATION OF NITROGEN USE EFFICIENCY IN RICE

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Nitrogen (N) is an essential macronutrient for rice production; however, excessive nitrogen fertilizer application increase crop production cost, environmental pollution and have negative impact on the grain quality (Cui et al. 2020). According to previous studies the recovery rate of nitrogen fertiliser is low (Garnett et al. 2009) and the remaining nitrogen may mix with groundwater as nitrate or volatilise to the atmosphere through microbial denitrification (Ju et al. 2009). Therefore, there is need to identify varieties that have higher nitrogen use efficiency and the can produced better grain yield with low nitrogen fertilizer input.

METHODOLOGY

One hundred eighty six lines derived from BVD109 x IR 20 cross were evaluated for nitrogen use efficiency. The experimental lines were grown under three different nitrogen level: 0 kg N/ha (low nitrogen), 60 kg N/ha (optimal nitrogen) and 120 kg N/ ha (high nitrogen) with two replications of each treatments in randomized block design. Based on the biomass and grain yield under three treatment, two lines with contrasting nitrogen use efficiency capacity was identified. Further, the chlorophyll fluorescence kinetics of the two contrasting lines was analysed using Handy PEA. For estimation of nitrogen use efficiency of the lines, total nitrogen content of different plant parts was estimated using Total Carbon Total Nitrogen auto Analyzer, SKALAR.

RESULTS

Field evaluation of the NILs from the BVD109 x IR 20 cross under three different nitrogen levels showed significant variability in grain yield and biomass production. Among all the lines tested, C822-102 had highest grain yield of 2.65 t/ha under '0' kg N/ha with

6.28 t/ha of total dry matter. Under 120 Kg N/ha, C822-102 had a grain yield of 5.39 t/ha and produced 14 t/ha of total dry matter. However, C822-143 produced 0.26 t/ha of grain yield under '0' kg N/ha and 1.49 t/ha of grain yield under 120 Kg N/ha. Agronomic nitrogen use efficiency of C822-102 was 19.27 whereas that of C822-143 was 8.97. Analysis of fluorescence transient curve of the two lines under different nitrogen treatment showed differential sensitivity towards nitrogen deficiency. C822-143 showed higher sensitivity to nitrogen deficiency than C822-102. Under 120 Kg N/ha no change in fluorescence transient curve was detected between C822-102 and C822-143. However, O-J-I-P polyphasic transient curve of C822-143 under 0 kg N/ha was more flattened compared C822-102 under 0 Kg N/ha and pooled data of 60 Kg N/ha. The response of the two tested lines under three different nitrogen doses was clearly distinguished on the basis of O-J-I-P polyphasic transient curve.

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ASSOCIATION AND PATH ANALYSIS STUDIES IN RIL POPULATION OF RICE FOR YIELD ATTRIBUTING AND NUTRITIONAL TRAITS

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Rice is the primary source of food for billions of people throughout the world, yet it contains insufficient levels of the key micronutrients iron, zinc and vitamin A to meet the daily dietary requirements. The experiment was conducted to study the character association and path analysis for yield, yield attributing and zinc concentration in 190 F₂ RILs derived from MTU1010 and BR2655 during Kharif 2016. The study revealed that grain yield per plant had significant positive association with panicle length (0.206^*) , number of productive tillers per plant (0.308*), number of filled grains per panicle (0.215*) and 1000-grain weight (0.307^{**}) . Path analysis demonstrated that 1000-grain weight (0.367), plant height (0.129), number of filled grains per panicle (0.050), days to 50 per cent flowering (0.014) and number of productive tillers per plant (0.016) exerted positive direct effect on grain yield indicating that selection for these characters was likely to bring about an overall improvement in grain yield per plant directly and the selected plants can be further used in future hybridization programme.

OBJECTIVE:

To identify the quantitative trait loci (QTLs) associated with grain zinc in 190 RILs derived from MTU 1010 & BR 2655.

MATERIALS AND METHODS:

The mapping population was derived from a cross of MTU1010 and BR2655 at ICAR-Indian Institute of Rice Research Farm, Rajendranagar, Hyderabad. MTU1010 being low in grain zinc (Zn =14.4ppm) was crossed with BR2655 having high grain zinc (Zn=23.7ppm). Twenty seven days old seedlings of each accession were transplanted in a Randomized Block Design with three replications during Kharif 2016 Rabi 2016-17. Data on seven metric parameters viz., days to 50% flowering, plant height, panicle length, number of productive tillers per plant, number of filled grains per panicle, 1000-grain weight and grain yield per plant were recorded on five randomly selected plants in each plot, while the data on days to 50% flowering were noted on plot basis. Linkage maps were constructed using ICI mapping version 4.1 (Wang et al., 2016) following Kosambi Function (Kosambi, 1944) and each of the scored traits along with phenotypic means was subjected to QTL mapping.

RESULTS:

The mean, range, variability, heritability and genetic advance for grain zinc concentrations in RILs and parents during both seasons. Grain zinc ranged from 12.60 ppm (J51) to 38.00 ppm (J146) with average of 24.16 ppm during *Kharif* 2016. While in *Rabi* 2016-17 mean value of 23.91 ppm, the values ranged from 13.06 ppm (J49) to 37.13 ppm (J146). A high GCV (20.10 & 20.19%) and PCV (20.43 &

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Fig 1. Selective genotyping of MTU1010, BR2655 and RILs with parental polymorphic SSR markers P1-MTU1010, P2-BR2655, 1-J1, 2-J2, 3-J3, 4-J4, 5-J6, 6-J6, 7-J7, 8-J8, 9-J9, 10-J10 (1-10 are RILs)

20.26%) were observed for this trait during *Kharif* 2016 and *Rabi* 2016-17 respectively, suggesting high range of genetic variability. Heritability estimate for this trait was very high (99.8 & 99.30%) with high genetic advance (37.90 & 39.39%), indicating that this trait is controlled largely by additive type of gene action.

Parental polymorphism survey between MTU1010 and BR2655 was studied using 948 Rice Microsatellite (RM) markers chosen based on their distribution throughout genome. Among 948 RM markers, 119 markers (12.55 %) were polymorphic between the parents distributed across the 12 chromosomes. A total of 60 out of 119 markers found polymorphic between parents and RIL population as shown in fig 1. These 60 markers distributed across 12 chromosomes of rice, five on each chromosome were utilized for genotyping of 190 RIL populations.

The linkage map covered 1874.09 cM distance employing Kosambi mapping function, resulting in an average marker interval of 331.23 cM. Among the 60 markers used, 41 markers showed segregation distortion to varied degrees on all the chromosomes. The segregation distortion of the markers was mostly skewed towards the parent BR2655.

A total of three QTLs during *Kharif* 2016 on chromosome 5 and 2, six QTLs during *Rabi* 2016-17 on chromosome 1, 2, 4, 9, 10 and 12 were detected. . In both seasons seven QTLs *viz.*, *qPH-5.1*, *qNPT-5.1*, *qDFF-1.1*, *qDFF-9.1*, *qGYP-4.1*, *qGYP-10.1 and qGYP-12.1* were identified for yield and related traits which accounts for 1.34-7.54 % phenotypic variance. One consistent QTL for grain zinc concentration (*qZn-2.1*) was mapped on chromosome 2, which accounts for phenotypic variance of 7.74% and 9.59% during *Kharif* 2016 and *Rabi* 2016-17 respectively. QTL for *qZn-2.1* wasflanked by RM13347-RM262 SSR loci at a distance of 26cM in both seasons, indicating that this genomic region is involved in controlling the grain zinc concentration.

CONCLUSION:

The identified QTL qZn-2.1 for grain zinc concentration was detected consistently on chromosome 2 was flanked by RM13347-RM262 SSR loci in both seasons indicating that this genomic region involved in controlling the grain zinc concentration. The identified QTLs should be validated



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in alternate population for future use in Marker Assisted Selection, fine mapping of identified QTL can be carried out, RILs with high zinc concentration and grain yield can be used as donors in crossing programmes and can be tested in multilocation trials.

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EVALUATION OF LUTEIN CONTENT AND ASSESSMENT OF ANTIOXIDANT POTENTIAL OF Á CAROTENOID IN MEDICINAL LANDRACE OF RICE 'KAVUNI'

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Antioxidants are the bioactive compounds which are vital for defending the cells/ body from the free radicals damage. The unpaired electrons in free radicals are formed due to oxidation as a process of normal metabolic activities in every day exposure to the environment. Reactive oxygen species (ROS) or free radicals when produced in excess amount overwhelming the scavenging ability of endogenous antioxidants like enzymes superoxide dismutase (SOD), glutathione peroxidase (GPX), and catalase [1], the ex-cess free radicals seek stability through electron pairing with biological macromolecules such as proteins, lipids and DNA in healthy human cells resulting the induction of lipid per-oxidation and mutation in DNA which leads to many human sufferings like cardiovascular and pulmonary diseases, some types of cancer, cataracts, immune/autoimmune diseases, inflammation, arthritis, atherosclerosis and brain dysfunction (Parkinson's, Alzhelmer's, Huntington's diseases) [2]. Due to the adverse side effects of synthetic antioxidants leading to car-cinogenicity their use in many countries has been tightly supervised. Therefore search for effective and natural antioxidants has become crucial and investigation of chemically active compounds of plants is of urgent need. Lutein, a dihydroxy xanthophyll, is the predominant plant carotenoid distinguished from other carotenoid compounds based on the chemical composition of hydroxyl group attachments to their structures and presence of â-ionone ring and a å-ionone ring (Fig. 1). It cannot be synthesized *denovo* and must be acquired from dietary food rich in lutein like green leafy vegetables, fruits and eggs and it is the major component of the macular pigment of the retina. The macula lutea or "yellow spot" in the retina is responsible for the central vision and visual acuity.

Lutein is one of the major therapeutic compounds among 600 naturally occurring carotenoids and is the only carotenoids found in both the macula







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and lens of the human eye, and acts as blocker of blue light damage, quencher of oxygen free radicals and prevent age related macular degeneration and cataracts and hence these macular pigments are considered as own set of 'Polarized Internal Sunglasses'. In addition to playing pivotal roles in ocular health, lutein and zeaxanthin (isomer of lutein) are important nutrients for the prevention of cardiovascular disease, stroke, and lung cancer. They may also be protective in skin conditions attributed to excessive ultraviolet (UV) light exposure. Coloured fruits and vegetables have higher antioxidants like lutein, than the cereal grains, Optimum quan-tity of coloured fruits and vegetables can't be in the diet of common man. So, an alternate staple food should quench the needs.

Rice is a staple food for more than three billion people in the world. India has been endowed with more than two lakhs rice varieties a rich biodiversity that no other country on earth. The ayurvedic treatise records show the existence of several medicinal rice varieties in India [2]. Kavuni, a traditional rice variety of Tamil Nadu is known for its nutritive properties and it is considered to be the best Antioxidant, Anti-arthritic and Anti-diabetic among other rice varieties (Fig. 2). Kavuni grains are brown-black in colour which were reported earlier to have reduced levels of total soluble sugar, low fat content, increased protein content, high levels of phenolic acid, flavonoids, carotenoids and minerals like iron, manganese, zinc, copper, sodium, potassium, magnesium. Kavuni is known as a long duration, poor





tillering and photosensitive traditional rice variety and owing to these traits it is not being cultivated widely.

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In our study, crosses were made with major high yield yielding white rice ASD 16 and Swarna Sub 1 to bring out threpeitic rice with good agronomical features. The present investigation reports the lutein content and the antioxidant potential of Kavuni in comparison with ASD 16 and Swarna Sub 1 and its derivatives. The objective of the present investigation was to characterize the lutein content and antioxidant potential of Kavuni and released mega varieties of rice (ASD 16, Swarna Sub1) and its derivatives obtained from crosses ASD 16 and Kavuni; Swarna Sub1 and Kavuni.

METHODOLOGY:

Lutein content was estimated using standard protocol of HPLC (High performance liquid chromatography) and antioxidant potential was measured using in vitro DPPH (2,2-diphenyl-1picrylhydrazyl) assay

RESULTS:

It was found that lutein was much higher in Kavuni (225 µg/100g) compared with white rice varieties (ASD 16-15 µg/100g and Swarna Sub1-21 $\mu g/100g$) and the DPPH (2,2-diphenyl-1picrylhydrazyl) scavenging ability were in the order (Kavuni >>ASD16, Swarna Sub1. Pigmented grain genotypes having higher lutein content had higher percentage of free radical scavenging activity of DPPH and lower IC₅₀ values compared to non pigmented genotypes. Genotypes having higher lutein content had higher percentage of free radical scavenging activity of DPPH and lower IC₅₀ values and exhibiting higher antioxidant potential. The IC_{50} values which indicates neutralizing 50% of free radicals of DPPH by the sample concentration and attaining IC550 values at lower concentration indicates higher antioxidant activity.



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CONCLUSION:

The phytochemical and in vitro antioxidant analysis confirms the methanolic extracts of Kavuni kernels as a potent antioxidant. Kavuni had broad spectrum in treating the health alignments due to rich source of bioactive molecules like lutein and it is a highly valuable source of natural antioxidants and free radical scavengers. Kavuni is a good choice for the plant breeders to develop new rice cultivars with high nutritive value along with a good yield which can lead to low cost production of natural antioxidants and can reach the bowl of common man. It is conceivable that the medicinal landraces of rice could be exploited as one of the potential sources for plant - based pharmaceutical products.

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. Indian Rice

HABITAT SHIFT RELATED ALLELIC DIVERSITY IN ANNUAL WILD RICE, ORYZA NIVARA FOR LOCI LINKED TO TOLERANCE FOR DIFFERENT ABIOTIC STRESSES

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Abiotic stresses are one of the major factors that limit crop growth and yield in large areas of the world. The major abiotic stresses worldwide causing risks to food security are drought, submergence and salinity. To minimize yield losses due to abiotic stresses, one of the cost effective and reliable methods of management is enhancement of host tolerance. Incorporation of trait enhancing alleles in the crop improvement programs is dependent on continuous infusion of land races, wild relatives and the use of modern breeding techniques (Tao and Ge, 2013). In this context, knowing the allelic diversity in Oryza nivara, the progenitor, photoperiod insensitive, annual wild species which is believed to have evolved from perennial O. rufipogon because of habitat shift (Sang and Ge, 2007) will be of great use. Ninety two O. nivara accessions, collected over a large geographical area of India, were characterized for the genes/QTLs that are known to be associated with tolerance to drought, submergence and salinity stresses in rice using associated/tagged molecular markers.

OBJECTIVES

To characterize a set of *O. nivara* accessions for the genes/QTLs that are known to be associated with tolerance to different abiotic stresses in rice using associated/tagged molecular markers.

MATERIALS AND METHODS

Seeds of 92 wild rice *O. nivara* accessions along with their passport data were obtained from rice gene bank of ICAR-National Rice Research Institute (NRRI), Cuttack. The seeds of the accessions along with known controls [N 22 (+ve) and IR 20 (-ve) for drought; FR 13A (with Sub1A region) (+ve) and IR42 (-ve) for submergence; FL 478 (with Saltol region incorporated from Pokkali, the well-known donor for saline tolerance) (+ve) and IR 29 (-ve) for salinity] were grown in pots till maturity and DNA was extracted from young leaves using a standard protocol. For allele mining of drought, submergence and salinity, SSR markers specific to their respective QTLs (5 for each trait) were used. PCR was performed in 10 µl reaction volumes and the master mix was prepared as per standard laboratory procedures. The PCR amplification products were visualized in 3% agarose gel stained with ethidium bromide using a Typhoon FLA 7000 fluorescent image analyzer. The sizes of the amplified fragments were estimated visually using 100 bp DNA ladder as the size standard. Markers were scored for the presence or absence of the corresponding amplicon among the genotypes. Genetic diversity parameters for each of the tested marker and the unbiased pair wise genetic distance among the accessions were calculated using POPGENE v 1.32. The neighbour-joining dendrograms based on unbiased pair wise genetic distances using drought, submergence and salinity markers were constructed separately using MEGA 6. The haplotype diversity pattern of the genotypes was constructed from the data generated from the QTL (drought, submergence and salinity) specific markers taking the positive controls as the reference.

RESULTS

The loci amplified with RM489 (root volume and growth under drought condition) recorded 5 alleles



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followed by RM324 (grain weight and number of spikelet) with 4 alleles and RM160 (root depth under drought) with 3 alleles. However, with markers RM240 and RM166, both related to yield and yield components under drought stress, 2 alleles were only amplified each case. The genetic diversity value ranged from 0.147 (RM166) to 0.712 (RM489) with an average of 0.463. The PIC values for the markers ranged from 0.979 (RM489) to 0.568 (RM166) with an average of 0.818. The neighbour-joining dendrogram constructed based on pairwise Nei's genetic distance grouped the accessions into 2 major clusters i.e. I and II. Two of the accessions, AC100431-1 and AC100316, though having allelic variation, showed close relationship with N 22 (+ve control). The haplotype structure constructed on the basis of allelic similarity of any given loci with N 22 detected 17 (H1 to H17) different haplotypes, where none of the accessions were found to be having same allele of N 22 for all the loci. From H2 to H16,

accessions were grouped according to their allelic similarity of N 22 for one or more tested loci in different combinations.

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The marker GNS2 present in *Sub1A1* region, detected maximum genetic diversity (He) of 0.705 followed by IYT3 (He = 0.432). Similarly the highest PIC value of 0.994 was detected for the marker SUB1BC2 followed by 0.993 for GNS2. The neighbour-joining dendrogram constructed based on pairwise Nei's genetic distance grouped the accessions into 2 major clusters. One of the accession i.e. AC 100010 showed close relationship with FR13A (+ve control). The haplotype constructed based on the allelic similarity of the tested loci with that of FR13A (+ve control), discriminated all the accessions into 8 different (H1 to H8) haplotype groups. A highest of 48 accessions was in H6 sharing same allele of *SUB1A203* and *IYT3* with FR 13A.



Figure 1. Genetic relationship and haplotypes of *O. nivara* accessions based on (a) drought linked SSRs, (b) *SUB1* linked SSRs and (c) *SALTOL* linked SSRs.



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A total of 5 Saltol QTL linked SSR markers (2 for SALT and 3 for SKC region) were used to study the allelic variation present in the O. nivara accessions for Saltol. The genetic diversity value detected for the tested loci was highest for RM3412 (He = 0.769) followed by RM10745 (He =0.613). The marker RM10745 was detected with a highest PIC value (0.864), whereas RM10864 was the lowest (0.684). The neighbour-joining dendrogram constructed based on pairwise Nei's genetic distance grouped the accessions into 2 major clusters, where 33 genotypes were grouped in one cluster and 61 were in another. Wide variation was detected among the accessions and only two of the accessions (AC 100293 and AC 100453) showed close relationship with FL 478 (+ve control). A total of 21 different haplotype groups and none of the accessions shared all the similar allele (for the tested loci) of FL 478. But, 3 accessions (AC 100154, AC 100328 and AC 100304) amplified similar alleles of FL 478 for 4 of the 5 tested loci (except AP 3206) and were grouped in H2.

Further, unique accessions which showed alternate amplicon/allele size than that of the positive/ negative control for drought, submergence and salinity were identified for any of the given loci. For drought, 20 such accessions were identified for each of the markers RM160 and RM 324, followed by 13 accessions for RM489. Similarly, for submergence trait related marker, 9 accessions were identified which amplified different alleles other than the positive control FR 13A or the negative control IR 42 with GNS 2. However, only one accession, AC 100313 amplified a different allele for the loci *SUB1BC2*. Highest allelic variation was detected for salinity trait related markers, where 49 accessions were detected to be having allelic variation with RM3412 followed by 31 accessions for RM10745 and 9 accessions for RM10864. Only 3 accessions, AC 100450, AC 100475, AC 100016, were observed as allelic variants for the loci AP3206.

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CONCLUSION

Data comparisons with the haplotypes observed in the accessions of wild rices from the same region, suggest an untapped reservoir of new alleles in the wild form which can be exploited profitably for the development of agronomically superior cultivars to mitigate the problem of different stresses in rice.

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INSILICO ANALYSIS AND HOMOLOGY MODELLING OF OsMYB6 GENE IN RICE (ORYZA SATIVA L.) Satya Sandeep Tata^{*1} and Sudhakar Godi²

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Many plants are subjected to various stresses, broadly classified as biotic and abiotic stresses. Out of many abiotic stresses, Drought can be considered as a major one. Rice (Oryza sativa L.), the crop which is cultivated widely all over the world is a staple food crop for mankind. It undergoes drought stress and a major loss in the productivity has been noted every year. Physiologically, MYB transcription factors were reported to have a key role in plant growth as well as abiotic stress responses. By considering the number of repeats in their MYB domain, the MYB family members are divided into four major groups, R2R3-MYB, MYB1-R, 4R-MYB, and R1R2R3-MYB in Arabidopsis. According to the previous literature, it was reported that OsMYB6gene, named by (Tang et al., 2019), is strongly induced by drought stress(Zhou et al., 2016) and the over expression of the same would leads to the enhanced drought tolerance when compared with the wild varieties. However, the knowledge of these gene interactions was still unclear in some aspects. In the present study we performed an insilico analysis of OsMYB6 gene, which could be a potent candidate gene for rice drought tolerance.

METHODOLOGY:

In this study we have conducted different analyses using various bioinformatics tools. The gene sequence have been drawn from NCBI and also as well as RAPDB online databases to retrieve DNA sequences of OsMYB6 gene and its transcript variants were also been studied. EXPASY was used to study different protein parameters and characteristics. A network map have been constructed to evaluate the interaction of other similar genes with OsMYB6, using STRING database. As we draw the trusted sequences of RNA and protein, we have executed homology modelling to build a protein model, by taking the "Crystal structure of the MYB domain of the RAD transcription factor from *Antirrhinum majus* (Snapdragon)" as a template, as it shows 49.21% similarity.

RESULTS:

The DNA sequences were retrieved and then they were virtually translated to get an amino acid sequence. This sequence, when used for the evaluation of protein it has given the molecular weight as 46300.22 Da and also a theoretical pI as 8.60. As the further analysis was done using STRING, it reveals the interaction of OsMYB6 with its predicted functional partners namely NAC077, P0485A7.2, HOX28, OS06T0105800-02 ,OS07T0496300-01,OsJ_20154, OS04T0543500-00, OsJ_12119, BZIP02. Using SWISS-MODEL a predicted protein 3D structure was created, which showed a local quality estimate upto 0.8 and also no similar ligand found. Ramachandran plot analysis was done and it has shown 95.08% favoured regions with a clash score and mol probity scores of 1.04 and 1.60 respectively.

CONCLUSION:

After various studies using online and offline bioinformatics tools, we conclude that the predicted protein structure of OsMYB6 gene could be used as a basis of the crystallographic analysis and it would extend



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a scope for further analysi. The OsMYB6 gene could act as a potential candidate gene for drought stress responses.

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Indian Rice

STUDIES ON GRAIN YIELD, PHYSICO-CHEMICAL AND COOKING CHARACTERS OF MID EARLY RICE GENOTYPES

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Rice is the most important cereal crop that it has been referred as "Global Grain" because of its use as prime staple food in about 100 countries of the world. Yield and quality are the most important aspects of rice breeding. Preference for rice quality varies among cultures and regions quality according to the preferences of local consumers. Efforts have been made to find out high yield, mid early rice genotypes having better quality characters during *Kharif* 2010 to 2019 at Main Rice Research Station, Nawagam and paddy Research station, Dabhoi of Anand Agricultural University and three paddy stations *viz*. Navsari, Baradoli and Vyara of Navasari Agricultural University.

METHODOLOGY

The NWGR 8001 was developed through cross of GR-3 x NWGR-97011 by pedigree selection method, than it was evaluated for yield with promising entries including check varieties, GR-7 and GAR-3 in different trials *viz.*, PET-ME, SSVT-L, LSVT-E-C and LSVT-E-F during *Kharif* season of 2010 to 2019 (Anonymous, 2010-20). The experiment framed in a Randomized Block Design with three replications. The all genotypes grown in 4.95 meters apart with two meters width by maintaining 20 cm \times 15 cm plant spacing of individual genotype. The agronomic characters listed in Table 2. The data pertaining to various characters analyzed as per the procedure of randomized block design given by Panse and Sukhatme (1978).

RESULTS

The grain yield differences among all the genotypes found significant. NWGR-8001 was found

13 times and 08 times significantly superior over GR-7 and GAR-3, whereas three time found significantly superior over both checks and overall mean performance the genotypes viz. NWGR-8001 (5196 kgha⁻¹) was found promising with 13.8 and 12.2 percent higher yield over best check variety GR-7 and GAR-3, respectively (Table 1). It was moderate resistance to all rice diseases and moderately tolerance to insects and pests (Table 2). Morphologically, NWGR-8001 found 127 days for maturity means recorded mid-early in maturity. The plant height found highest in NWGR-8001 (135.5 cm), number of effective bearing tillers (9.0) found at par with checks. The NWGR-8001 has highest test weight 24.7g than GR 7 (21.7g) and GAR-3 (20.0g) and have 25.5 cm, higher length of panicles than both checks. The highest kernel length found in NWGR-8001(6.98 mm.) than GR7 (6.22 mm.) and GAR-3 (6.60 mm.), Kernel length after cooking is very important character found 9.6 mm of NWGR-8001 than GR 7 (9.0 mm.) and GAR-3 (9.2 mm.), respectively. The best Alkali spreading value of NWGR-8001 (5) was at par with GAR-3 (6.0mm.) than GR 7(3.0 mm). Kernel elongation ratio ranged between 1.38 and 1.45. While, amylose content reported intermediate 24.78%. Mild scent reported in NWGR-8001 (Table 3).

CONCLUSION

The highest length breadth ratio exhibited by NWGR 8001 (4.47) along with highest Kernel elongation ratio (1.38). The grains of NWGR 8001 found long slender may be best suited to farmers and consumers and propose to release.




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Table 1. Yield performance of NWGR-8001 in comparison with check varieties in Gujarat

Trial	Year	Locations		Grain yiel	d (kg/ha)	C.D. at 5%	C.V %
			NWGR 8001	GR-7 ^a	GAR-3 ^b		
PET-ME	2010	NWG	5556	3788		456.3	4.6
		DAB	5032	5628		1015.9	10.7
SSVT-L	2011	NWG	3153	3378		1208.6	16.3
		DAB	4978	5032		999.9	11.2
		DAH	4167	2760		877.0	12.0
		VYA	3756	4931		754.0	12.0
LSVT-E-C	2012	NWG	5189ª	4421		354.6	5.5
		DAB	7094 ^a	5299		562.6	5.4
		DAH	5553ª	4103		784.5	10.3
		BAR	4296	3997		611.2	9.2
LSVT-E-F	2013	NWG	4414		5216	806.9	10.0
		DAB	4416		4274	392.8	5.9
		DAH	4396		3972	800.0	13.6
		BAR	2265		2239	389.2	9.6
LSVT-E-F	2014	NWG	7026 ^b		5882	813.8	7.5
		DAB	6638 ^b		5028	722.3	8.1
		DAH	5823 ^b		4724	770.6	9.7
		BAR	3775 ^b		3742	765.1	10.3
LSVT-E-C	2015	NWG	6405 ^a	5294		471.2	4.9
		DAB	6952ª	5157		996.4	10.0
		DAH	6761	6741		1496.4	11.9
		BAR	4843	4986		960.9	11.2
LSVT-E-C	2016	NWG	4394	5011		797.4	10.1
		DAB	5791ª	4850		615.9	6.4
		DAH	8293	7578		1158.8	8.6
		BAR	4330	4017		1093.3	14.2
LSVT-E-M	2017	NWG	5735 ^b	4659	5137	1242.0	14.3
		DAH	4712 ^a	3416	5937	739.0	9.3
		NAV	5044	4961	4996	649.0	8.0
		VYA	3309	3353	2849	758.0	14.5
LSVT-E-M	2018	NWG	5741ª	3794	5061	1242.0	14.3
		DAB	6715 ^a	4946	6818	739.0	9.3
		NAV	5892 ^{ab}	4327	4926	649.0	8.0
		VYA	4148	4453	4917	758.0	14.5
LSVT-E-M	2019	NWG	5905 ^{ab}	4397	4103	1253.0	16.9
		DAB	5607 ^{ab}	4274	4231	1206.0	13.4
		NAV	5917ª	4129	5423	1186.0	13.0
		VYA	3422	3351	3162	913.9	14.9
Over all % Inc.	5196	4568	4632				
% increase ove	r check		13.8	12.2			

Note: 1. *a*=*GR*-7*b*= GAR-3*indicates Significant at 5% level than respective check.*

2. NWG= Nawagam, DAB= Dabhoi, BAR=Bardoli, NVS= Navsari, VYA= Vyara locations.



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Table 2. Ancillary observations of NWGR 8001 along with disease & pest reactions*

Treatment	DFF	Maturity	PH (cm)	PL(cm)	Test wt. g	EBT	Disease & Pest Reactions**							
							BLB	ShR	GD	LB	NB	SB	LF	WBPH
NWGR-8001	97.0	127	135.5	24.7	24.7	9.0	3	2	3	2	2	2	2	1
GR-7(C)	82.5	123	106.5	21.7	21.7	9.5	4	4	4	3	2	4	2	1
GAR-3(C)	91.5	122	117.5	20.0	20.0	9.5	5	4	5	5	4	2	2	1

*mean of four locations and last two years ***Unprotected field conditions*DFF, PH, PL and EBT indicating days to 50% flowering, plant height, panicle length and effective bearing tillers, respectively.

Table 3. Grain quality of NWGR-8001 along with checks at MRRS, Nawagam (Kharif-2019)

Treatment	Kernel	Kernel	L/B	KLAC	KER	VER	Water	Alkali	Scent*	Amylose%
	length mm.	breadth mm.		mm.			uptake ml.	Spreading		
								value		
NWGR-8001	6.98	1.56	4.47	9.6	1.38	4.71	340	5	1	24.78
GR-7(C)	6.22	1.95	3.19	9.0	1.45	4.54	355	3	0	24.85
GAR-3(C)	6.60	1.62	4.07	9.2	1.39	4.30	315	6	1	24.91

KLAC - Kernel length after cooking KER- Kernel elongation ratio VER- Volume expansion ratio L/B -Length breast ratio 1= Mild aroma 2= Strong aroma 0= Absent *indicting organoleptic test

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PHYSICO-CHEMICAL PROPERTIES OF SOME INDIAN GLUTINOUS RICE

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Glutinous rice (GR) contains low (0-5%) amylose, making it very soft and sticky. It is also called as waxy rice. Glutinous rice (GR) is very popular in Greater Mekong Sub-region (GMS) and ASEAN. It is a preferred staple for consumption in China (mainly Yunnan Province and the Guangxi Zhuang Autonomous Region), Japan, Cambodia, Thialand, Korea, Vietnam, Laos, Taiwan, Philippines, Mayanmar, Bhutan, Nepal and the North Eastern states of our country. Glutinous rice makes up 5% (23.8 mt) of the global white rice production (476 mt). Thailand and Laos PDR are the two major sticky rice producing countries in Southeast Asia. Thialand and Vietnam are the major global exporters of this rice while Korea and Japan are its major importers (Somporn et al, 2015). With the rapid growth of food and beverage industries and the changing rice cultivation scenario in countries like China, the demand for glutinous rice in the global market seems to increase in near future.

In India, glutinous rice is a preferred staple in the North Eastern states and therefore the traditional varieties in the area are found to be glutinous after cooking. Huge variation for glutinous rice exist in the local varieties of these states (Roy et al, 2020) and therefore an effort was undertaken to characterize 17 glutinous rice varieties for their physico-chemical and cooking quality parameters which is presented hereby.

Two High-yielding glutinous rice varieties Kmj 3-292 (Bhogali) and Kmj 3-296-3 (Rongili) have also been developed (Ahmed et al 1996) from Ghew Bora, a traditional tall, glutinous rice. The developed varieties have not been included for the study due to lack of their seed in the ICAR-NRRI gene bank .However, the donor parent for glutinous trait in these varieties i.e. Ghew Bora has been involved for the study..

Glutinous rice is used in preparing many traditional Asian processed foods. It is also used in making rice wine, pasta, rice balls, and rice cakes (Wittenberg, 2007). Besides, waxy rice flour is utilized in various food processing ingredients such as thickener for sauces and gravies.

METHODOLOGY

Seventeen rice cultivars, namely Aghoni bora, Bhogali bora, Gandhi birion, Ghew bora, Gundhi birion, Joha bora, Kola bora, Lal birion, Lusai biroin, Nal bora, Pamoi bora, Pani birion, Sona birion -2, Tilbakol bora, Putti birion, Ranga bora1 and Kalobhat were collected from North-Eastern states of India and were collected from the genebank module at ICAR- NRRI, Cuttack during Karif-2019. The physico-chemical properties and cooking quality were analysed through standard laboratory method (Pal et al.,2019) at 12% moisture content. Data was analyzed using the online standard software package of ICAR-IASRI, New Delhi.

RESULTS AND DISCUSSION

The physico-chemical properties of some waxy rice are presented in table1. The amylose content (AC) of these cultivars varied between 4.3 to 6.6%. The lowest AC was found from Sona birion-2 followed by Pani birion, whereas highest was found in Nalbora (6.6%). The head rice recovery percentage (HRR) varied between 35.5 to 66.5%. The highest HRR was found in Putti Birion and lowest in Joha bora. The genotyoes under study varied for thir grain type viz.



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Table1.Physico-chemical and cooking properties of some Indian Glutinous rice.

Sl. No	Varieties	Hull %	Mill %	HRR %	KL	KB	L/B	Grain	ASV	VER	KLAC	ER	AC%
					(mm)	(mm)		Туре			(mm)		
1	Aghoni bora	76.00 ^M	64.00 ^G	60.00 ^F	5.40 ^M	1.53 ^Q	3.53 ^G	SS	2.00 ^Q	3.75 ^Q	9.64 ^B	1.98 ^A	4.85 ^I
2	Bhogali bora	76.50 ^K	65.00 ^F	63.00 ^c	5.78 ^F	1.61 ^N	3.59 ^E	SS	2.00 ^p	5.30 ^E	9.45 ^D	1.63 ^D	5.50 ^B
3	Gandhibirion	78.00 ^E	63.00 ^H	59.00 ^I	6.38 ^A	1.68^{L}	3.80 ^B	LS	2.00 ^o	5.30 ^D	8.57 ^G	1.34 ^M	4.83 ^K
4	Ghew bora	80.00 ^A	66.50 ^E	64.00 ^B	6.06 ^E	1.68 ^K	3.61 ^D	LS	3.00 ^L	5.66 ^A	8.30 ¹	1.36 ^L	4.75^{L}
5	Gundhibirion	77.00 ^I	62.50 ^I	59.00 ^H	6.14 ^c	1.60 ^P	3.84 ^A	LS	2.00 ^N	4.00 ^N	8.21 ^J	1.33 ^o	5.36 ^D
6	Joha bora	74.50 ^Q	60.00 ^o	35.50 ^Q	5.15 ^Q	1.84 ^c	2.80 ^p	MS	3.50 ^H	5.00 ^K	8.00^{L}	1.50 ^H	5.02 ^G
7	Kola bora	76.50 ^J	61.00 ^м	49.50 ^L	5.24 ^N	1.71 ^J	3.06 ^M	SS	2.00 ^M	5.60 [°]	7.00 ^o	1.33 ^N	4.57 ^N
8	Lal birion	77.00 ^H	60.00 ^N	40.50 ^P	5.40 ^L	1.92 ^B	2.81 ^o	MS	3.00к	5.30 ^H	8.30 ^H	1.53 ^G	5.25 ^F
9	Lusai biroin	75.00 ^p	62.00 ^K	60.50 ^E	5.44 ^J	1.76 ^G	3.09к	SS	6.00 ^B	5.00 ^J	9.10 ^E	1.67 ^B	4.87^{H}
10	Nal bora	76.00 ^L	62.00 ^J	58.00 ^J	6.06 ^D	1.83 ^D	3.31 ^H	LS	3.00 ^J	5.30 ^G	9.60 ^c	1.58^{E}	6.63 ^A
11	Pamoi bora	78.50 [°]	68.00 ^B	43.00 ^N	5.18 ^P	1.74^{H}	2.98 ^N	MS	3.00 ^I	5.00 ^I	6.71 ^P	1.29 ^p	4.68 ^M
12	Pani birion	77.00 ^G	68.00 ^A	61.50 ^D	5.65 ^H	1.60 ^o	3.53 ^F	SS	5.00 ^E	4.66 ^L	7.71 ^N	1.36 ^K	4.35 ^P
13	Sona birion2	78.00 ^D	67.50 ^c	60.00 ^G	5.58 ^I	1.78^{E}	3.13 ^J	SS	5.00 ^D	4.00 ^M	9.64 ^A	1.64 ^c	4.27 ^Q
14	Tilbakolbora	78.50 ^B	58.50 ^p	48.50 ^M	6.16 ^B	1.66 ^M	3.71 ^c	LS	5.00 ^c	5.66 ^B	8.85 ^F	1.43 ^I	4.42 ^o
15	Putti birion	77.00 ^F	67.00 ^D	66.50 ^A	5.40 ^K	1.76 ^F	3.07 ^L	SS	6.00 ^A	3.75 ^P	6.61 ^Q	1.22 ^Q	4.83 ^J
16	Ranga bora1	75.00 ^o	55.50 ^Q	41.50 ^o	5.65 ^G	1.72 ^I	3.28 ^I	SS	4.50 ^G	5.30 ^F	7.80 ^M	1.38 ^J	5.32 ^E
17	Kalobhat	75.00 ^N	61.67 ^L	52.00 ^K	5.23 ^o	2.55 ^A	2.05 ^Q	SB	5.00 ^F	3.75 ^o	8.10 ^K	1.55 ^F	5.44 ^c
	Mean	76.79	63.07	54.24	5.64	1.76	3.25		3.65	4.84	8.33	1.48	5
	p-Value	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001		<.0001	<.0001	<.0001	<.0001	<.0001

*Hull: Hulling%, Mill: Milling%, HRR: Head rice recovery%, KL: kernel length(mm), KB: Kernel breadth, L/B: Length breadth ratio, ASV: Alkali spreading value, VER: Volume expansion ratio, KLAC: Kernel length after cooking, ER: Elongation ratio, AC: Amylose content

short slender (SS) to medium slender (MS) and long slender(LS). The kernel length of these genotypes varied between 5.2 to 6.4 mm and kernel breadth was found between 1.5 to 2.6mm. The Alkali spreading value, a measure of cooking time was observed highest in Putti birion and Lusai birion-2 while lowest was observed in Aghonibora and Kalobhat. The kernel length after cooking (KLAC) was highest in Aghonibora and Sona birion-2 whereas lowest was observed in Kolabora (7.00mm). The elongation ration (ER) after cooking was observed highest in Aghonibora. The volume expansion ration (VER) after cooking was highest in Ghewbora and Tilbakolbora. Kang et al.(2010) reported the minerals content, protein, carbohydrates and fatty acids composition and pasting properties of some glutinous cultivars of Korea. Setyaningsih et al, (2015) reported that glutinous rice

contains lower antioxidant compounds that nonglutinous rice varieties.

CONCLUSION

Assessment of physicochemical properties is necessary to determine the quality preferences and possible food industry applications of rice. In addition, the quality of different rice products made from these cultivars will greatly depend on their physicochemical properties and nutritional quality. Therefore the cahercterization of glutinous rice egermplasm is critical to determine their end-use quality. The results of this study will help the food processors in selecting glutinous rice genotypes with desirable characteristics for different specialty food. Furthermore, this can help plant breeders for refinement and improvement of glutinous rice to suit the specific consumers' preferences.



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MAPPING QTL HOTSPOTS LINKED TO RICE ROOT SYSTEM ARCHITECTURE THROUGH METAQTL ANALYSIS

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Rice is one of the major staple food crops for about 3.5 billion people across the globe and is grown under diverse ecosystems. Rice is the most important crop of India in terms of area, production and the percentage of population involved in cultivation. Recently abiotic stresses gained severity in magnitude thus affecting the sustainability of rice production. Moisture deficit stress accounts for more than 50% of average agricultural yield losses worldwide. Drought is the single largest yield reducing factor in rainfed areas of South and Southeast Asia, affecting more than 23 million ha area. Root traits are important for plant productivity especially in the environments characterized by various stresses including drought and nutrient deficiency. Root system architecture (RSA) refers to spatial and temporal distribution of roots along with their components in terms of root length, root number, root diameter, surface area, volume, lateral roots and root hairs in a defined pattern in rhizosphere. RSA is governed by genetic factors and environmental conditions majorly abiotic factors as well as their interactions for adaptive plasticity of root development. Understanding the genetic basis of root traits would facilitate transfer of desirable alleles into preferred genetic backgrounds. Therefore the present study was undertaken to identify QTLs/genes associated with rice RSA.

METHODOLOGY

Publications related to root traits were surveyed and the data was extracted according to the format prescribed by software BioMercator. The analysis was performed as per the algorithms built in the software. The meta-analysis was performed in three steps (1) Construction of consensus map (2) QTL projection and (3) meta-analysis. Meta-analysis was performed chromosome by chromosome basis. Some of the studies may not contain data for a particular chromosome. For meta-analysis two types of input data files are required (1) Map information file and (2) QTL information file. Headers for input files are provided by BioMeractor v4.2 software. Data for population size, crosstype, mapping function, mapping crosstype, map data over which QTLs were mapped, QTL positions, flanking markers, peak markers, LOD value and r^2 value etc were mined from published studies. The studies for which any of this information was not available were discarded. The data was first compiled on Microsoft excel worksheet and the Map data text file and QTL data text file were created and saved separately before loading on to the software. QTL meta-analysis was performed chromosome by chromosome basis. Data from only those studies which have all the required information was loaded on to the software. A consensus map can be developed only if there are at least 2 or more common markers between the maps. In first step the connectivity of all the maps

Meta-analysis of root traits related QTLs was 354 Drmed using Bewerbert 8: 9, 42920 It Kare NRRI, Cuttack 753006, Odisha, India



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was checked with infomap connectivity and MMap view functions of the software. Consensus map was developed for only those maps for which the connectivity was shown true. In consensus map development, map data from 47 studies were integrated in a single consensus map through a one-step procedure using weighted least squares (Veyrieras et al. 2007). QTL projection was performed by superimposing the QTLs on the consensus map using the QTL projection function of BioMercator. Meta-analysis is a two step process. In first step, meta-analysis-1/2 (Veyrieras), in which three text files are generated. One of them meta_vX_model.txt shows the number of models of AIC criterion. This model number needed to be feed in second step of meta-analysis. In second step i.e. meta-analysis-2/2 (Veyrieras), a text file is generated which shows the position of the metaQTL models on a particular chromosome and the weight of that metaQTLs among others and the CI and UCI values for the respective metaQTLs. Here meta-analysis is finished. All the relevant figures, maps and text files were then extracted from software and saved accordingly.

RESULTS

Meta-QTL analysis for root traits in rice has been carried out to identify the consensus QTLs from the QTLs reported independent genetic mapping studies from 1995 to 2018. 47 QTL mapping studies were selected for meta-QTL analysis of root traits. The individual mapping population size varied from 26 to 250. In majority of studies RILs, BILs and DH populations were used except few where F2 or F3 were used. Genetic linkage maps were constructed using RFLP, ALFP, isozymes, RAPD, SSRs and Indels. A total of 1108 QTLs associated 93 root traits including their associated traits were reported from 47 genetic studies out of which 576 QTLs were utilized in metaanalysis. The phenotypic variance explained among the QTLs utilized in meta-analysis ranged from 0.01 to 0.42 of the total variance. Chromosome wise consensus genetic maps were developed for all chromosomes except chromosome 7, 10 and 12. The distribution of projected QTLs in meta-analysis showed that chromosome 1 has highest number of QTLs followed by chromosome 3, 4, and 9 (Fig.1). Integrating all the



Fig 1. Consensus map showing the meta-QTLs detected on chromosome 1 for MRL

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maps, there were 4386 markers on the consensus map with a total map length of 2147cM with a mean distance of 0.48cM between markers. The confidence interval (CI) of markers for individual QTLs varied from 0.31 to 66.76 cM. A total of 77 meta-QTLs with CI of 95% were identified from 576 QTLs detected from different studies projected for root traits. Ten meta-QTLs were identified each on chr.1 (mQTL1.1 to mQTL1.10), chr.2 (mQTL2.1 to mQTL2.10) and chr.6 (mQTL6.1 to mQTL6.10); nine meta-QTLs on chr.3 (mQTL3.1 to mQTL3.9); eight meta-QTLs each on chr.4 (mQTL4.1 to mQTL4.8), chr.8 (mQTL8.1 to mQTL8.8), chr.9 (mQTL9.1 to mQTL9.8) and chr.11 (mQTL11.1 to mQTL11.8), while seven meta-QTLs were detected on chr.5 (mQTL5.1 to mQTL5.7).

CONCLUSION

Meta-analysis has redefined the CI of QTLs to a smaller physical and genetic interval. Several

candidate genes were mapped in the metaQTLs detected in present study which is a valuable resource to integrate and utilize them for improvement of rice RSA. Fine mapping of the robust meta-QTLs using the markers developed from candidate genes with in meta-QTL regions can be used for marker assisted breeding and pyramiding of QTLs governing different tolerance mechanisms for genetic improvement of rice RSA.

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. Indian Rice

ASSESSMENT OF GENETIC DIVERSITY IN RICE (ORYZA SATIVA L.) GERMPLASM BASED ON AGRO-MORPHOLOGICAL TRAITS

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Rice (Oryza sativa L.) is the most important food crop and a primary food source for more than one third of the world's population. Different breeding strategies such as introduction, selection, recombination breeding, heterosis breeding etc. were practiced during and after green revolution to increase the yield levels of rice. Although, yield was improved using these breeding strategies, the yield levels have stagnated subsequently. Breaking the yield ceiling through genetic improvement becomes the priority in current rice research programme. Aggressive introduction of modern high yielding varieties has resulted in the loss of a large number of landraces especially from irrigated lands, which leads to narrowing down the gene pool of the rice diversity (Roy and Sharma, 2014). The diversity of rice genetic resources is depleting. The diversity of rice has been well used in efforts to solve today's food problems (Khush and Virk, 2000).

The D² technique developed by Mahalanobis (1936) had been found to be a potent tool in quantifying the degree of divergence in germplasm. This analysis provides a measurement of relative contribution of different components on diversity both at inter-cluster and intra-cluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generation (Rao, 1952). Thus, the purpose of the present study was to identify rice genotypes having high yield potential and stability under drought stress condition, particularly at reproductive stage and to study genetic divergence among 48 genotypes to help the breeders in selecting promising and genetically diverse parents for desired improvement in rice under rainfed condition of eastern India.

MATERIALS AND METHODS

A set of fourty-eight tice genotypes including two checks viz., Sahbhagi Dhan and Sabour Deep were evaluated at reproductive stage under drought stress conditions during kharif, 2018-19 at rice research Farm of Bihar Agricultural University, Sabour, Bihar in randomized block design with three replications. All the recommended package of practices was followed to raise a healthy crop. Data were recorded on five randomly and competitive plants of each genotype from each replications for nineteen quantitative characters viz., number of effective tillers per hill, plant height (cm), panicle length (cm), number of fertile grains per panicle, spikelet sterility (%), panicle density index, total number of spikelet per panicle, 1000 grain weight (g), grain yield per plant (g), biological yield (g), harvest index (%), proline content, chlorophyll content index, canopy temperature, leaf area, relative water content and root biomass. Data on days to 50 % flowering and days to maturity were recorded on plot basis. Genetic divergence was determined by using D² statistics of Mahalanobis (1936) and clustering of genotypes was done according to Tocher's method. The percentage contribution of studied characters towards genetic divergence was computed according to Singh and Chaudhary (1985).



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RESULTS AND DISCUSSION

The analysis of variance revealed significant differences for all the nineteen characters studied indicating that there was significant amount of genetic variability present in the breeding material. On the basis of D² statistics, all the genotypes were grouped into nineteen clusters in control condition with cluster I containing the maximum of 24 genotypes followed by 7 genotypes in cluster III. The highest inter-cluster distance was observed between cluster XVIII and XIX, followed by cluster X and XVIII, cluster XIII and XVIII and cluster VII and XVIII in control condition while in stress condition the highest inter-cluster distance was observed between cluster IX and X, followed by cluster VII and IX, cluster V and IX and cluster VII and VIII indicating wider genetic diversity among the genotypes between the genotypes of these clusters. The hybridization programme involving genotype of cluster XVIII (IR 107891-B-B-447-3-1) and cluster XIX (IR 13L378) under control condition and the genotypes of cluster IX (IR 14L157) and X (IR 95817-5-1-1-2) under stress condition could be undertaken to isolate high yielding segregants, since these genotypes have high yielding potential, effective tiller per hill, relative water content, leaf area, root biomass, panicle length, biological yield, harvest index, plant height, number of fertile grains per panicle, total number of grains per panicle, leaf area and proline content with more genetic distances. The parents for hybridization could be selected on the basis of their large inter-cluster distance for isolating useful recombinants in the segregating generations. Therefore, progenies derived from such diverse crosses are expected to show wide spectrum of genetic variability and a greater scope for isolating transgressive segregants in the advanced generations. Hence, these genotypes might be used in a multiple crossing programme to recover transgressive segregants.

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. Indian Rice

KNM 1638, GALL MIDGE RESISTANT EARLY DURATION RICE (*ORYZA* SATIVA L.) GENOTYPE SUITABLE FOR TELANGANA STATE IN INDIA

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More than half of the world's population use rice as an essential staple food and Asian countries produce and consume 80% of the world's rice. It is also most important staple food crop of Telangana state of India and cultivated in varying climate and soil conditions in almost all the districts. Though enormous progress has been made in recent past in improving yield levels with the use of high yielding varieties, still there is a pressing need for improving productivity, quality requirements of consumers and resistance to major pests and diseases to reduce the cost of cultivation and to get the premium price in the market. Milled rice of rice variety, BPT 5204 fetches premium market price in Telangana and Andhra Pradesh of Southern India. However, BPT 5204 which is popularly cultivated in the Telangana state during rainy season is susceptible to the gall midge biotype 3, and also requires more water to complete its crop growth period as it is a long duration variety results in increasing the cost of cultivation. The Asian rice gall midge, Orseolia oryzae (Wood-Mason) is one of the important insect pests in Northern Telangana. In India, it is rated as third most important pest of rice in terms of spread, severity of damage and yield loss (Bentur, 2015). More recently, gall midge incidence has been increased in almost all the rice growing states of India which results in considerable yield losses as affected tillers bear no panicles or grains. In contrast, the maggots fail to induce gall formation on the resistance varieties and perish in 2-4

days after hatching. Hence, breeding for gall midge resistant varieties has been important strategy with more yield and acceptable grain quality (Henrichs and Pathak, 1981).

OBJECTIVES

Keeping in view of the above gap, breeding programme was taken up with an objective of developing short duration (120-125 days) high yielding gall midge resistant non lodging medium slender rice genotype without compromising quality.

METHODOLOGY

The breeding at Agricultural Research Station, Kunaram focused on combining various traits desired by farmers, including high yield, gall midge resistance, earliness, and improved quality. In this connection, pedigree method of breeding was followed to develop a variety with the required objective by selecting two parents i.e. JGL 11727 and JGL 17004. The female parent, JGL 11727 is noted for its good cooking quality with medium slender grains, high yielding potential, medium duration, as well as having gall midge (biotype-3) resistance developed at Rice Research Scheme, Regional Agricultural Research Station (RARS), Jagtial. JGL 17004 is a short statured medium slender non lodging variety with good quality and is selected for its extra earliness and multiple gall midge resistance developed at Rice Research Scheme, RARS, Jagtial used



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as male parent. Field screening by planting the test materials to coincide with high pest populations has been a successful technique. The gall midge resistance can be easily transferred to the desirable genotypes due to its simple inheritance. These two parents were crossed and raised the F1 and crossed plants were confirmed, based on the characters at RARS, Jagtial. The seeds of F₂ were collected by Agricultural Research Station (ARS), Kunaram and F₂ was evaluated with, approximately 10,000 population in the year, 2012. Pedigree method of breeding was followed in the F_2 , F_4 and F_5 populations by selecting single plants for the characters, such as medium slender grain, semi dwarf, long panicle, with more number of grains. Simultaneously, segregating material was left unprotected and allowed for gall midge incidence and the susceptible plants were removed leaving the resistant plant in the field and the selection was practiced only among the gall midge resistant plants. This process was continued up to F_6 till these lines attained uniformity in height, panicle length, grain type along with gall midge resistance. The breeding line with Index No. KNM 1638 resulted from the bulk harvest of a F6 family in 2014 and it was subsequently evaluated in the yield trials from the year 2014 to 2016 at ARS, Kunaram.

REUSLTS

KNM 1638 is a semi dwarf rice variety with moderate tillering, erect flag leaf, all plant parts green, semi compact well exerted semi erect attitude of branching panicle, and straw colored awn less grains culture and its grain classified as translucent medium slender grain. It is a relatively short duration variety, with total growth duration of about 120-125 days. This culture has high yield potential (7386 kg/ha) with resistance to gall midge biotype 1, 3 and 4. It is also resistant to leaf blast, moderately resistant to neck blast. It out yielded the best checks with 9.7% yield superiority over the station trials and it stood second position among all the entries tested in MLT (Early) across all the six locations (pooled locations) during kharif, 2016 in Telangana State. It also recorded nil damage against various biotypes (1 and 3) across the locations in National Gall midge Screening Trials (IIRR, 2016). It is a non shattering culture, and showing insensitivity to photoperiod. Quality wise, it recorded 58.3% head rice recovery and 21.47% amylose content with good cooking and eating quality (IIRR, 2016). The kernels are with a 1000 grain weight of 15 to 16gm without any abdominal white resemble BPT 5204. It is having around 336 to 380 ear bearing tillers $/m^2$ and the height is in the range from 100 to 105cm with strong culm having the internodal thickness of 6-7 mm. The panicle length ranged from 23.7 to 27.6 cm with 248 to 312 no. of grains per panicle. The panicle with compact nature showing full exertion without any awns and sterility. It is suitable for both Kharif and rabi seasons.

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CONCLUSION

KNM 1638 has been widely accepted by the farmers, millers and consumers due to its high yield potential, earliness (120-125 days), gall midge and blast resistance, and non shattering with good head rice recovery and excellent cooking and eating quality.

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THEME - II

Sustainable rice farming

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PATH MODELLING APPROACH FOR ELUCIDATING RELATIONSHIP BETWEEN NITROUS OXIDE EMISSION AND FUNCTIONAL SOIL MICROBES FROM RICE SOIL EXPOSED TO ELEVATED CARBON DIOXIDE

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Due to extensive anthropogenic activities present atmospheric concentration of CO₂ has surpassed 400 µmol mol"¹, which is predicted to go beyond 550 µmol mol"¹ by 2050; and 700 µmol mol"¹ by 2100 (IPCC 2013; Kumar et al. 2019). Understanding the effect of elevated atmospheric CO₂ (eCO₂) on nitrous oxide emission (N₂O) and plantmicrobe interactions in rice soils is of great significance for predicting the long-term response of rice ecosystems to eCO₂ concentration. Elevated atmospheric CO₂ concentration has the potential to augment rice production (Kumar et al., 2017) and alter the soil nitrogen (N) dynamics. Because N₂O emission is controlled by microbial activity, we hypothesised that changes in soil N chemistry and activity of soil microbes may affect N₂O flux from rice soil.

METHODOLOGY

We designed a field experiment to examine the influence of eCO_2 on N_2O emission from rice soil under different water regimes and N doses. In this study, path analyses using partial least square path modelling (PLS PM) approach was used to distinguish the direct and indirect factors influencing N_2O emission under ambient and elevated CO_2 conditions.

RESULTS

Labile N fractions such as microbial biomass-N increased by 32% (p d" 0.03) whereas there was a decrease in NH_4^+ -N(40%; p d" 0.0005) and NO_3^- -N (32%; p d" 0.001) concentration under eCO₂ over ambient CO₂ (aCO₂). Rhizosphericdenitrifier population was increased (39%; p d" 0.001) whereas, nitrifier population decreased (41%; p d" 0.001) under eCO₂ as compared to aCO₂. Exposure of eCO₂ decreased (20%; p d" 0.001) N mineralization whereas it increased N₂O emission (43%; p d" 0.001). Elevated CO₂ level increased activities of â-glucosidase, urease, dehydrogenase and Fluorescein diacetate showing significant effects on soil N dynamics. The PCA biplot constructed using the scaled dataset explained 66.55% (PC1) and 12.16% (PC2) for ambient, 61.81% (PC1) and 14.82% (PC2) for 550 µmol mol"1 (Fig. 1) and 72.83% (PC1) and 8.09% (PC2) for 700 µmol mol"1 CO₂ regime. Under ambient CO₂ concentration, N₂O emission was higher under panicle initiation stage and positively correlated with N_{min} (R²=0.972; p<0.001), nitrifier (R²=0.968; p<0.001) and denitrifier (R²= 0.902; p<0.001) population. At 550 µmol mol^{"1}CO₂ concentration, the parameters demonstrating higher positive correlations were amoA ($R^2 = 0.988$; p<0.001), nitrifier ($R^2 = 0.979$; p<0.001) and denitrifier ($R^2 =$ 0.969; p<0.001) population under panicle initiation stage. With further increase in CO₂ concentrations (700 µmol mol"1), the highly positive correlated parameters under panicle initiation stage were nitrifier ($R^2 = 0.980$; p<0.001) and denitrifier ($R^2 = 0.909$; p<0.001) population. At panicle initiation stage, the $\rm N_{p}$ and $\rm N_{min}$ decreased with increase in CO2 concentration, which was accompanied by decrease in MBN and soil

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Principal component analysis (PCA) of soil enzymes Fig.1. and functional soil microbes across two dimensions under elevated atmospheric CO₂ concentration ($550 \pm 20 \mu mol mol^{"1}$). The factors represents soil enzymes and functional soil microbes associated with soil nitrous oxide emission at MT = maximum tillering stage and PI = panicle initiation stage. FDA = Fluorescein diacetate (μg fluorescein $g^{-1} h^{-1}$), â GLU = âglucosidase (µg PNP g⁻¹ h⁻¹), Urease (µg urea hydrolysed g⁻¹ h^{-1}), MBN = Microbial biomass nitrogen (µg N g⁻¹ soil), NH₄⁺-N = Ammonical nitrogen ($\mu g g^{-1}$), NO₃ - N = Nitrate nitrogen $(\mu g g^{-1}), N_{min} = Nitrogen mineralization (\mu g N g^{-1} soil), N_n =$ Nitrification potential ($\mu g N g^{-1} dry weight day^{-1}$), NIT = Nitrifier population (\log_{10} population g⁻¹ soil), DENT = Denitrifier population (\log_{10} population g⁻¹ soil), URS = Urease (µg urea hydrolysed $g^{-1} h^{-1}$), NOE = Nitrous oxide emission (kg ha⁻¹), amoA = amonia mono oxygenase (log copy number g⁻¹ soil),nirK = nitrite reductase (log copy number g^{-1} soil), nosZ = nitrous oxide reductase (log copy number g⁻¹ soil).

nitrogen fractions (NO₃⁻-N and NH₄⁺-N) under elevated CO₂ conditions. Furthermore, the soil enzymatic activities like \hat{a} -glucosidase, FDA and Urease were positively influenced with increase in CO₂ concentration and found to be strongly associated with N_{min}.

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CONCLUSION

Path modelling indicated that under aCO_2 condition nitrogen mineralization, NH_4^+ -Nand NO_3^- -N concentration were significantly (p < 0.001) and positively correlated with N₂O emission, whereas under eCO_2 condition nitrogen mineralization, nitrification potential and microbial population were significantly (p < 0.001) and positively correlated. Regression analysis revealed complex interactions among the important variables influencing N₂O emission under ambient and elevated CO₂ conditions.

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INTEGRATED NUTRIENT MANAGEMENT FOR SUSTAINABLE RICE PRODUCTION IN THE CLIMATE CHANGE SCENARIO- LESSONS FROM LONG TERM FERTILIZER EXPERIMENTS

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The Long term Fertilizer Experiments (LTFE) serve as important tools to understand the changes in soil properties due to intensive cropping and continuous fertilizer/manure application. The All India Co-ordinated Project on Long term fertilizer experiment and Permanent manorial trial have been laid out at Regional Agricultural Research Station, Pattambi with the main objective of studying the effect of continuous application of plant nutrients (NPK) in organic and inorganic forms and in combinations on sustainable production in the rice-rice cropping sequence. The present paper discusses the sustainability of integrated nutrient management in rice-rice cropping system based on the lessons from long term fertilizer experiments.

METHODOLOGY

The co-operating centre of All India Coordinated Project on Long term fertilizer experiment have been laid out at Regional Agricultural Research Station, Pattambi with the main objective of studying the effect of continuous application of plant nutrients (NPK) in organic and inorganic forms and in combinations on sustainable production in the rice-rice cropping sequence. Permanent manorial trial in dwarf rice variety Jaya is also operation at Pattambi since 1973. PMT consists of 8 treatments while the LTFE consists of 12 treatments. The treatments included sole application of fertilizers, organic manures and integrated nutrient management practices. To analyse the effect of fertilizers/ manures, the effects on biomass yield, soil biological properties, carbon accumulation pattern and carbon pools were studied in the soils collected from both the experiments. An incubation study was also conducted at four different temperature regimes (15, 25, 35 and 45°C) using the soil collected from the plots of LTFE as well as PMT to analyse the thermal stability of carbon under LTFE and PMT.

RESULTS AND DISCUSSION

In PMT, the organic nutrient management (T_1) wherein whole of the mineral N was applied as cattle manure and Integrated Nutrient Management (INM) practice(T_5) where 50 per cent N was substituted by cattle manure were equally superior in growth and productivity to other treatments. Treatment T_{5} (45 kg N ha⁻¹ as cattle manure + N:P₂O₅:K₂O 45:45:45 kg ha ⁻¹) was found to be significantly superior with respect to the soil biological properties including dehydrogenase activity and microbial biomass carbon. The LTFE experiment with 20 years cropping history revealed the superiority of integrated nutrient management with 100 Per cent NPK along with FYM over the sole use of fertilizers. Howeverin situ growing of dhaincha (Sesbania aculeata) also offer a good solution for integration of manures and fertilizers. Integrated nutrient management and in situ green manuring with daincha recorded higher grain and straw yield and the growth parameters corroborated the trends in yield.Hemalathaet al., (2000) also observed that in situ incorporation of Sesbania registered highest plant height, number of tillers and dry matter production.

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In LTFE with 20 years history, it was seen that all the carbon pools (active, slow and passive) contributed towards yield whereas in PMT, with 44 years history, it was the slow pool of carbon that showed higher correlation with crop yield. Data on analysis of different carbon pools revealed that slow pool is the most predominant yield determining pool in the long run. The percent share of slow pool to the total carbon was higher under INM than the sole application of organic manures/ fertilizers, indicating the sustainability of INM.

An incubation study was conducted at four different temperature (15, 25, 35 and 45°C) using the soil collected from the plots of LTFE as well as PMT. The activation energy and the rate constants, calculated, provide a good insight into decomposability of organic matter and the pace of mineralization in soil. In general, all the treatments in PMT, except T_s (at high temperature - 35°C and 45°C), had comparable amounts of carbon decomposition rates at the studied temperatures. The reaction rates in all the organic treatments were found to decrease at 45°C indicating the exhaustion of carbon pools accessible for microbial decomposition. The values on activation energy and the rate constantsprovided a good insight on decomposability of organic matter and the pace of mineralization in soil. Treatments with inorganics recorded lowest activation energies indicating the instability of even recalcitrant or passive pools while carbon developed under INM had highest activation energy. The results are in confirmation to the results of Sandeep et al. (2016) wherein it was

observed that application organic manures were more effective in enhancing the activation energy of SOC than mineral fertilizers.

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CONCLUSIONS

Integrated nutrient management and in situ green manuring with daincha recorded higher grain and straw yields and In situ green manuring is a cost effective and farmer friendly technology, which can save cost of 5 tonnes of farmyard manure. 50% reduction in inorganic fertilizer dose is possible with the incorporation of in situ green manuring with daincha or FYM @ 5t/ha into the fertilizer schedule of paddy. Though the organic carbon buildup is higher under organic nutrient management, the share of the slow pool to the total carbon is higher under INM, which is the predominant yield determining pool. Moreover, the INM practice increases the thermal stability of the carbon. Hence integrated nutrient management will be the stable practice in rising temperature scenario for sustaining the soil carbon and crop productivity in the long run.

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SRI (SYSTEM OF RICE INTENSIFICATION) AND ITS MODIFICATIONS ON WATER INPUT SAVING FOR SUSTAINABLE PRODUCTIVITY

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Traditional transplanting of rice seedlings 5-8 weeks old is the most common method of crop establishment under irrigated lowland ecosystems with continuous flooding not only consumes more water, but it also causes wastage of water as it does not enhance yield. There is considerable scope to increase the productivity of rice by manipulating the plants' environmental conditions to modify their microclimates and soil conditions. System of Rice Intensification(SRI) method of cultivation works by reducing plant population (plant density) for enhanced root and canopy growth, by careful transplanting of single young seedlings to conserve their growth potential, by wider and square planting for more access to soil nutrients and light interception, by mechanical weeding that actively aerates the soil, by need-based fertilizer application with an emphasis on increasing the soil's organic matter content, and by optimum use of water to get better plant growth through more aerobic soil conditions and more beneficial soil biota.

Manual transplanting of rice is laborious and time-consuming. The non-availability of labourers for transplanting at an appropriate time leads to late planting, which results in poor yield. Transplanting rice manually requires about 30-35 man-days/ha, which is nearly 25% of the total labour requirement for irrigated rice production (Swain et al. 2013). To counteract the labour problems, mechanization of transplanting and weeding is a desirable innovation. Mechanical transplanting that is plant-friendly would not only facilitate timely completion of operations but would also enhance production potential, labour-saving, energy efficiency, and the profitability of rice production if SRI's principles can be combined with its methods. In this context, a field experiment was conducted in both wet and dry seasons to evaluate and assess the water productivity, grain yield with the mechanization of SRI methods with the original practices of SRI method.

METHODOLOGY

Field experiments were conducted at the Indian Institute of Rice Research (IIRR) (17°33'^N latitude, 78°38'E longitude), formerly the Indian Council of Agriculture Research (ICAR) – Indian Institute of Rice Research (IIRR), Rajendranagar, Hyderabad, Telangana state. The soil is clay loam soil having medium fertility, slightly acidic (pH 5.6) with low nitrogen (245.96 kg ha⁻¹), medium phosphorous (33.90 kg ha⁻¹) and medium potassium (184.50 kg ha⁻¹). The trials were carried out during the wet and dry seasons of 2013-14 and 2014-15 to assess the comparative efficiency of MSRI (wherein SRI practices such as transplanting has been mechanized) and manual SRI.

RESULTS

The System of Rice Intensification (SRI) method was found to result in significantly higher yields of grain (5.91 t ha⁻¹) compared with mechanized SRI (5.74). SRI methods with wider spacing of plants and less competition between them plus careful transplanting enable the plants to grow more vigorously. The larger

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roots help to capture the essential nutrients important for plant growth, and this in turn leads to higher tillering and dry matter production. Variations in water use, water-saving and water productivity of rice under different irrigation methods indicated the Water productivity (kg ha mm⁻¹) was significantly higher with SRI (5.02) over MSRI (4.91). It was reported that with a longer irrigation interval of 5 days, the yields are reduced in SRI method, but only by <6%; with the significant saving of water, a much larger total area could be irrigated, more than compensating for the reduced yield per hectare (Hameed et al. 2013).

Table 1. Effect of crop establishment and Irrigation management on grain yield, Energy efficiency, B:C ratio and Water Productivity (mean of 4 seasons)

Crop	GY	Energy	B:C	Water
Establishment	(t/ha)	Productivity	Ratio	Productivity
Methods/		(kg/MJ)		(kg/mm
Irrigation				
M1 I1	6.15	0.78	1.163	5.189
M1 I2	5.85	0.76	1.111	4.968
M1 I3	5.23	0.71	0.934	4.573
	5.74	0.75	1.069	4.910
M2 I1	6.25	0.88	1.136	5.237
M2 I2	6.05	0.86	1.116	5.098
M2 I3	5.43	0.78	0.949	4.727
	5.91	0.84	1.067	5.021
I1	6.19	0.82	1.15	5.21
12	5.94	0.80	1.12	5.03
13	5.32	0.74	0.94	4.64
Methods (M)	0.07	0.01	NS	0.06
Irrigations (I)	0.19	0.03	0.06	0.16

Methods: M1 = Mechanized system of rice intensification (MSRI); M2 = System of rice intensification (SRI) Irrigation methods: I1 = Saturation; I2 = Irrigation @ 3 DADPW; I3 = Irrigation @ 5 DADPW

The lowest energy productivity (0.75 kg MJ⁻¹) was observed in MSRI as compared to SRI. This was mainly due to higher cost of cultivation with lower output energy for MSRI. The system of rice intensification registered significantly higher energy productivity (0.84 kg MJ⁻¹) compared to the other production method evaluated. The SRI method is not necessarily more labour-intensive once farmers have gained proficiency

with and confidence in this methodology, but initial labour requirements can be a barrier to adoption, and farmers with large land areas cannot find the labour needed to use these more productive methods (Sharif, 2011).

Mechanised transplanting together with other SRI practices thus appears to be justified for promoting SRI on a large-scale in areas of where labour is scarce. A further need is to develop appropriate motorized implements for mechanical weeding

The planting methods did not differ significantly between MSRI and SRI for B:C ratio during both years of study. Irrigation at saturation recorded a significantly higher B:C ratio (1.15) followed closely by 3 days of disappearance of ponded water (DADPW) (1.11) while irrigation at 5 DADPW recorded the lowest B:C ratio (0.94).

CONCLUSION

Alternate wetting and moderate-dryingsoilwater regimes as followed for both SRI and MSRI enhanced root development and also facilitate a number of other physiological processes such as tiller number and dry matter production and enhanced the grain yield. Although the saturation irrigation method is successful compared to usual flooding practices, promoting alternate wetting and drying will further reduce the water consumed in rice production (by 4-12%) and will enhance water productivity, and maintain sustainability of the rice productivity. There is need for learning and refining the SRI method especially mechanization in transplanting (to reduce labour requirement)need to be promoted at large scale without compromising yield.

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Theme - II : Sustainable rice farming

AN UNFOLDING SUCCESS STORY OF ENDOPHYTIC DIAZOTROPH Azotobacter chroococcumAvi2: A SUBSTANTIAL SUBSTITUTE OF N-FERTILIZER IN RICE

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Nitrogen (N) is deprived in most of the world's soil which would directly hamper the sustainability of crop production. More than 50% of exogenous applied N-fertilizer is lost in rice field, causes negative impacts on soil environment thereby affecting its yield and nitrogen use efficiency. Nitrogen fixing microbes are one of the possible alternatives of chemical N; however, potentiality of these microbes is really a question at field level mainly due to environmental constraints. Inoculation of the native, polyvalent diazotrophs can aid and uphold production of non-leguminous crops like rice. Azotobacter is known N-fixing bacteria in cereal crops including rice, however, its dizotrophic potential in rice as endophytes was not known. Hence, AzotobacterchroococcumAvi2, a native endophytic has been explored as a potential diazotrophs exclusively for rice crop. The present document represents how A.chroococcumAvi2 could substitute substantial amount of chemical N in rice.

METHODOLOGY

All the experiments, from isolation to formulation followed by characterization, localization, quantification and tremendous evaluation in both *in vitro* and field conditions were performed at ICAR-National Rice Research Institute (NRRI), Cuttack, Odisha, India. Out of 325 endophytes and epiphytes from Indian cultivated and wild rice genotypes, 20 promising nitrogen fixing bacteria were identifiedbased on acetylene reduction assay on nitrogenase activity, biochemical tests, BIOLOG and 16S rRNA gene sequencing.These promising diazotrophs were systematically studied under *in vitro* and *in vivo* condition for their diazotrophic efficacy in rice and identified the best straini.e.A. chroococcum Avi2, which was used for liquid formulation and monitored for shelf-life. The efficacy of the formulationwastested further at farmer's field. A. chroococcum Avi2 was also evaluated under oxidative (H_2O_2) as well as water deficit stress(-60kPa) condition and made an effective combo formulation along with ascorbic acid based on extensive experiments viz. its nitrogen fixation (nifH gene quantification) efficiency, antioxidants (SOD, CAT, H₂O₂), stress indicator proline, photosynthetic efficacy (chlorophyll content and chlorophyll florescence imaging), and plant-growth promotion traits. Absolute quantification of nifH gene was calculated by using five points standard curve, following the protocol of Kumar et al. 2017. Measurement of antioxidants viz. catalase, superoxide dismutase, hydrogen peroxide activities and proline were measured by Aebi (1984), Dhindsa et al. (1981), Sergiev et al. (1997) and Bates (1973), respectively.

RESULT

Avi2 was isolated from Swarna root and its endophytic nature has been proved through FRETbased technique. Further, *in vitro* and *in vivo* analyses of Avi2 were done in rice to prove its diazotrophic efficacy. Root colonizing ability of Avi2 was confirmed by scanning electron microscopewherebacterial biofilm was observed at the junction of primary and lateral root confirming. The findings of the study were encouraging as Avi2exhibited better vegetative and reproductive growth of rice in both pot and field experiment compared to the available commercial product of rhizospheric *Azotobacter* sp.

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Finally, a liquid formulation of Avi2, having shelf life of more than one year was developed. Continuous evaluation of Avi2 at thirty different locations of rice field in Odisha, revealed that it can save 4 25% of chemical-N without compromising its yield. Chlorophyll imaging study revealed the efficacy of Avi2 in terms of quantum yield of PSII. Inoculations with Avi2 exhibited higher yield as well as maximal chlorophyll fluorescence of flag leaves in flowering and grain filling stages indicating higher photosynthetic rates. Molecular data also suggested that the higher abundance of nifH gene was found in Avi2-treatment compared to the recommended N (RDN). The data from Flagship Experiment on "Nitrogen Use Efficiency in rice" conducted at NRRI, Cuttack for last two seasons also showed at paryield in Swarna and CRDhan310 in Avi2-treatment compared to RDN. Diazotrophic efficacy of endophytic A.chroococcumstrain Avi2was evaluated in rice cultivars (Var. Naveen and Sabita) and compared with commercialized bioinoculants (IFFCO product) and recommended dose of nitrogen for rice crop.

CONCLUSION

The present study concludes that the potentiality of Avi2 to save around 25% of chemical-N fertilizers without compromising the rice yield. Besides subsidy given by Indian Government, input cost of nitrogenous fertilizers for rice production is too high which can bring down drastically through intervention of Avi2 and will help to enhance the farmers' income.Overall, the field experiment suggested that Avi2 strain may have ability to save approximately 12-25% of N without compromising the rice yield. Besides, a simple formulation of A. chroococcum was made to alleviate moisture stress vis a vis enhancing the PGP efficacy in rice. The combined application of A. chroococcum Avi2 and ascorbic acid could improve plant growth by alleviating the water deficit stress through increasing relative water content, chlorophyll pigments, antioxidant enzyme activities, nifH gene copy number and ChlF-based photosynthetic coefficients and reducing electrolytic leakage content and proline activity in drought-tolerant (Satyabhama and Ankit) and susceptible (IR64 and Naveen) cultivars.

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Fig.1 Schematic diagram of rice-specific endophytic diazotroph A. chroococcumAvi2formulation from isolation to field evaluation.



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ENHANCING PRODUCTIVITY AND RESOURCE USE EFFICIENCY OF RICE-MAIZE SYSTEM THROUGH CONSERVATION AGRICULTURE

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Sustainable nutrient management in maize of rice maize system is a tough challenge in southern India (Timsina*et al.*, 2010). Conservation agriculture (CA)based tillage and crop establishment options such as reduced tillage, and maintaining stubble mulch may hold potential to increase yield, reduce crop establishment costs, and increase income of the farmers. Keeping this in view the present experiment is initiated in *kharif* 2016 to study the effect of different rice establishment methods, mulching stubbles and tillage on system productivity of rice-maize system.

METHODOLOGY

In *kharif* the trial consists of two main treatments i.e. normal manual transplanting and direct wet seeding and 3 sub plots as date of sowing i.e.1st July, 15th July and 30th July replicated four times. The seeds were sown on the same date of sowing for both establishment methods (date of nursery raising and direct sowing in wet seeding is same). Similarly, in *rabi* two tillage treatments (convenventional and minimum tillage) were imposed over the *kharif* treatments. High yielding rice variety RNR 15048 was taken in *kharif*. In *rabi* single cross maize hybrid variety DHM 117was taken. All the agronomic package and practices were followed as per recommendation.Four years (2016-2020) data were analysed and presented here. The plots were kept fixed for all the four years.

RESULTS

The highest rice grain yield (5.14 t/ha) was recorded in transplanted plots sown at 1stJuly.In*rabi*, conventional tilled plots resulted in the highest maize yield (9.1 t/ha). Manual transplanting method transplanted on 1st July followed by conventional tillage in *rabi* maize resulted significantly higher system productivity of 13.2 t/ha than those of other treatment combinations (Fig.1). Minimum tillage in maize resulted low system productivity compared to conventional tillage irrespective of treatments. Similarly, higher bacteria (193 x 10⁶) and actinomycetes (105 x 10⁴) population were observed under transplanted plots compared to those under direct wet seeded plots.

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CONCLUSION



Fig.1. Effect of different date of sowing, establishment method and tillage intensity on system productivity of rice-maize cropping system.

In initial year of conservation agricultural practices in rice-maize system revealed that *kharif* rice transplanted at 1st July followed by *rabi* conventional tilled maize resulted in the highest system productivity (13.2 t/ha).

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IMPROVING RESILIENCE AND PRODUCTIVITY OF RICE-BASED SYSTEMS IN DROUGHT-PRONE RAINFED ENVIRONMENT

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Rainfed rice-based systems are mostly characterized by fragile environments and poverty extremes. In India, rainfed rice covers an area of 20.4 million hectares (m ha). Eastern India alone accounts for nearly 60% of country's total rice area, of which about 80% is confined to rainfed ecologies. However, the productivity of rainfed environment continues to remain low in comparison to input-intensive irrigated ecosystem because of multiple (biotic and abiotic) stresses related to different bio-physical and socio-economic issues including weak extension systems, poor diffusion of improved technologies, etc. (Ismail et al., 2013). Among different stresses, drought is a recurrent phenomenon that becomes a significant constraint to agricultural production and productivity under rainfed environment. In eastern India, rainfed rice is grown on approximately 16.2 m ha, of which about 6.3 m ha of upland and 7.3 m ha of lowland areas are drought-prone.

Rice production and productivity gets adversely affected due to frequent drought, especially in the red and lateritic zone (RLZ) which belongs to the western tract of West Bengal (comprising the districts of Bankura, Birbhum, Jhargram, Paschim Bardhaman, Paschim Medinipur and Purulia). The RLZ is mainly characterized by undulating topography with red or laterite, coarse loamy to fine loamy soils, less rainfall as well as occurrence of drought, leading to low soil water holding capacity, low cropping intensity (mostly mono-cropping) and low rice productivity. Even vast areas remain fallow after the harvest of *kharif* rice due to lack of irrigation, late harvesting of long-duration high-yielding rice varieties, faster depletion of soil moisture after rice harvest causing moistures stress at the sowing time of *rabi* crops because of early monsoon withdrawal, *etc*. All these ultimately lead to the risk-averse sub-optimal inputmanagement.

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METHODOLOGY

Development and identification of stresstolerant rice varieties, which fit well into changed climatic conditions, is a common denominator for sustainable crop production in rainfed agro-ecosystems. Many of these rice varieties have been developed by the International Rice Research Institute (IRRI) and disseminated through mega-projects like STRASA(Stress Tolerant Rice for Africa and South Asia) and EC-IFAD (European Commission-International Fund for Agricultural Development) with the help of NARES (national agricultural research and extension systems) partners and State Departments of Agriculture. A number of short duration droughttolerant rice varieties (DTRVs) like Sahbhagi Dhan, Shusk Samrat, Abhishek, CR Dhan 40, DRR Dhan 42 (IR 64-Drt1) and DRR Dhan 44 are now available in India, and they can withstand up to 15-20 days of exposure to dry spells with a yield gain of 1.5-2.0 t ha-¹ over the traditional of farmers' preferred rice varieties (Dar et al., 2020). Besides, conforming best-bet agronomic management practices like appropriate tillage options, seed priming, integrated weed management, foliar nutrition through organic and inorganic sources, use of soil conditioner (hydrogel), straw mulching or dust mulching, etc. during the kharif season can further add 1.0-1.5 t ha-1 yield benefit to these DTRVs, besides widening the opportunities for introducing a second crop in rice-fallows under rainfed



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environment. If managed properly, these rice-fallows offer huge potentials as suitable niches for growing *rabi* pulses which not only help in augmenting total pulse production, but also ensure better soil moisture conservation as well as soil health improvement in drought-affected areas.

RESULTS

As experienced from research activities at Zonal Drought Resistant Paddy Research Station, Hathwara, Purulia along with on-farm validation experiments at farmers' fields in Purulia District of West Bengal during last three years (2017-19), the highest grain yield of rice was recorded under unpuddled transplanted condition (3.72 t ha⁻¹), compared with puddled transplanted condition (3.59 t ha⁻¹) although both the crop establishment (CE) methods did not display significant yield differences during kharif season. Amongst the moisture conservation practices, higher grain yields were recorded with straw mulching at 5.0 t ha⁻¹ (3.75 and 3.90 t ha⁻¹) and Pusa Hydrogel at 3.75 kg ha⁻¹ (3.71 and 3.97 t ha⁻¹) under puddled and unpuddled condition, respectively during kharif season. Unpuddled rice establishment (0.99 t ha⁻¹) was also found superior to the puddled one (0.90 t ha⁻¹) for paira (utera) cropping of rabi pulses with effective utilization of residual soil moisture in rice-fallows. Of different moisture conservation practices, higher seed yields of pulses were recorded with Pusa Hydrogel (0.95 and 1.05 t ha⁻¹) and straw mulching (0.91 and 1.03 t ha⁻¹) under puddled and unpuddled condition, respectively, during rabi season. Amongst pulses,

lathyrus proved to exhibit more drought hardiness although chickpea was more productive, followed by lathyrus and lentil in rice-fallows.

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CONCLUSION

Improved CE methods and matching agrotechnologies during *kharif* season under drought-prone rainfed environment would help to accommodate a second crop in succession through appropriate moisture conservation. Pulse crops deserve huge opportunities for exploitation of rice-fallows owing to less water requirement, more hardiness, soil health improvement, and higher prices. Short duration DTRVs, appropriate moisture conservation practices and minimum tillage as un-puddled condition during *kharif* along with successful pairing of suitable *rabi* pulses in water-limited rice-fallows would be an effective strategy for improving system resilience, productivity and profitability of ricebased cropping systems.

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GREEN ALGAE DIAGNOSIS AND MANAGEMENT IN LOW LAND PADDY FIELDS OF CAUVERY DELTA ZONE, TAMIL NADU

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Wet land rice cultivation contributes maximum grain yield than dry land rice. Cauvery delta is a predominant area for rice cultivation in Tamil Nadu. Green algae growth during Kuruvai (June - August) season is a serious problem in wet land rice. Laboratory and field experiments were conducted to find out the remedial measures. The results of soil and water analyses showed that use of bore well water and dumping of phosphatic fertilizers leads to salt accumulation which favours the algal growth. The results of the laboratory experiment revealed that the CuSO₄ londox power, propiconazole and hexaconazole showed moderate inhibition on 5th day after treatment. The findings from field experiment indicated that use of conoweeder and $CuSO_4$ drenching at the rate of 2.5 kg/ha when green algae appearance has just noticed or 5.0 kg/ha when severe growth occurred is effective in managing the green algae. Biofertilizers application, crop rotation, green manure trampling to be practised to control the algae growth was not rectified by CuSO₄ application.

OBJECTIVES

To find the reason behind green algae growth in low land rice field

To identify the management practices to control green algae growth in low land rice field

METHODOLOGY

Soil and water physical parameter analysis

Soil and water sample were collected from algae noticed fields for analysing the reason behind the excess algae growth. Micronutrients *viz*. HCO₂, S, Cl,

Ca, Mg, Na and K were estimated using Atomic Adsorption Spectrophotometer (AAS) method and expressed in ppm. The electrical conductivity (EC) and pH were estimated using EC and pH meter respectively (Table 1 and 2).

LABORATORY EXPERIMENT

Laboratory experiments were carried out at Tamil Nadu Rice Research Institute, Aduthurai. Green algae were collected from infected rice fields. Ten gram of algae was placed in the Petri dish. Fungicides, weedicides and algicides were added at the rate of 2ml/plate each separately, closed with lid and left for 7 days. The observations were recorded every day after incubation.

PRELIMINARY FIELD EXPERIMENT

A field experiment was conducted at Tamil Nadu Rice Research Institute, Aduthurai during June to August 2015 (*Kuruvai* season) to determine green algae management practices under wet land rice ecosystem. Experiments were laid out in a randomized block design with11 treatments and 3 replications. Fertilizers were applied at the rate of 150: 50: 50 kg



Fig. 1. Green algae growth in rice field



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NPK/ha. N was applied 50% as basal and two top dressings of 25% each at the time of active tillering and panicle initiation stages. The size of the experimental plot adopted with 3 x 4m and 2 seedlings / hill. Selected weedicide, fungicides were applied in the field for green algae control.

CONFIRMATORY FIELD EXPERIMENT

Field experiments were conducted during *Kuruvai* season in Tamil Nadu Rice Research Institution, Aduthurai during June to August 2016 and 2017. Fertilizers were applied as in the case of preliminary field experiment. The experiments were laid out in a randomized block design with 12 treatments and 3 replications. The plot size was 4m x 3m with 20 x 15 cm spacing having 2 seedlings / hill. ADT 45 variety was used in this experiment

RESULT AND DISCUSSION

Physical parameters of the soil and water sample in algae infected field

Green algae growth usually occurred during Kuruvai season. This might be due increase in salt concentration of the bore well water and soil pH. Use of borewell water, P fertilizers accumulation, dumping of complex fertilizer and herbicides application increases the soil pH.

Effect of fungicides, weedicides and algicides on algae growth under laboratory and field conditions

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The laboratory experiments revealed that the application of propiconazole, hexaconazole, CuSO₄ and londox power showed moderate inhibition on algae growth at 5th day of incubation. The algae became shrunken and black in colour. Other chemicals don't have negative impact on the algae growth as given below (Table 1). Field experiment results revealed that CuSO₄ application inhibited algal growth 100%, whereas, londox power exhibited 50% inhibition of algal growth (Table 1) while, other chemicals don't have inhibition on algal growth. Chemicals réaction on algae under invitro and invivo conditions were significantly different. Eventhough CuSO₄ inhibit algae growth under field conditions, itwas not observed in labortory conditions. This might bé due to the change in the soil pH due to CuSO₄ application.

Effect of CuSO₄ application on green algae growth under field conditions

The results of the confirmatory field experiment at Aduthurai revealed that by simple physical management practices like alternate wetting and drying, manual trampling of algae and use of conoweeder reduces the green algae growth (Table 2). Repeated stagnation of bore well water increases the phosphorus

Fable 1.	Effect of w	eedicides,	fungicides	and algicid	les applicat	ion on alg	gae growth	under la	boratory/f	field	conditions

Treatments	Recommendeddose /ha	Laboratory conditions (dosage: 2ml/plate)	Field conditions
T ₁ -Bispyriphos sodium	20 g	No inhibition	No inhibition
T_2 – Almix	20 g	No inhibition	No inhibition
T ₃ –Pyrosulfuran	200 g	No inhibition	No inhibition
T_4 - Londox power	10 Kg	Moderate inhibition	Moderate inhibition
$T_5 - CuSO_4$	2.5 Kg	Moderate inhibition	Inhibition
T ₆ -CaO	25 Kg	No inhibition	No inhibition
$T_7 - CuSO_4 + CaO$	$2.5 \mathrm{kg} + 25 \mathrm{Kg}$	Moderate inhibition	Moderate inhibition
T ₈ -Butachlor	2.5 lit	No inhibition	No inhibition
T ₉ –Propiconazole	250 ml	Moderate inhibition	No inhibition
T ₁₀ -Hexaconazole	250 ml	Moderate inhibition	No inhibition
T_{11}^{-} control	-	No inhibition	No inhibition

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Treatments	Dosage/ha	Field condition
T ₁ -Alternate wetting and thawing the	-	Inhibition
algal growth with conoweeder if algal		
growth occurred		
T_2 - CuSO ₄	Soil application-1 Kg	Inhibition
$T_3 - T_1 + T_2$	As indicatedAbove	Inhibition
T_4 - CuSO ₄	Soil drenching-0.5%	Moderate inhibition
T_5 -Cu(OH) ₂	Soil application – 1 Kg	Moderate inhibition
$T_6 - T_1 + T_5$	As indicatedAbove	Inhibition
$T_{7}Cu(OH)_{2}$	Soil Drencing-0.5%	Moderate inhibition
T ₈ -Londox power	Soil application – 1 Kg	Moderate inhibition
$T_9 - T_1 + T_8$	As indicatedAbove	Inhibition
T ₁₀ =Londox power	Soil drenching -0.5%	Moderate inhibition
T_{11} -Soil extract with cell free extract	10%	No inhibition
containing Rhamnolipids from		
Pseudomonas chlororamphis		
T ₁₂ -Control	-	No inhibition

Table 2. Effect of CuSO₄ application on algae growth under field conditions

content in soil leads to the stimulation of algae spore. When stimulation of algae spores observed, water was completely drained, $CuSO_4$ drenching at the rate of 2.5 kg/ha was done. But during tremendous algae growth, $CuSO_4$ drenching at the rate of 5.0 kg/ha was done. In most cases action to eradicate green algae is taken only when filaments are present in huge numbers and the treatments available are limited. Generally Australian farmers use water control, bluestone ($CuSO_4$) and coptrol (2.5 lit/ha), both of which are drastic answers to a problem where a lot of damage has already been done (Hrudey*et al.*, 1999, Jones and Burch, 1997; Jones and Orr, 1994 and http// www.affa.gov.au/nra/welcome.html accessed January 2002)

PAK[™]27 (BioSafe Systems, 2008 and Hazardous Substances Data Bank, 2009) is a granular product that attacks planktonic and filamentous algae on contact. The active ingredient is sodium carbonate peroxyhydrate and creates a powerful oxidation reaction that destroys algal cell membranes and chlorophyll providing immediate control of algae. Fast acting within 60 seconds of application and leaves behind no harmful residues and adds 13% bio-available oxygen to the water.

CONCLUSION

It is concluded that soil is consider as a buffer that can tolerate the pH change. Even though continuous dumping of DAP and other chemical fertilizers changes the soil pH, innate capacity and fix more amount of the salt in the soil, which indeed difficult by reclamation practices ($CuSO_4$). In this situation continuous treatments like gypsum (bring the pH in acidic), infiltration with water (leach excess ions viz. Na, HCO₃), biofertilizers treatment (to move the accumulated P) and periodical soil and water sample analysis are important. It is always advisable to prevent the excess algae growth by fertilizer and water management practices rather than control, since chemicals are toxic to soil microorganisms. However, when situation warrants, application of 2.5 kg of $CuSO_4$ /ha when the growth of algae is mild and 5.0 kg/ha when severe algae growth is noticed is the best management practices.

GRATITUTE: Sincere thanks to Tamil Nadu Rice Research Institute, Aduthurai

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RICE AND WATER STRESS - A RETROSPECTIVE ANALYSES ON SOIL-CROP-WATER INTERFACE FOR CLIMATE RESILIENCY & SUSTAINABLE SYSTEMPRODUCTIVITY

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Adversity of climate change foot-printemerges as the paramount challenge in the usual rice-growing micro-environment to achieve the target of 120-125 MT production target of rice by 2030 taking account the current demographic growth rate (1.5%). One of the major detrimental consequences of climatic aberration is the water stress that could appear with its two different dimensions, viz., deficit water stress and excess water stress situations. Ostensibly, rice, unlike other field crops, has remarkable merits of wide range adaptability at variable hydrological conditions. Although, both the stress situations occurs on account of erratic rainfall, location specific special trait rice variety supplemented with improved crop, nutrient and irrigation management could help the crop migrate the detrimental effects ofstress situations substantially.

Therefore, understanding the causes and concerns of water stresses, advance technological interventions have been developed so as to address the mitigation mechanism alleviating the intensity of stresses forenhancing sustainable rice production.

METHODOLOGY

Since last more than twenty five years, several field studies addressing both the stress situations were conducted at the on station situations, ICAR-NRRI, Cuttack and ICAR-IARI, New Delhi which were simultaneously fine-tuned following validation at Onfarm situations in district Odisha and NCR-Delhi. Addressing the excess water situation at rainfed lowland rice ecology, several studies were conducted on stand establishment, stand management, nutrient management and cropping system; while mostly water, nutrient and cropping system research were conducted addressing the deficit water at aerobic rice ecology.

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RESULTS

As a result, advance rice production technology was developed constituted with improved crop management, nutrient management and water management in a system mode perspective.

a). Improved agro-technology under excess water stress situations

Results showed that dry seeding rice (DSR) with 400-600 seeds/m² at an inter row spacing of 20 cm in 4-5 cm deep furrow and fertilized with 30 kg N /ha was found advantageous under rainfed semideep water (0-100 cm) situation (Ghosh, 2007). In rainfed lowland rice, dry direct seeding high density seeds provided 64% more grain yield; while, transplanting fertilized seedling ensured 57% more grain yield than that with unfertilized seedlings. Manipulating seeding geometry with skipping gone row after every four rows at 15 x 20 cm spacing arrangement was reported a 20% saving of the major resources mainly seeds, labor and fertilizer without affecting the yield under semi-deep lowland (0-100 cm) situations. Clonal propagation with 50% tillers removed from a 50-day old DSR crop was found ensuring comparable grain yield with DSR stands and superior to that using conventional nursery seedlings. At post-flood situation, planting robust seedling of medium-duration rice variety treated with 1 kg/m² of rice hull ash (8% Si) and FYM increased 25% seed use efficiency and resulted in 10-25% more yield benefit. In rainfed lowland rice, hand weeding twice at 20 and 40 DAS along with beushening

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at 40 DAS followed by gap filling was reported to enhance grain yield by 12-15% over other methods. Efficacy of weed suppression was more with two summer/offseason ploughings at 2 months and 1 month before sowing. In dry season irrigatedrice, applying preemergence herbicide, butachlor at 1.5 kg a.i. / ha 3 days after sowing resulted in grain yield comparable with two hand weedings. Intercropping long-duration (> 160 days) and short duration (~ 80-100 days) rice varieties was found to ensure 15-17% more yield in rainfed medium deep water situation.

Similarly, studies on nutrient management showed that combined application of FYM (10 t/ha) with urea (20 kg N/ha) gave grain yield comparable with 40 kg urea-N/ha under flood-prone situations. Green manuring rice with intercropped Sesbania (GM) (1:1 or 2:1 stand ratio) supplemented with 20 kg N/ha achieved grain yield comparable with that of 40 kg N/ ha under flood-prone situations. In flood-prone lowland rice, integrated N management with Sesbania and FYM, and urea N at 20 kg N/ha (10:10:20ratio) along with 20 kg P₂O₅/ha gave grain yield comparable with that of 40 kg urea - N/ha with higher N uptake (55.5 kg/ ha), NUE (29.5 kg grain/kg N), PUE (12 kg grain/kg P) and apparent N recovery(38.32%). Applying 20 kg urea-N/ha in greengram (GM) intercropped rice produced grain yield comparable with that of 40 kg urea-N/ha with higher NUE (40 kg grain/kg N) under rainfed medium deep lowland. In a jute-rice cropping system, applying 75% N from urea and FYM at 3:1 ratio following soil test-crop response- based target yield equation achieved higher N, P and K productivity of 32.1, 16.3 and 26.8 kg grain/kg nutrient applied. Therefore, on-farm assessment -cum-validation of studies established that optimum productivity could be achieved only when both modern HYV of rice and improved crop management goes hand to hand.

b) Improved agro-technology under deficit water stress situations

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Studies conducted under water deficient situations showed that In aerobic rice cultivation, scheduling irrigation at 40 kPa soil moisture content increased water saving (40-44%), water productivity (0.45-0.50 g grain/lit water) without affecting grain yield compared with 0 kPa(Ghosh and Singh, 2010). In transplanted rice, alternate wetting and drying cycle of irrigation maintaining 0.1 bar soil moisture content resulted in higher WUE (3.0-3.5 kg grain/lit water) and grain yield comparable grain yield with usual irrigation. Maintaining semi-aerobic (20 kPa SMC) soil condition alleviated 20 - 24% yield penalty caused on account of 25% increase in concentration of H_2O_2 and proline, and 20% decrease in total soluble protein concentration in successively grown aerobic rice. Zero-till sown forage sorghum after kharif rice registered 50% saving in irrigation water without affecting green forage yield.

Regarding weed management, results showed that maintaining lesser crop-weed competition during initial 75, 60 and 45 days of crop growth promoted higher N uptakes of 106.0-106.6 kg/ha, 105.5-105.8 kg/ ha and 100.0-101.2 kg/ ha that achieved significantly higher grain yield of 5.25-5.56 t/ha, 5.00-5.40 t/ ha and 4.70-5.15 t/ ha, and also higher residual soil N (250.0 kg/ ha). Again, studies on different schedules of weed management, results showed significantly higher grain yield of 3.70 - 3.89 t/ha with integrated weed management followed by 3.61 - 3.62t/ha with twice manual weeding at 2^{nd} and 4^{th} week stage of crop. However, combined practice of applying Butachlor @ 2.5 lit/ha, a pre-emergence weedicide at 3 days stage followed by manual weeding at 4th week stage, although produced comparatively lesser grain yield resulted in higher net return of INR 15250.0 and B:C ratio of 1.48 for the lowest cost of weed management (INR 6075.0).



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CONCLUSIONS

Therefore, the above information could advocate improved varieties as well as agromanagement for thriving over the stressful rice growing environment. Negotiating with the water-logged situation in rainfed lowland ecology, ICM and INM of flood water tolerant varieties could be suggested as paramount important factors. While, at water scarcity situation, optimizing irrigation and weed management of deficit moisture stress resistant varieties could be of prime concern sustaining rice production successfully.

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Rice Research and Development for Achieving Sustainable Development Goals

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EFFECT OF TYPE AND METHOD OF PHOSPHORUS SOLUBALISING BIOFERTILIZER APPLICATION ON RICE YIELD

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Rice (Oryza sativa) is the most important grain satisfying more than one-fifth of the caloric requirement of humans globally. Cultivation of rice crop needs external application of fertilizers. At present, to increase rice production, chemical fertilizers and pesticides are applied in abundance in the paddy fields. This led to several environmental problems and hence, sustainable agriculture demands replacement of agrochemicals with the eco-friendly soil microbiota. Phosphorus is the one of the major macronutrients required by plants. A large amount phosphorus existing in soil is insoluble type and not exploitable by the plants . Additionally, phosphorus is applied to the soil in the form of phosphatic fertilizers and a large portion of it is rapidly immobilized and thus become unavailable to plants. The soil microbes, referred to as phosphate solubilizing microbes, having solubilizing ability dissociate these forms and make it available to the plants. These phosphorus solubalising biofertilizers were available both in solid and liquid formulations, hence present study was conducted to find out the comparative effect of liquid and carrier based biofertilizers applied in both soil and foliar methods on rice yields, phosphorus uptake and the soil phosphorus content.

METHODOLOGY:

A field experiment was conducted at Regional Agricultural Research Station, Maruteru during *Kharif*,2016 with an objective to reduce the use of chemical phosphatic fertilizers applied to soil and also to find out the comparative effect of liquid and carrier based biofertilizers applied in both soil and foliar methods on rice yields, phosphorus uptake and the soil phosphorus content. The treatments imposed were, control with three graded doses of recommended phosphorus application (Control,75%,100%) along with two types of bio fertilizers (Liquid and Carrier based) and also with two methods (soil and foliar) of application in a randomized block design. Remaining nitrogen and potassium fertilizers were applied as per recommended dose.(Recommended dose of fertilizers for kharif season 120-80-40 kg NPK per ha). Variety tested under this experiment was MTU-1061.

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RESULTS:

Among all the treatments, treatment with 100% Recommended dose of Phosphorus along with application of Liquid bio fertilizers as soil application recorded highest grain and straw yield (6.24 t/ha and 9.87 t/ha respectively)(Padmshree Patel *et al*,2015) which was on par with 75% Recommended dose of Phosphorus application along with application of both liquid (6.0 t/ha and 9.79 t/ha respectively) and Solid bio fertilizers as soil application (6.10 t/ha and 9.50 t/ ha respectively). Liquid biofertilizer application as foliar spray has got no impact on grain and straw yields of rice. Duarah*et al.*, (2011).

CONCLUSION:

Application of bio fertilizers along with chemical phosphatic fertilizers, reduced the 25% usage of chemical phosphatic fertilizers and also improved the uptake of phosphorus in rice grain and straw. However, while comparing the liquid and carrier based bio fertilizers, both had the similar impact on rice grain and straw yields. However, comparing the method of application of liquid bio fertilizers, application of liquid





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biofertilizers as foliar spray doesn't shown any positive impact with regards to rice yield and phosphorus uptake in low land rice ecosystem of Godavari delta.

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PERFORMANCE OF RICE VARIETIES UNDER DIFFERENT CROP ESTABLISHMENT METHODS IN COASTAL IRRIGATED ECOSYSTEM

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Rice (Oryza sativa L.) is the staple food crop for more than half of the world's population and plays an important role in food security of many rice growing countries. It is grown in more than 100 countries across the globe. In India, it is cultivated over 43.79 m.ha. area with a production of 112.91 m.t. of milled rice and an average productivity of 2578 kg ha-1 (DES, 2018). In Andhra Pradesh, rice is grown in an area of 2.1 m ha with an annual production of 12.0 m.t. and a productivity of 5.70 t ha⁻¹ (Anonymous, 2018). Godavari delta is the Rice bowl of Andhra Pradesh, which is one of major contributors of rice production in the country. The production and productivity of rice growing areas are fluctuating every year due to different biotic and abiotic constraints. Besides climate change, continuous cultivation of rice for longer periods with low system productivity, and often with poor crop management practices, results in loss of soil fertility (Dwivedi et al., 2001) and decline in factor productivity and crop yields in high productivity areas (Yadav, 1998). In Godavari zone, the area under traditional manual transplanted rice is decreasing and farmers looking for alternate planting methods like mechanical transplanting, line transplanting, drum seeder and bengal planting to achieve more productivity due to shortage of man power and cultivation expenses. So, there is need to identify suitable crop establishment method to increase the productivity of rice. Though the mechanical transplanting of rice has been considered most promising option, as it saves labour, ensures timely transplanting, the area under Bengal planting also increasing due to labour constraint in Godavari zone. Bengal planting is similar kind of line planting by maintaining proper row to row and plant to plant spacing. Hence this study is proposed to identify best and suitable method of planting to achieve maximum yields with lead rice varieties of Andhra Pradesh.

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IRC/TM-2/PP-4

METHODOLOGY

A field experiment was conducted during Kharif, 2018 at Regional Agricultural Research Station, Maruteru, West Godavari District, Andhra Pradesh under Deltaic alluvial soils with canal irrigated conditions, to assess the best suitable method of planting to the rice varieties released from this station to get maximum yields under puddled conditions. The experimental site is located at 16.38° N latitude, 18.44° E longitude with an average elevation of 5 m mean sea level altitude. The experiment was laid out in split plot design with four methods of planting (Manual transplanting, Machine transplanting, drum seeder planting and bengal method of planting) and four rice varieties (MTU 1061, MTU 1140, MTU 1075 and MTU 7029) and replicated thrice.

RESULTS AND DISCUSSION

The result of present investigation showed that highest average rice grain yield of 4933 kg/ha was recorded under manual transplanting which was followed by Bengal method of planting with 4483 kg/ ha. Drum seeder method recorded significantly poor yields during kharif, 2018. Method of stand establishment influences the performance of rice through its effect on growth and development. Although, transplanting has been reported to be the best establishment method (Singh *et al.*, 1997). Among rice varieties tested under different crop establishment methods, MTU 1075 responded well and recorded



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Methods/Varieties	MTU 1061	MTU 1140	MTU 1075	MTU 7029	Mean Yield
Manual Transplanting	5733	4200	5267	4532	4933
Machine Planting	3605	3833	4467	3295	3800
Bengal Planting	4825	3540	5450	4117	4483
Drum seeder	3950	2865	3567	2750	3283
Mean	4528	3610	4688	3673	
	C.D.	SE(d)	SE(m)		
Methods	394	161.40	114.13		
Varieties	369	178.53	126.24		
V at same level of M	766	357.06	228.26		
M at same level of V	748	348.81	246.65		

Table. Grain yield (kg/ha) of Rice varieties under methods of planting during Kharif, 2018

significantly higher rice grain yield of 4688 kg/ha which was followed by MTU 1061 with 4528 kg/ha grain yield. Least performance was observed with MTU 1140 rice variety with 3610 kg/ha grain yield. In case of varieties with methods of planting, MTU 1061 was performed better with manual transplanting (5733 kg/ ha) followed by MTU 1075 with Bengal method of planting (5450 kg/ha). Similar results are in confirmed with Lakshmi Bhavani *et.al*, 2017.

CONCLUSION

Manual transplanting methods like line planting or bengal planting are always advantageous under canal irrigated ecosystem and recorded highest rice grain yield if the adequate labour is available and among rice varieties tested MTU 1061 and MTU 1075 are proved to be promising varieties under any kind of crop establishments due to wider adoptability and uniform growth habit.

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IRC/TM-2/PP-5

Indian Rice

OPTIMIZATION OF IRRIGATION AND FERTILIZERS THROUGH DRIP FERTIGATION IN DIRECT SEEDED RICE (ORYZA SATIVA L.)

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Rice is an important staple food crop of India grown over an area of 44 million ha. Water resources for rice cultivation are dwindling and to feed the increasing population there is a greater need for producing more rice with less water resources. Water saving technologies like alternate wetting and drying and maintenance of saturation are working well for the rice. To continue further micro irrigation is the new area where water and nutrients can be more efficiently used for producing rice. Advantages if drip irrigation includes lower water and NPK requirements and efficient utilization of resources for grain production. However, work on micro irrigation and fertigation in respect of water and NPK requirement in rice is very limited. In this connection an experiment was conductedat Agricultural Research Station Gangavathi, Koppaldist, Karnataka, India during 2018-19 to study the effect of different ET levels and fertigation levels on the performance of direct seeded rice using conventional NPK fertilizers.

METHODOLOGY

The drip cum fertigation experiment consisted of three ETc levels as main plot treatments viz., I_1 :Irrigation at 1.2ETc, I_2 : Irrigation at 1.4Etc and I_3 : Irrigation at 1.6ETc and six fertigation levels as sub plot treatments viz., F_1 :75%RDF(112:56:56 kg N,P₂O₅&K₂O/ha)with N applied in five equal splits, F_2 : 75%RDF(112:56:56 kg N,P₂O₅&K₂O/ha)with N applied in tenequal splits, F_3 :100%RDF(150:75:75 kg N,P₂O₅&K₂O/ha)with N applied in five equal splits, F_4 :

100%RDF(150:75:75 kg N,P₂O₅&K₂O/ha) with N applied in tenequal splits, F₅: 125%RDF(188:94:94 kg N,P,O,&K,O/ha) with N applied in five equal splits and F₆: 125%RDF(150:75:75 kg N,P₂O₅&K₂O/ha) with N applied in tenequal splits and were compared with soil application of 100% RDF with flooding as control. The experiment was conducted in split-plot design with three replications. The rice crop variety GNV-10-89 was direct seeded under dry conditions using seed cum fertilizer drill with a line spacing of 20 cm. The crop was manually irrigated and after 20 days of sowing treatments were imposed. 16 mm Laterals were spaced at 80 cm covering four rows and within laterals inbuilt drips were placed at 40 cm spacing. The drippers had an emitting rate of 2lph. Water was regulated as per the treatments. Conventional phosphorous and potassium fertilizers were soil applied at sowing. Conventional nitrogen(Urea) was given by fertigation through ventury. Observations on yield and yield parameters and water recorded, water quantified and water use efficiency worked out.

RESULTS

The numbers of panicles per square meter were significantly higher in the case of ETc 1.6(261) as compared to ETc 1.4 (235) or ETc 1.2 (225). Among fertigation levels applying 125%RDN in five splits recorded significantly higher number of panicles as compared to other levels except 100%RDN applied in five splits. Among the treatment combinations ETc 1.6 x 100%RDN recorded more number of panicles



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followed by ETc 1.6 x 125%RDN. Panicle weight was not significantly influenced by ETc levels. Among the fertigation levels it was significantly higher with 75% RDN applied in five splits followed by 100%RDN applied in five splits. The interaction was non significant. There was no significant difference in test weight for different ETc levels. Among the fertigation levels 125%RDN applied in ten splits recorded higher test weight than other levels.

The grain yield was significantly higher with ETc 1.6 (5.218t/ha) as compared to Etc 1.2(4.624 t/ha) or Etc1.4(4.755t/ha). Among the fertigation levels 125%RDN applied in five splits recorded significantly higher grain yield(5.397t/ha) than other levels but remained on parwith 100%RDN applied in five splits. The interaction effect revealed that among the treatments a combination of 16.ETc x 125%RDN applied in five splits recorded higher grain yield(5.807t/ ha) but remained on par with 1.6 ETcx 100%RDNapplied in five splits(5.580t/ha). These combinations were significantly superior to the control treatment of soil application of 100%NPK with continuous flooding(4.907q/ha). The higher grain yield in the combination of 16.ETc x 125%RDN and 1.6 ETcx 100%RDNwere mainly attributed to significantly higher number of panicles per square meter. The results are in line with Parthasarathiet al (2013) who reported 15-20% higher grain yields with drip irrigation over conventional flooding.

The water requirement was 747,843 and 940 mm in ETc1.2,Etc 1.4 and ETc1.6 respectively as compared to 1260 mm in the case of traditional flooding controlresulting in 40.71,33.10 and 25.40% saving

respectively.Parthasarathi*et al* (2013) and Singh *et al* (2019)reported lower water requirement under drip irrigation compared to flooded irrigation in transplanted rice.

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The water use efficiency did not vary significantly among ETc levels. Mean WUE varied from 6.6 kg/ha.mm in ETc 1.2 to 5.5kg/ha.mm in the case of ETc 1.6. These findings are in agreement withParthasarathi*et al* (2013) and Singh *et al*(2019) who reported higher water use efficiency with drip irrigation than flooded irrigation. Among fertigation levels application of 125%RDN in five splits recorded significantly higher WUE (6.42 kg/ha.mm) than all other levels which however remained on par with fertigation with 100%RDN applied in five splits.

CONCLUSION

The above study can be concluded that under drip fertigation a combination of 16.ETc x 100%RDF(150:75:75 kg N,P₂O₅&K₂O/ha)with P and K soil applied and fertigation of conventional N in five equalsplits at 15 days interval recorded higher grain yield and found optimum for direct seeded rice.

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IRC/TM-2/PP-6

Indian Rice

PERFORMANCE OF RICE VARIETIES UNDER ORGANIC FARMING

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ABSTRACT:

Performance of modern cultivars in terms of yield under organic farming differs from that of conventional system. As the demand for organic rice is increasing, so to maintain high productivity, there is a need to evaluate modern high yielding rice varieties under organic farming systems. Field experiment was carried out using factorial randomized complete block design involving two methods of rice cultivation and four high yielding rice varieties with four replications during E.Kharif,2015. Results of the study revealed that higher yield attributes viz. Plant height, filled grains per panicle, 1000-grain weight, and grain yieldsdwere recorded with inorganic cultivation. There was 11% yield reduction in organic cultivation. Among the varieties tested highest grain yield was obtained with NLR 40024 (8016 kg/ha) which was onpar with NLR 34449 (7975 kg/ha) and NLR 30491(7772 kg/ha) and the lowest grain yield was obtained with NLR 33358 (6878 kg/ha)

INTRODUCTION

Organic farming is gaining momentum during recent times due to awareness of people towards environment and food safety.Rice is the staple food crop of world after wheat and the demand of organic rice is increasing due to its export potential.There is always a continuous search for agronomic improvement to optimize farming system under organic farming and needs suitable varieties to realise its potential (Kokare et al., 2012).Despite the potential benefits of organic farming in terms of better soil health and quality of produce, maintenance of high yields is one of major challenge under organic farming systems (Tilman et al., 2002).Modern cultivars have been selected by Plant breeders under conventional systems and they may notperform well under organic farming systems where they are grown in stressed environment without addition of external inputs that is entirely different to those in which they were selected (Ceccarelli, 1996; Murphy et al., 2007). So, there is a need to select varieties for organic farming which is believed as a stressed environment as crops are not supplied with chemicals for either supplying nutrients or to protect the crop from pests and diseases.

MATERIALS AND METHODS:

Field experiment was carried out at Agricultural Research Station, Nellore during E.Kharif, 2015. The soil of the experimental site was sandy clay loam with pH: 8.1; electrical conductivity: 0.5 dS/m; low in organic carbon (0.45%), low in available N (152 kg/ha), high in available P (97 kg/ha), medium in available K (258 kg/ha) and high in available S (30.8 kg/ha). The experiment was set up in a factorial RBDdesign with two factors namely F₁: cultivation methods and F₂: rice varieties. F₁ includes cultivation methods namely C₁: Organic and C2: in organic and F2 includes rice varieties namely V₁: NLR 34449, V₂: NLR 30491, V₃: NLR 40024 and V_4 : NLR 33358 which were replicated four times. C1: Organic package includes Soil incorporation of FYM @ 10 t/ha, Incorporation of green manure (dhaincha @ 30 kg/ha seed rate), Application of vermicompost @ 1 t/ha at 10 DAT, Azospirillum& PSB each @ 5 kg/ha (in 2 equal splits) at basal and 15 DAT and neem cake (a) 500 kg/ha in two equal splits at basal and 15 DAT and crop protection was followed by spraying of neem oil @ 5 ml/l and Psuedomonas fluorescence @ 4ml/l as and when required. Inorganic





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Treatments	Pl.ht(cm)	No.of	Panicle	Filled	Test Wt	GrainYield
		panicles/hill	Length(cm)	Grains/panicle	(g)	(kg/ha)
Cultivation practice						
Organic	77.6	8.4	19.2	110	19.9	7211
Inorganic	81.9	8.7	19.7	118	20.8	8109
Sig	**	NS	*	NS	*	* *
P value	0.005	0.617	0.047	0.061	0.038	0.004
Rice varieties						
NLR34449	71.4 ^b	9.0	18.4 ^b	129ª	17.2 ^d	7975 ^a
NLR30491	87.3ª	8.3	20.2ª	113 ^b	21.1 ^b	7772ª
NLR40024	74.3 ^b	8.6	18.9 ^b	115 ^b	19.5°	8016 ^a
NLR33358	86.1ª	8.4	20.2ª	101°	23.7ª	6878 ^b
Sig	**	NS	**	**	**	*
P value	0.000	0.710	0.000	0.002	0.000	0.022
Interaction						
Sig	NS	NS	*	NS	NS	*
P value	0.483	0.815	0.957	0.628	0.366	0.001

Table: 1 Yield attributes and yield of rice varieties under organic and in organic farming (Early kharif- 2015)

method includes RDF: 120:60:40 N:P₂O₅; K₂O kg/ha and plant protection includes spraying of cartap hydrochloride and propiconazole as and when required. The crop was transplanted with a spacing of 15x10 cm spacing.Observations were recorded and the data was subjected to statistical analysis.To control weeds, two hand weedings were done at 20 days after transplanting (DAT) and 40 DAT.

RESULTS AND DISCUSSION:

Highest plant height (81.9 cm), Panicle length (19.7 cm), test weight (20.8 g) and grain yield (8109 kg/ha) was recorded under inorganic method of cultivation when compared with organic cultivation. There was 11% yield decrease with organic method of rice cultivation. Among the varieties tested, highest plant height (86.1 cm), Panicle length (20.2 cm) was recorded with NLR 30491 and NLR 33358 and the highest filled grains per panicle was recorded with NLR 34449 (129) and the highest grain yield was recorded with NLR 40024 (8016 kg/ha), NLR 34449 (7975 kg/ha) and NLR 30491 (7772kg/ha).

CONCLUSION:

During Early kharif (2015), highest grain yield of 8109 kg/ha was obtained in inorganic when compared with organic cultivation (7211 kg/ha). There was 11% yield reduction in organic cultivation. Among the varieties tested highest grain yield was obtained with NLR 40024 (8016 kg/ha) which was onpar with NLR 34449 (7975 kg/ha) and NLR 30491(7772 kg/ha) and the lowest grain yield was obtained with NLR 33358 (6878 kg/ha).

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EFFECT OF AGE OF SEEDLINGS OF RICE VARIETIES UNDER MACHINE TRANSPLANTING

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With the increasing scarcity of the rural labour force, mechanical transplantation has become a prevalent and simplified cultivation method to replace hand transplantation. In India, mechanical transplanters were developed and now popularized among the farmers. Reducing manpower availability for agricultural work and increasedlabor wages for transplanting forced the farmers to go for alternate methods like direct sowing and machine transplanting. Present COVID 19 pandemic situation forced the farmers to transplant rice with machine transplanters. Predominant rice varieties generally grown in Nellore are Nellore mahsuri(NLR 34449), Cotton dorasannalu(MTU 1010) and Samba mahsuri (BPT 5204). Due to different duration groups, different seedling vigor, varieties differ in their growth.Many researchers have demonstrated that the achievement of high grain yield for mechanically transplanted rice requires an optimal seedling age¹. Shen et al. reported that among all agronomic practices influencing grain yield of mechanically transplanted rice, seedling age is the most important factor followed by the use of fertilizer and sowing density². Generally, 15-20 days aged seedlings are recommended for transplanting with machines. Most of the times farmers are not able to prepare the land well in advance due to electricity or labour problems and farmers are transplanting old age nursery. Hence present trial has been taken up to know the age of seedlings for machine transplanting of popularly grown different duration group rice varieties.

METHODOLOGY:

Evaluation of most popularly grown rice varieties in Nellore district during rabi under machine transplanting was taken up at Agricultural Research Station, Nellore during *rabi*, 2019-20. The experiment was conducted in sandy clay loam soil with 0.4 % O.C, 7.93 PH & 0.620 dsm⁻¹. The available nitrogen, Phosphorous and Potassium were 301, 19.48, and 528 kg/ha respectively. Present trial has been taken up in split plot design with three rice varieties as main plots i.e V₁: MTU 1010, V₂: NLR 34449, V₃: BPT 5204 and four age of seedlings as sub plots i.e, A₁: 15 days, A₂: 20 days, A₃: 25 days, A₄: 30 days, replicated thrice. The data collected is analysed in SPSS.

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RESULTS:

Highest plant height (77.6 cm) was recorded with MTU 1010 when compared to NLR 34449 and BPT 5204. Highestnumber of filled grains per panicle (183) and highest grain yield was recorded with NLR 34449 (5428 kg/ha) followed by MTU1010 (4828 kg/ha) and BPT 5204 (4572 kg/ha) which were in turnon par with each other under machine transplanting. Among the age of seedlings tested, plant height was not significantly different with age of seedlings and the highest grain yield (5399 kg/ha) was recorded with transplanting of 20 days aged seedlings and which was inturnonpar with transplanting of 15 days aged seedlings (5333 kg/ha) followed by 25 days aged seedlings (4933 kg/ha). The lowest grain yield (4106 kg/ha) was observed with 30 days aged seedlings in machine transplanting. NLR 34449 when transplanted at 15 days aged seedlings recorded highest grain yield which inturn on par with 20- and 25-days aged seedlings under machine transplanting. MTU 1010 can be transplanted from 15 to 20 days and NLR 34449 and BPT 5204 can be transplanted from 20 to 25 days aged seedlings. Under delayed situations, NLR 34449 and BPT 5204

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Treatments	Pl.ht	No. of	PanicleLength	Filled	Test	GrainYield
	(cm)	panicles/ hill	(cm)	Grains/panicle	Wt (g)	(kg/ha)
Rice varieties						
MTU 1010	77.6 ^a	18	20.8 ^b	115°	20.1ª	4828 ^b
NLR 34449	71.5 ^b	17	20.5 ^b	183 ^a	13.8 ^b	5428ª
BPT 5204	72.4 ^b	16	22.0ª	169 ^b	14.4 ^b	4572 ^b
Sig	**	NS	**	**	**	* *
P value	0.000	0.463	0.000	0.000	0.000	0.000
Age of seedlings						
15 days	73.0	17	20.5 ^b	152	17.1ª	5333ª
20 days	73.4	19	21.0 ^{ab}	149	17.9ª	5399ª
25 days	73.9	16	21.7 ^a	163	15.4 ^b	4933 ^b
30 days	74.8	16	21.1 ^{ab}	158	14.9 ^b	4106 ^c
Sig	NS	NS	*	NS	**	* *
P value	0.545	0.199	0.04	0.223	0.000	0.000
Interaction						
Sig	NS	NS	NS	NS	NS	NS
P value	0.405	0.556	0.08	0.072	0.518	0.368

can also be transplanted up to 30 days with machine transplanters.

CONCLUSION:

Among the three rice varieties (NLR 34449, MTU 1010 and BPT 5204), highest grain yield was recorded with NLR 34449 and among the age of seedlings, the highest grain yield was recorded with transplanting of 20 days aged seedlings which inturn on par with transplanting of 15 days aged seedlings under machine transplanting.

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IRC/TM-2/PP-8

Indian Rice

MANAGEMENT OF WEEDS IN DRUM SEEDED RICE THROUGH SEQUENTIAL APPLICATION OF HERBICIDES

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In recent years, rice (Oryza sativa L.) production systems are undergoing several changes and one of such changes is shifting from transplanted rice to direct sown rice due to increased cost of labour and non availability of labour during peak periods of agricultural operations. Sowing of sprouted rice seeds in wet puddled soils offers an attractive alternative and labour saving technique for stand establishment to the traditional transplanting. Wet seeded rice is gaining momentum in India and it have the advantages of quick and easier planting, reduces labour requirement and increased water use efficiency. Wet seeding in puddled soil is done by using drum seeder. However, direct seeded rice is associated with several constraints like heavy weed infestation, water management immediately after sowing and lack of perfect levelling etc. Among them, heavy infestation of heterogenous weed flora becomes the biggest biological constraint as rice and weed seeds germinate simultaneously. The yield loss due to unchecked weed growth was reported upto30-48% in direct seeded rice (Naseeruddin and subramanyam, 2013). The failure and success of the drum seeded rice depends on weed and water management practices. Hence, use of sequential application of pre-fb post-emergence herbicides or pre-emergence herbicides fb manual weeding could be more convenient in containing the weed menace.By keeping above information in view, the present investigation was carried out to study the optimization of suitable weed management practices for drum seeded rice under Southern dry zone of Karnataka.

METHODOLOGY

A field experiment was conducted during Kharif season of 2014 and 2015 to know the efficacy of sequential application of herbicides in drum seeded rice under Southern dry zone of Karnataka at Zonal Agricultural Research Station, V.C. Farm, Mandya in red sandy loam soils. The experiment was carried out in a complete randomizedblock design comprising of eight treatments and 3 replications. The sowing of rice variety 'MTU-1001' was done through 8 row drum seeder with a row to row spacing of 20 cm on well puddled and levelled field in June 2014 and 2015 with a seed rate of 62.5 kg/ha. The crop was fertilized with 100:50:50 kg N:P2O2:K2O/ha and 50% nitrogen, entire dose of phosphorous and potassium was applied as basal in addition to zinc sulphate @ 25 kg/ha. The remaining 50% of the nitrogen was top dressed at two equal splits at tillering and panicle initiation stage. Preemergence herbicides were mixed with sand 100 kg/ ha and applied uniformly in the field on 5 DAS. A thin film of water was maintained at the time of preemergence herbicide application. The post-emergence herbicides were sprayed at 3-4 leaf stage of weeds by using knapsack sprayer fitted with deflectornozzle mixed with water 750 liter/ha. Mechanical weeding with two row cono weeder was carried out at 40 DAS as per the treatments. Hand weeding was carried out as per the treatment schedule. All other agronomic and plant protection measures were adopted as per the recommended packages of UAS, Bangalore. Bensulfuron-methyl 0.6% + pretilachlor 6% GR is





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combination of two herbicides and is in granular form and found safe to rice and sold in the trade name of LondaxPower.Standardpackage of practices were adopted andgrowth, yield parameters and yield were measured and estimated using standardprocedures.

RESULTS

Among the weed management treatments, hand weeding thrice at 20, 40 and 60 DAS recorded significantly lower weed density (13.6 and 23.75/m² at 30 and 60 DAS, respectively) and weed dry matter production (2.66 and 5.75 g/m² at 30 and 60 DAS, respectively) as compared to other treatments in the two year pooled data. However, it was at par with pre-emergence application of bensulfuron-methyl 0.6% + pretilachlor 6% GR 10 kg/ha*fb* post-emergence application of bispyribac sodium 25 g/ha (15.7 and 23.85/m² weed density; 2.57 and 7.00 g/m² weed dry weight respectively at 30 and 60 DAS). While, the lowest weed density and dry weight of weeds were observed in weed free check and the highest was recorded in weedy check. The crop yield is directly proportional to weed control efficiency. As a result of effective control of weeds hand weeding thrice (86.10 and 82.80% at 30 and 60 DAS, respectively) and sequential application of bensulfuron-methyl 0.6% + pretilachlor 6% GR 10 kg/hafb post-emergence application of bispyribac sodium 25 g/haregistered higher weed control efficiency (86.55 and 78.65% at 30 and 60 DAS, respectively) among the weed management treatments.

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The highest grain yield was observed in weed free check. While, the lowest was recorded in weedy check.Unweeded check registered 50.88% reduction in grain yield as compared to weed free check owing to sever competition offered by uncontrolled weeds for nutrients, soil moisture, space and light.Among the weed managementtreatments,hand weeding thrice at 20, 40 and 60 DAS recorded significantly higher grain yield(5506 kg/ha) as compared to other treatments in the two year pooled data. However, it was at par with pre-emergence application of bensulfuron-methyl 0.6% + pretilachlor 6% GR 10 kg/hafb post-emergence

 Table 1: Influence of weed management practices on weed parameters, yieldandyield attributes and in drum seeded rice (Pooled data of two years)

Treat.	Total weed of (No./m ²)	density	Total weed d weight (g/m ²	ry)	WCE (%		No. of tillers at	Grain weight/ panicle (g)	Grain yield (kg/ha)
	30 DAS	60 DAS	30 DAS	60 DAS	30 DAS	60 DAS	harvest	-	
T ₁	4.88 (23.35)	5.85 (33.8)	2.17 (4.25)	3.02 (8.70)	77.95	73.70	14.53	2.63	5037
T ₂	4.17(16.9)	5.05 (25.05)	2.28 (4.71)	2.98 (8.38)	75.45	74.45	14.98	2.78	5173
T ₃	4.63 (21.2)	5.70 (32.05)	1.94 (3.29)	2.84 (7.57)	82.75	77.15	15.21	2.99	5287
T ₄	4.00(15.7)	4.93 (23.85)	1.75 (2.57)	2.73 (7.00)	86.55	78.65	15.50	3.21	5429
T ₅	7.90(61.9)	8.41 (70.15)	3.33 (10.65)	4.50 (19.80)	44.45	40.85	12.73	1.48	2979
T ₆	3.74(13.6)	4.89 (23.75)	1.78 (2.66)	2.50(5.75)	86.10	82.80	15.80	3.50	5506
T ₇	0.71 (0.00)	0.71 (0.00)	0.71 (0.00)	0.71 (0.00)	100.00	100.00	16.55	3.72	5764
T ₈	10.59(112.1)	11.36(70.6)	4.44 (19.23)	5.85 (33.90)	0.00	0.00	9.98	1.60	2831
S.Em±	0.18	0.20	0.11	0.17	-	-	0.63	0.09	183
CD(P=0.05)	0.54	0.60	0.32	0.51	-	-	1.90	0.28	556

T1-Pyrazosulfuron ethyl @ 25 g a.i. ha-1 (PRE) + passing of one conoweeder at 40 DAS, T2 - Bensulfuron methyl 0.6% + Pretilachlor 6% GR@ 10 kg ha-1 (PRE) + passing of one conoweeder at 40 DAS, T3 - Pyrazosulfuron ethyl @ 25 g a.i. ha-1 (PRE) + Bispyribac sodium @ 25 gm a.i. ha-1, T4 - Bensulfuron methyl 0.6% + Pretilachlor 6% GR@ 10 kg ha-1 (PRE) + Bispyribac sodium @ 25 gm a.i. ha-1, T5 - Bispyribac sodium @ 25 gm a.i. ha-1 (EARLY POST), T6 - Hand weeding thrice at 20, 40 and 60 DAS, T7-Weed free check, T8 - Weedy check





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application of bispyribac sodium 25 g/ha (5429 kg/ha) (Table 1). These results were in accordance with Dhanapal*et al.* (2018). This increased in above treatment was mainly attributed to enhanced weed attributes *viz.* number of tillers per plant and grain weight per panicle due to effective control of weeds throughout the critical crop growth period.

CONCLUSION

In drum seeded rice, application of bensulfuron-methyl 0.6% + pretilachlor 6% GR 10 kg/ hafb post-emergence application of bispyribac sodium 25 g/hafound most effective and economical in controlling the weeds.

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Theme - II : Sustainable rice farming

PRODUCTION AND PRODUCTIVITY OF AEROBIC RICE AS INFLUENCED BY SOURCES AND LEVELS OF PHOSPHORUS WITH BIO-FERTILIZER

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Aerobic rice is gaining importance as one of the alternative methods of rice production for effective utilization of resources in recent years. Aerobic rice is a production system in which potentially high yielding, fertilizer responsive rice varieties are grown in fertile aerobic soils that are non-puddled and have no standing water. Supplementary irrigation, however, can be given in the same way as to any other upland cereal crop. Phosphorus (P) is considered as a major constraint for successful crop production in India, particularly for rice because finite reserve of this non-renewable resource is getting exhausted rapidly and on other hand, P deficiency is becoming wide spread with high intensity cropping. Phosphorus deficiency has been recognized as one of the main limiting factor in upland rice. Again, naturally occurring immobilization of P by microbes can help ration plant available P to crops over the course of a growing season. Dry and aerobic soil can reduce the indigenous supply of phosphorus (P), hence the application of fertilizer P can be more critical for aerobic rice. Chemical P fertilizer is the main source of plant available P in agricultural soils, but almost 75 to 90% of added P fertilizer is precipitated by iron, aluminum and calcium complexes present in the soils (Turanet al., 2006). The P diffusion to plant roots may be too low to acquire the requirements of crops if soils have less P solubility and a high P fixation capacity (Hoberget al., 2005).

Thus, management of phosphorous is an important issue in aerobic rice to be addressed to have a sustainable higher productivity of rice. With this background, an investigation was carried out to study the production and productivity of aerobic rice using different sources and levels of phosphorus with biofertilizer.

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METHODOLOGY

A field experiment was carried out in the Instructional-cum-Research (ICR) Farm, Assam Agricultural University, and Jorhat during autumn season of 2016. The treatment consisted of three phosphorus sources viz., single super phosphate, diammonium phosphate and rock phosphate, three doses of phosphorus viz., 10kg P2O5ha-1, 20 kg P₂O₅ha⁻¹ and 30 kg P₂O₅ha⁻¹ and two biofertilizer treatment i.e. without biofertilizer and Azospirillum PSB. One absolute control was included for comparison. The experiment was laid out in factorial randomized block design (RBD) with three replications. The soil of the experimental site was sandy loam in texture, medium in available N (285.36 kgha-¹), P₂O₅ (22.85 kgha⁻¹) and K₂O (138.04 kgha⁻¹) and organic carbon (0.62%) with pH value of 5.2. The rice variety "Inglongkiri" was shown on 11th March, 2016 and harvested on 08th July. 2016. The rainfall received during the crop season was only 1330.9mm. The weekly average maximum temperature ranged from 24.9 to 32.9°C and minimum temperature 16.0C to 26.1°C, respectively.

RESULTS

Among the different sources of phosphorus, rock phosphate recorded the highest values of plant height, number of total tillers and dry matter accumulation at all the growth stages of aerobic rice. In most of the yield attributing characters *viz.*,number of effective tillers per meter square, number of grains per panicle, number of filled grains per panicle and per



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cent filled grains rock phosphate exhibited significantly highest values but was at par with single super phosphate. The highest grain (2619 kg ha⁻¹) and straw (4705 kg ha⁻¹) yield of aerobic rice was observed with application of phosphorus through rock phosphate.

Among the doses, application of $30 \text{ kg P}_2\text{O}_5\text{ha}^{-1}$ ¹recorded significantly higher plant height, population (number of tiller m⁻²) and dry matter accumulation over 10 and 20 kg P₂O₅ha⁻¹. The highest number of effective tillers per meter square was observed under 30 kg P₂O₅ha⁻¹which was statistically at par with 20 kg P₂O₅ ha⁻¹and significantly higher over the 10 kg P₂O₅ha⁻¹. Application of 30 kg P₂O₅ha⁻¹registered significantly higher number of grains panicle-1 and number of filled grains panicle-1 than both 10 and 20 kg P₂O₅ha⁻¹. The highest grain and straw yield of 27.43 qha⁻¹ and 49.39 qha⁻¹, respectively was obtained at 30 kg P₂O₅ha⁻¹.

In case of bio-fertilizer, the plant growth parameters like plant height, plant population in terms of tiller number and plant dry matter accumulation observed were higher in bio-fertilizer treatment i.e. Azospirrilum + PSB than without bio-fertilizer treatment.Biofertilizer treatment(Azospirillum+PSB) recorded significantly higher number of effective tillers m⁻², number of grains panicle-¹ and number of filled grains panicle-¹ than that of without biofertilizer.Significantly higher grain (26.17 qha⁻¹) and straw (48.21 qha⁻¹) yield noted with Azosprillum + PSBtreatment proved it to be superior towithout biofertilizer treatment with an increase of 14.42 % and 20.04% in grain and straw yield, respectively.

Indian Rice

CONCLUSION

Among the three sources of phosphorus, in rock phosphate applied treatments, the crop performed better in terms of growth, yield and phosphorus use efficiency. In case of various application doses , application of $30 \text{ kg P}_2\text{O}_5\text{ha}^{-1}$ resulted in higher grain and straw yield. Similarly, in bio-fertilizer treatments, Azospirillum + PSB recorded better growth, higher values of yield attributes and yield as compared to without bio-fertilizer treatment. Thus, application of rock phosphate at the rate of $30 \text{ kg P}_2\text{O}_5 \text{ ha}^{-1}$ inoculated with Azospirillum + PSB appeared to be the best treatment combination so far the yield performance of aerobic rice is concerned.

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Rice Research and Development for Achieving Sustainable Development Goals

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Indian Rice

NUTRIENT PRESCRIPTIONS IN RICE (ORYZA SATIVA L.)

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ABSTRACT

Rice (Oryza sativa L.) is the dominant cereal crop in many developing and Asian countries and is a staple food for more than half of the world population. Rice is a staple food crop not only in India but also in entire South Asia. Of the total rice (Oryza sativa L.) production in the world, more than 90 % is in Asia, and it is increasing annually at the rate of 2.7 % (IRRI, 1986). Rice is cultivated in 111 countries of all continents, except Antarctica. India and China are the leading producers as well as consumers of rice. In India, it is grown in an area of 43.9 m ha with a production of 99.24 m t and productivity of 2494 kg ha⁻¹. For enhancing rice productivity from the existing rice growing areas, which have been under rice cultivation over decades, soil fertility monitoring and management need to be strengthened. During the last two decades, due to crop intensification and increased availability of chemical fertilizers at subsidized prices and decreased availability of organic sources of nutrients resulted in substantially declined use of organic manures such as farm yard manure. Organic manures also enhance fertilizer use efficiency when applied in conjunction with inorganic fertilizers (Baskar, 2003). Integrated approach of nutrient supply is gaining importance as it reduces the excessive use of inorganic fertilizers and sustains the crop productivity by improving soil health.Application of fertilizers without information on soil fertility status and nutrient requirement of crop causes adverse effects both nutrient toxicity and deficiency either by over use or inadequate use, respectively (Ray et al., 2000).

Managing the location specific variability in nutrient supply is key strategy to overcome the current mismatch of fertilizer rates and crop nutrient demand in irrigated rice environments. Soil test based application of plant nutrient helps to realize higher response ratio and benefit- cost ratio as the nutrients are applied in proportion to the magnitude of the deficiency of a particular nutrient and the correction of the nutrients imbalance in soil helps to harness the synergetic effects of balanced fertilization (Rao and Srivastava, 2000). Location specific fertilizer recommendations are possible for soils of varying fertility, resource availability and levels of targeted yield for similar soil classes and environment. Field specific balanced amounts of NPK could be prescribed based on crop estimates of the indigenous supply of NPK and by modelling the expected yield response as a function of nutrient interaction.

METHODOLOGY:

The experiment was conducted with variety BPT-5204 in a Randomized Block Design with ten treatments and three replications during *kharif* season, The experimental soil was clay loam in texture, slightly alkaline in reaction, non saline, low in available nitrogen, low in organic carbon, high in available phosphorus and potassium. The application of nutrients was done following the soil test based fertilizer recommendations as per the treatment. Target yield fertilizer recommendations were based on using the target yield equations developed for Krishna Godavriagro ecological region.



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RESULTS:

Results indicated that performance of the soil test based fertilizer recommendation with 10 tha-1 FYM application was found superior in terms of total pooled rice grain yield, Total N-P-K nutrient recovery percentage and nutrient use efficiency (5570 kg/ha, 33.3%, 68.4%, 37.3% and 33.71% respectively). Twenty five days old seedlings were used for transplanting. By the time of transplanting, soil test based fertilizer recommendation with 10 t ha-1 FYM application crop started flowering. Hence, soil test based fertilizer recommendation with 10 t ha⁻¹ FYM application practice is the best method for N-P₂O₅-K,O of Rice. Among the nutrient management practices, grain yield, straw yield and harvest indices (5570, 6268 kg/ha and 47.30%) were significantly higher with combined application of organic and inorganic fertilizers (10 t ha-1 FYM + 156-42-28 N-P₂O₅-K₂O kg ha⁻¹) compared to sole application of either inorganic or organic fertilizers. Fertilizer use efficiency (FUE) was significantly the highest with application of 5.5 t ha⁻¹ target yield recommendation with FYM compared to all other treatments. Application of soil test based fertilizer recommendation recorded

the highest returns per rupee investment and found significantly superior to the rest of the treatments.

Indian Rice

CONCLUSION:

Overall soil test based fertilizer recommendation with FYM followed by soil test based fertilizer recommendation alone found superior in increasing growth, yield and maximum returns in rice.

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PERFORMANCE OF RICE (ORYZA SATIVA L.) UNDER DIFFERENT DOSES AND COMBINATIONS OF HYDROGEL

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Rice (Oryza sativa L.) is one of the three major food crops of the world. Globally India stands first in rice area and second in rice production after China. Within the country, rice occupies one quarter of the total cropped area, contributes about 40-43 percent total food grain production and continues to play a vital role in the national food and livelihood security system.Rice is a high water demanding crop. Water requirement of rice is approximately 900-2500mm. Availability of water influences the growth and yield characters of rice. By considering above factors water is considered as most important input for rice growth, so from soil and water conservation point of view the main objective is to efficiently utilize the available water resources. In order to maintain water in the soil for longer period after rainfall or irrigation some additional materials such as soil conditioners, organic matter areadded to the soil. Soil conditioners are natural and synthetic in nature, they contribute significantly to provide reservoir of soil water to plant on demand in the upper layers of the soil where root systems normally develop. The synthetic water holding substances are known as super absorbent polymers(SAP). The SAP's hold water more than its weight. These polymers increase soil physical environment especially aggregate stability, infiltration rate, water retention capacity and aeration porosity of soil to create more porous and favorable environment for better root growth. SAP had been applied to stabilize soil structures, causing an increase in infiltration and a decrease of water usage and soil erosion in the furrows of fields (Khadem, S.A., 2010).Hydrogel is one of the SAP. Hydrogel polymer can absorb pure water up to 500-600 times their weight forms gel. These are used to increase water holding

capacity of soil and forms gel. Hence hydrogel help to reduce to water stress of plants resulting increased growth and plant performance. Farm yard manure (FYM) is the major source of organic matter in field crops. The composition of well decomposed farm yard manure contains 0.5 % N 0.2% P and 0.5% K and also small amounts of micronutrients. It helps to increase crop production and improve soil physical properties. The vermicompost is nothing bur earthworm castings consisting of 3%N, 1%P, 1.1%K and trace amounts of micronutrients. It also shows considerable diversity in physical, chemical, biological properties and their effectiveness in crop production depends upon the agro-biological environment where the crop is grown. Keeping this in view, pot culture experiment was conducted with an objective to study the effect of different doses and combinations of Hydrogel on growth and yield performance of rice.

METHODOLOGY

A Pot culture lab study was conducted during *kharif*, 2018 at Rajiv Gandhi South Campus, Banaras Hindu University, Mirzapur to study the effect of hydrogel and its combination with FYMand Vermicompost on growth and yield of rice crop. Experiment was laid out in Completely Randomized Design and replicated thrice with twelve different treatments of Hydrogel. Different doses of hydrogel from 2.5 kg/ha to 7.5 kg/ha and also combination with FYM @ 10 t/ha and Vermicompost @ 5 t/ha. TheHydrogel, FYM and vermicompost were incorporated directly before the sowing of seed. The seed was directly sown in the pot and recommended dose of inorganic fertilizer were applied. The nitrogen

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Table, Rifect of HAdrodel, R	y vi and vermicomnos	TIVE INDORNWIN	and vield of rice

Treatments	Plant height	Root length	No. of panicles	Test weight	Grain yield	Straw yield
	(cm)	(cm)	per pot	(g)	(g/pot)	(g/pot)
T1 :Control	70.33	14.92	16.33	20.10	19.32	47.52
T2 :2.5 kg/ha Hydrogel	72.00	16.56	18.67	20.33	20.68	52.41
T3 :5 kg/ha Hydrogel	78.19	17.75	19.33	20.53	21.98	52.75
T4 :7.5 kg/ha Hydrogel	78.53	19.58	21.33	20.60	25.64	62.97
T5:2.5 kg/ha Hydrogel+FYM@10 t/ha	79.40	19.69	21.33	20.73	27.61	65.72
T6:5 kg/ha Hydrogel+FYM@ 10 t/ha	79.75	21.22	21.33	20.90	30.70	74.00
T7: 7.5 kg/ha Hydrogel+FYM@10 t/ha	80.92	22.22	21.67	21.13	33.67	74.95
T8: 2.5 kg/ha Hydrogel+VC @ 5 t/ha	83.17	22.87	22.67	21.27	38.34	75.15
T9: 5 kg/ha Hydrogel+VC@ 5 t/ha	84.17	22.89	23.33	21.40	39.20	84.91
T10: 7.5 kg/ha Hydrogel+VC@ 5 t/ha	86.50	23.31	24.33	21.77	46.89	95.39
S.E.m±	1.278	1.054	1.109	0.288	3.090	6.889
C.D. (P=0.05)	2.671	2.203	2.318	NS	6.459	14.398

and potash were applied in splits (Panicle initiation and heading). Entire phosphatic fertilizer applied as basal. In order to draw reliable conclusions, the data obtained on plants were statistically analyzed by using the method described by Gomez, (1984).

RESULTS AND DISCUSSION

Plant height is one of the most important characteristics indicating nutrient absorption capacity as well as plant health. It is evident that there was significant increase in plant height recorded at harvest time. No. of panicles per pot, grain yield, straw yield per pot and root length of plant shows significant variation. Among all the treatments, hydrogel @ 7.5 kg ha⁻¹along with vermicompost @ 5 t/ha combination recorded higher values of growth parameters and grain yield (46.89 g/pot) compared to all other treatments and also over control (19.32 g/pot). The performance of hydrogel in combination with either FYM or vermicompost was found superior over Hydrogel alone doses. This hydrogel helps to increase the water availability to the crop and also reduces the loss of available nutrients and vermicompost comprises the more nutrients. Application of hydrogel significantly improved the plant height and no. of fertile tillers; Similar results were also reported by Rehamanet al. (2011) and Yezdaniet al. (2007).

CONCLUSION

From the present research study findings stated that, application of Hydrogel @ 7.5 kg/ha in combination with 5 t/ha Vermicompost was found good and produced higher growth and yield of rice under normal conditions, it increased the nutrient content and uptake of nutrients in straw and grain. Hence application of 7.5 kg ha⁻¹ hydrogel in combination with 5 t ha⁻¹ vermicompost may be suggested to apply in direct seeded rice for obtaining better yield.

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EFFECT OF NUTRIENT MANAGEMENT PRACTICES ON PADDY

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Results of several long term fertilizer trials conducted in different countries have demonstrated the favorable effects of combined application of chemical fertilizers and organic manures on crop yields and soil eco-systems. These results have conclusively shown the need for meeting the nutrient requirements of plants at least partly through organic manures. This helps ultimately in achieving the goal of environmentally benign sustainable agriculture. The nutrient leaching losses are less because of more intense microbial activity leading to mineralization, immobilization and greater turnover of nutrients in soil by microbes. Exploitation of natural resources in the form of farm and animal waste, decomposed organic matter and crop specific microbial inoculants may replenish the soil by returning its lost share of organic matter and reverse the process of yield stagnation. Rice being a staple crop is widely consumed by Indian community. Its production needs to be increased by another 40 % to provide food security to the growing population by 2030.

METHODOLOGY

A field experiment was conducted on effect of nutrient management practices on paddy duringKharif and Rabi seasons from 2016-17 to 2019-2020 at Regional Agricultural Research Station, Maruteru. The experimental area was under sub tropicalclimateThe experiment was laid out in randomized block design with seven treatments replicated thrice.The recommended dose of fertilizers for kharif season 90: 60 : 60 kg N, P,K /ha and for Rabi 180:90:60 kg N :P : K /ha The treatments consists of control, 100% RDF, 50% RDF + organic farming, organic farming, natural farming, 50% RDF + Natural farming and 100 % RDF + organic farming + natural farming. Recommended dose of fertilizers included application of urea as N source SSP as phosphorus source and MOP as K source. Urea applied in three splits as basal, tillering and panicle initiation stage, SSP applied as basal dose and potassium in two splits at maximum tillering and panicle initiation stage. Organic farming practices included incorporation of green manures, neem cake and vermicompost @ 500kg/ha in two splits at maximum tillering and panicle initiation stage, FYM @ 10 t/ha and biofertilisers as basal. The natural farming practices included with application of Ghana Jeevamrutham as basal and dravaJeevamrutham spraying at 15 days interval throughout the crop period. The experimental soil was normal in reaction and conductivity, low in available nitrogen, medium in available phosphorus with high potassium content. The tested variety was MTU 1075 (Pushyami) during Kharif and MTU 1121 (Sridruthi) during Rabi season.

RESULTS

The results indicated that the highest grain yield was recorded with the application of 100% RDF along with Organic farming and Natural farming practices which was on par with the application of 100% RDF and significantly higher than control, organic farming and natural farming practices. Application of 50% RDF + Organic farming and 50% RDF along with natural farming practices are on par with each other but was significantly differed with organic farming and natural farming. The nutrient content (N,P,K) in grain and straw did not show any significant difference among the treatments. Uptake of nutrients by the grain and straw also showed significant difference between the application of 100% RDF along with organic and natural farming practices and control, organic farming and natural farming. The available nutrients and organic carbon status was high with the application of 100%





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Pooled data on nutrient management practices on grain and straw yield of paddy during Kharif

Treatments	Grain	Straw
	yield	yield
	(kg/ha)	(kg/ha)
T1-Control	3746	4016
T2-100% RDF	5926	6806
T3-50 % RDF + Organic farming	5545	6561
T4-Organic farming	4661	5834
T5-Natural farming	4323	5279
T6-50 % RDF + Natural Farming	4985	5972
T7-100% RDF + Organic farming +		
Natural Farming	6693	7550
Mean	5025	6002
CV%	4.74	5.09
Sem	137.61	210.24
CD (0.05%)	424.05	647.87

RDF along with organic and natural farming practices and was significantly differed with control, organic and natural farming practices. The microbial population during kharif was more with the application of 100% RDF along with organic and natural farming practices which was significantly higher with control but was on par with the organic farming practices and 50% RDF along with natural farming practices.

CONCLUSION

Application of recommended dose of fertilizers along with organic farming package of practices and natural farming practices is better even though the Pooled data on nutrient management practices on grain and straw yieldof paddy during Kharif

Treatments	Grain	Straw
	yield	yield
	(kg/ha)	(kg/ha)
T ₁ Control	3300	4009
T2-100% RDF	6623	7853
T3-50 % RDF + Organic farming	6016	7467
T4-Organic farming	5595	6964
T5-Natural farming	5169	6241
T6-50 % RDF + Natural Farming	5918	7225
T7-100% RDF + Organic farming +		
Natural Farming	7228	8161
Mean	5478	6846
CV	8.02	9.17
Sem	63.96	82.02
CD	497.11	652.74

cultivation expenses were more when compared to recommended dose of fertilizers.

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INTEGRATED WEED MANAGEMENT IN WET SEEDED RICE -DYNAMICS AND ECONOMICS

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Direct seeding of rice excludes nursery and transplanting which in turn decreases labour requirement and cost of cultivation. Due to shortage of labour during peak periods of agricultural operations and high labour wages, there is a shift from transplanted to direct seeded rice which include wet seeded rice and dry seeded rice. In the state of Kerala, the majority of rice farmers practice wet seeding during kharif season where weeds are the major biotic constraints. Competition due to weeds is more severe in directsown rice due to age similarity of rice and weed seedlings whereas in transplanted rice aged seedlings are able to compete better (Saha, 2008). Also, both the crop and weed emerge simultaneously in wet seeded rice resulting in maximum extent of crop weed competition. Various grasses, sedges and broadleaved weeds compete with crop and cause significant loss to direct seeded rice. The various methods adopted for weed control include hand weeding which cannot be profitably employed as a soul source in direct seeded rice due to its high cost and difficulty in identifying the weeds at initial stage and it necessitate time for attaining the size to be pulled out. Hence suppression of weeds during the initial stage itself by integration of pre-emergence or postemergence herbicide followed by manual weeding need to be tested as an efficient and economical approach to weed management in wet seeded rice.

METHODOLOGY

A field experiment was conducted in the rice fields of Integrated Farming System Research Station (8°47'N,76° 96' E),Karamana, Thiruvananthapuram during *kharif* season extending from June to October 2019. The mean rainfall during the crop growing season was 99.05mm with the soil under the textural class of sandy clay loam. The rice variety Uma (MO-16) extensively grown in Kerala was used in this experiment. The crop was grown and managed in line with the cultivation practices as per the recommendations of Package of Practices (KAU, 2016). Eight weed management practices including preemergence and post-emergence herbicide along with hand weeding were evaluated in a randomized complete block design with three replications. Herbicides included in the study were bensulfuron methyl+ pretilachlor, pyrazosulfuron ethyl, bispyribac sodium, penoxsulam + cyhalofop-p butyl, metsulfuron methyl+chlorimuron ethyl and ethoxysulfuron. The field was thoroughly ploughed, puddled and levelled andthe experimental unit consisted of plots each of size 5m x 4m. The amount of spray volume utilized was 500 L ha-1. Manually operated knapsack sprayer was used for herbicide spraying. Pre-emergence, early post emergence and post emergence herbicide application were done at 5, 15 and 20 DAS respectively followed by hand weeding at 40 DAS. In weed free check, hand weeding was done at 20 and 40 DAS and weedy check plot maintained devoid of weed control practices.

RESULTS

A total of 15 weed species belonging to 14 genera within 10 families were identified across the growing season of rice in the field. Overall, 7 broadleaf weeds (BLW), 3sedges, 4 grass species and one fern were recorded in the field. Based on density and frequency, the dominant weed species were *Sphenocleazeylanica*, *Ludwigia parviflora*, *Bergia capensis* and *Linderniarotundifolia* along with

Indian Rice

IRC/TM-2/PP-13



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Monochoria vaginalis. Sedges associated with the crop were Fimbristylismiliacea, Cyperus difformis and Cyperus iria. Amonggrass weeds Echinochloa colona, Leptochloa chinensis, Isachnemiliacea and Ischaemumrugosum were seen in crop field.Broad leaved weeds dominated the weed flora as they comprised 40 % of the total weed population whereas grasses and sedges accounted for 37% and 23%, respectively. Broad leaved weeds were emerged as early flush and abundant although the density was not significant than sedges and grasses because of the previous seed bank of the dominant weed Sphenocleazevlanica and appropriate moisture content of the soil as the field was non-flooded for the first month of seeding. At 45 DAS, all categories of weeds appeared in equal proportion with grasses dominating the flora. The third flush of weed was counted at 60 DAS after the hand weeding on 40 DAS, mostly characterized by grassesvery similar to rice like weedy rice and Leptochloa chinensis. Broadleaved weed such as Ludwigia parviflora emerged significantly at a later phase in a continuously flooded situation and appeared throughout the seasonreplacingSphenocleazeylanicawhich began decreasing continuously.

At 15 DAS, pre-emergent spraying of bensulfuron methyl+pretilachlor @60+600g ha⁻¹ at 5 DAS fb HW at 35-40 DAS resulted in better weed control efficiency (WCE) of 99.28 % which is statistically on par with pyrazosulfuron ethyl @ 25g ha⁻¹ at 5 DAS fb HW at 35-40 DAS recording WCE of 98.16 %.At 45 DAS, penoxsulam+cyhalofop butyl 6 % OD (*a*) 150 g ha⁻¹ at 20 DAS fb HW at 35-40 DAS recorded better WCE of 99.54 % which is significantly at par with metsulfuronmethyl+chlorimuron ethyl (*a*) 4gha⁻¹ at 20 DAS fb HW at 35-40 DAS with a WCE of 98.98%. In weedy check (T_8), higher yield reduction of 59.75 % was noticed.

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From the results, it was evident that weed management practices had a significant influence on the benefit: cost ratio of wet seeded rice cultivation. Plots treated with bensulfuron methyl +pretilachlor @60+600g ha⁻¹at 5 DAS fb HW at 40 DAS recorded higher B: C ratio of 1.83. This was followed by penoxsulam + cyhalofopbutyl 6% OD at 150 g ha⁻¹at 20 DAS followed by hand weeding at 40 DAS with a B:C ratio of 1.77. The extent of yield reduction due to presence of weeds in wet seeded rice was estimated to be 57 per cent. Hand weeding twice at 20 and 40 DAS realized a B: C ratio of 1.50 while weedy check (T_8) recorded a lower B: C ratio of 0.97.

CONCLUSION

Application of bensulfuron methyl + pretilachlor @ 60+600 g ha⁻¹at 5DAS followed by hand weeding at 40 DAS turned out to be the most economic weed management practice with a higher B:C ratio of 1.83.

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MODELLING SOIL WATER BALANCE IN SUB-SURFACE DRIP IRRIGATED RICE UNDER CA USING HYDRUS-2D

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Rice is the principal crop of dominant ricebased systems and staple food of the country sharing 24% of gross cropped area (195Mha), 42% total food grain production and 45% of total cereal production in India (Agricultural statistics division, 2017). The declining ground water table, water scarcity and rainfall aberration has put forth a big question mark for the cultivation of traditional water guzzling puddled transplanted rice (PTR). In the conventional tillage system (CT), repeated tillage and burning of crop residue are the two major causes of concern for soil health deterioration and environmental pollution; the key indicators of unsustainability. Conservation agriculture (CA) based new innovative agronomic management practices like zero-tillage (ZT), direct seeded rice, residue recycling, precision water and nutrient management etc. have been used as an alternative to CT. Therefore, to improve crop productivity and farmers' profitability and looking to the constraints of water shortages in future, it is imperative to put more efforts on re-designing/diversify rice-based systems through developing efficient and remunerative CAbased practices. One such practice for water saving is bundling of conservation agriculture (CA) with subsurface drip irrigation termed as CA+ and has immense benefits over CA alone and conventional tillage-based flood irrigated (PTR/farmer's practice) rice. Further, direct seeded rice with CA+ have twin benefit of improvement in crop productivity vis a vis soil health and is a possible alternative to PTR in rice-wheat cropping system belts. Irrigating the crop plant with drip system can also tackle the water scarcity problem and can enhance the water use efficiency. Although many researchers have reported higher crop productivity and less water use under sub-surface drip irrigation (SSDI) system, but the information accounting the complete soil water balance in high water requiring crop like rice grown under SSDI in CA are not available. That's why the present experimentation was framed for partitioning of soil water into various input (rainfall, irrigation and initial soil moisture) and output (RWU, evaporation and drainage) components to reckon the soil water balance (SWB) using HYDRUS-2D model.

METHODOLOGY

A rice variety PR 126 was sown during Kharif, 2019 at experimental farm of Borlaug Institute for South Asia (BISA)-CIMMYT, Ladhowal, Punjab, India. The experiment was framed in randomized complete block design with 9 treatment combinations and replicated thrice. Sub-surface drip fertigation was pre-installed (4 years before) with lateral at 15cm fitted with in line emitter. The treatments under CA+ system were zerotilled direct seeded rice (ZTDSR) + sub-surface drip irrigation: without N (SSD-N0), 50% of recommended dose of N (RDN) (SSD-N50), 75% of RDN(SSD-N75) and 100% of RDN(SSD-N100); likewise CA treatments are ZTDSR + flood irrigation system: without N (ZT-N0), 50% of RDN(ZT-N50), 75% of RDN (ZT-N75) and 100% of RDN (ZT-N100); PTR system + flood irrigation system @ 120N kg/ha. Out of 9 treatments, 5 treatments (SSD-N0, SSD-N100,

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ZT-N0, ZT-N100 and PTR) were simulated using were used to calibrate and validate the HYDRUS-2D model for 80 days simulation period (35 to 114 days after sowing). HYDRUS-2D model is a mathematical model to simulate the two-dimensional movement of water by using Richard's equation for unsaturated flow in different soil layers and to estimate each component of the soil water balance (Šimùnek, et al., 2008). Nitrogen in CA and PTR system was broadcasted and fertigated through venturi in CA+ system. The water productivity (WP) was calculated based on the ratio of biomass produced by selected representative plants from each treatment and total amount of water applied during the simulation period.

RESULTS

In our study on rice, 131.7cm of total water (rainfall+irrigation) was applied in PTR plots which was 1.37 time and 2 times higher than CA system and CA+ system, respectively. Out of the applied water, PTR transpired only 18.4% through root water uptake than to 24% in ZT-N100, 36.28% in SSD-N100, 12.5% in SSD-N0 and 8.8% in ZT-N0. SSD-N100 plots had 20.62% and 23.54% less water loss through evaporation and 45% and 66% less deep drainage loss than ZT-N100 and PTR, respectively. ZT-N0 incurred 41.5% higher drainage loss and 5% higher evaporation than SSD-N0. So, switching to CA+ system with 100% RDN application saved 50.1% and 31.3% of water with proportionately increase in the crop yield resulting in 2 and 1.45 times water productivity (WP) than PTR and ZT-N100, respectively.

CONCLUSION

CA+ based practices with precise application (right rate and amount) and direct root feeding (right placement) curtailed the unproductive water loss components like evaporation, drainage loss and diverted maximum applied water towards consumptive



Fig. 1 Dry matter produced, soil water balance components and water productivity (WP) of rice under different crop establishment, N and irrigation management treatments during the simulation period.

Where, DM: dry matter produced (t/ha); CRWU: cumulative root water uptake; CI: cumulative inflow (rainfall+ irrigation water applied);CE: cumulative evaporation; WP: dry matter (kg/ ha)/ total water use (mm)

use. Therefore, the results of our study on bundling of complementing agronomic innovations including subsurface drip irrigation (SSDI) systems for rice would be of immense interest to farmers, policy planners and civil society for addressing the current and future challenges of rice cultivation. In future, the N dynamics and N loss studies in SSDI installed CA-based systems (CA+) using HYDRUS-2D model may provide further insight into this aspect.

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EFFECT OF HERBICIDES ON WEED FLORA, GROWTH AND YIELD OF SCENTED GOBINDABHOG RICE DURING KHARIF SEASON

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Gobindabhog, a popular short-grainnon-Basmati scented rice, is traditionally cultivated in lower *gangetic* plains of South Bengal for a long period. Weed infestation in aromaticrice field not only results in low yield, but also affects the quality to some extent. Chemical weed control is a quick, cost-effective and less laborious method, but continuous use of the same herbicide(s) for a long period have caused environmental hazards (Aktar*et al.*, 2009) and shifts in weed flora (Holt, 1994). So, identification of suitable new generation herbicide(s) with proper dose and application schedule in *Gobindabhog* rice is need of hour to keep the weed population under control, better production and sustained quality.

METHODOLOGY

A field experiment was conducted in a randomized block design (R.B.D.) with 3 replications during kharif season of 2019 at the Instructional Farm of Bidhan Chandra KrishiViswavidyalaya, Jaguli, Nadia, West Bengal, India. The experiment consisted of 11 weed control treatments: T₁ (Untreated control), T_2 (Pretilachlor 50% EC @750ml a.i. ha⁻¹ at 3 DAT), T_3 (Pyrazosulfuron ethyl 10% WP @ 25g a.i. ha⁻¹ at 3 DAT), T₄ (Cyhalofop Butyl 10% EC @ 800 ml a.i. ha-¹ at 15 DAT), T₅ (Fenoxaprop-p-ethyl 69EC @ 750ml *a.i.* ha⁻¹ at 15 DAT), T_6 (Fenoxaprop-p-ethyl 69EC (a) 1000ml a.i. ha⁻¹ at 15 DAT), T_7 (Fenoxaprop-pethyl 69EC @ 1250 ml a.i. ha-1at 15 DAT), T₈ (Fenoxaprop-p-ethyl 69EC @ 2500 ml a.i. ha⁻¹ at 15 DAT), T_o (Fenoxaprop-p-ethyl 6.7% w/w EC @ 875 ml a.i. ha⁻¹ at 15 DAT), T_{10} (Two hand weeding at 25 and 40 DAT) and T₁₁ (Continuous weed free). Seedlings of Gobindabhog rice @ 3 hill-1 were transplanted at a spacing of 20 cm \times 15 cm in 4 \times 3 m² plots in puddled field, which was fertilized with the recommended dose of N₆₀P₃₀O₃₀kg ha⁻¹.

Numbers of weeds were counted species-wise from each experimental plot at 30 and 60 DAT. A quadrate of 1 m \times 1 m was used for recording the data for each observation. The data collected on weeds were transformed to square root transformation ("x +0.5) for statistical analysis. Weed control efficiency (WCE) was calculated as per the formula:

Weed Control Efficiency (%) =

 $\frac{WDC - WDT}{WDC} \times 100$, where WDC = Weed dry weight in untreated control plot (gm⁻²); WDT = Weed

dry weight in treated plot (gm⁻²). The dry weight of weeds wererecorded as per standard procedures.

RESULTS

Plant height, tiller production, LAI and dry matter accumulation of *Gobindabhog* rice, irrespective of weed management treatments, were increased progressively upto 90 DAT in the study. Among eleven weed control practices, continuous weed free (T_{11}) plots were generally noted with greater number of tillers and better foliage growth than rest of the treatments. The plant height was found to vary between 115.6 (T_1) and 132.5 cm (T_{11}) at harvest, while the number of tillers m⁻² between 224 (T_1) and 356 (T_{11}), and LAI between 3.01 (T_1) and 3.66 (T_{11}) at 60 DAT.

Mean number of total weeds in 1 m² area was 13.4, 28.2 at 30 and 60 DAT, respectively. The weed control efficiency varied among other nine weed control methods (T_2-T_{10}) over the untreated control (T_1) as:





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Table 1: Effect of weed management practices on density of total weeds, weed control efficiency, growth parameters and yield of *Gobindabhog* rice during *kharif* season

Treatment	Total wee	eds	Weed co	ontrol	Plant height	Tillers m ⁻²	Dry mat	tera	LAI		Grain yield
	(No.m ⁻²)		efficienc	y(%)	(cm)at	at60 DAT	accumul	ation			$(t ha^{-1})$
					harvest		(g m ⁻²)				
	30 DAT	60 DAT	30 DAT	60 DAT			30 DAT	60 DAT	30 DAT	60 DAT	-
T ₁	6.5(42.1)	9.0(80.1)	0.0	0.0	115.6	224	49.9	220.1	1.38	3.01	1.88
T ₂	3.3(10.1)	4.8(22.2)	75.5	72.3	127.9	316	66.4	264.9	1.63	3.47	2.70
T ₃	3.7(13.1)	5.5(29.8)	69.0	59.8	126.3	268	61.0	240.1	1.47	3.09	2.53
T ₄	4.1(16.5)	5.9(33.9)	60.3	55.6	124.3	235	53.8	227.7	1.43	3.04	2.49
T ₅	4.2(17.2)	6.0(35.6)	58.3	52.5	126.8	294	62.9	247.4	1.54	3.24	2.58
T ₆	4.0(15.1)	5.6(30.8)	63.9	58.1	127.4	304	64.0	258.7	1.56	3.34	2.62
T ₇	3.4(11.1)	4.9(23.8)	73.4	69.3	129.4	309	65.6	263.9	1.61	3.45	2.66
T ₈	3.0(8.8)	4.4(18.9)	78.9	76.1	125.1	254	58.8	232.3	1.45	3.08	2.30
T ₉	3.3(10.7)	4.8(22.9)	74.4	70.2	126.6	276	62.5	246.6	1.51	3.13	2.55
T ₁₀	1.7(2.3)	3.6(12.1)	94.6	85.5	129.6	326	68.6	270.9	1.67	3.54	2.78
T ₁₁	0.7(0.0)	0.7(0.0)	100.0	100.0	132.5	356	70.2	275.5	1.72	3.66	2.85
CD at 5%	0.18	0.09	2.3	2.19	1.58	4.7	5.55	8.46	0.01	0.09	0.10

Figures indicate square root transformed values, and figures in parentheses indicate original values.

58.3-94.6% at 30DAT and 52.5-85.5% at 60 DAT. Fenoxaprop-p-ethyl 69EC (a) 2500 ml a.i. ha⁻¹ at 15 DAT (T_o) effectively controlled all types of weeds throughout the cropping period, but failed to improve the growth and yield performance of Gobindabhog rice compared to other chemical weed management treatments, which might be due to the phytotoxic effect of highest dose of Fenoxaprop on Gobindabhog paddy. Gobindabhog rice in continuous weed free (T_{11}) plots produced highest grain yield (2.85 t ha⁻¹), which was 34.0% greater over weedy check (T₁) units. Based on grain yield, the eight herbicidal weed managements could be arranged as: $T_2(2.70 \text{ t ha}^{-1}) >$ $T_{7}(2.66 \text{ t ha}^{-1}) > T_{6}(2.62 \text{ t ha}^{-1}) > T_{5}(2.58 \text{ t ha}^{-1}) >$ $T_{9} (2.55 \text{ t ha}^{-1}) > T_{3} (2.53 \text{ t ha}^{-1}) > T_{4} (2.49 \text{ t ha}^{-1}) >$ T_{s} (2.30 t ha⁻¹).

CONCLUSION

Pretilachlor 50% EC @ 750 ml *a.i.* ha⁻¹ (T_2) could be recommended as pre-emergence herbicide for *Gobindabhog* rice due to >70% WCE and greater grain yield (2.70 t ha⁻¹). Fenoxaprop-p-ethyl 69EC @ 750 ml *a.i.* ha⁻¹ at 15 DAT (T_5) might be an alternative post-emergence herbicide for near-similar grain yield (2.58 t ha⁻¹), but less WCE (58.3% at 30 DAT) n Gobindabhog rice field.

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STCR BASED NUTRIENT MANAGEMENT INFLUENCES THE FRACTIONS OF POTASSIUM UNDER RICE BASED CROPPING SYSTEMS IN MIDDLE INDO-GANGETIC PLAIN

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Soil nutrient status has declined due to intensive monocropping in the same field as well as injudicious fertilizer application. Efficient application of fertilizers has become a necessity to fulfil the increasing demand of food grains. For an efficient fertilizer recommendation, crop requirement as well as available nutrient status of the soil needs to be considered before applying the fertilizer. Balanced use of fertilizers based on soil test crop response (STCR) fertilizer application has an important role in nutrient supply from both organic and inorganic sources, and in return maintaining the health of the soil in addition to productivity of crops. Sustainable soil potassium (K) management has long been neglected in the Indian agriculture scenario which needs to be overcome. Over exploitation of K from soil is due to continuous imbalance between crop demand and external supply, and this resulting in depletion of K reserve. K in soil exists in different forms i.e., water soluble K, exchangeable K, nonexchangeable K, mineral K, and total K. K dynamics in soil depends on magnitude of equilibrium among different forms. Study of different fractions of K is very important as 80% of the K requirement of crops is fulfilled by the non-exchangeable form of K. The reduction of amount in one form shifts the equilibrium to different pools to replenish it. Knowledge and understanding of K dynamics in soil proves to be the best approach for recommendation of fertilizers for different crops. Hence, the present study gives rise to various information regarding issues with the objective to study the effect of STCR based nutrient management on fractions of K and rice yield.

METHODOLOGY

A field experiment was conducted during Kharif 2017-2019 at Bihar Agricultural College research farm, Sabour, Bhagalpurto evaluate the influence of STCR based fertilization on different fractions of soil K on third crop cycle of rice based cropping systems. The experiment was consisted with nine treatments viz., general fertilizer recommendation, farmers' practice, STCR with and without IPNS for low (30 q ha^{-1}) , medium (40 q ha^{-1}) and high (50 q ha^{-1}) ¹) target yield in a randomized block design. IPNS represents the integrated plant nutrient system and with IPNS means use of organics (vermicompost was used in this study) with inorganic fertilizers and without IPNS means no use of organics in the treatment. The fertilizer adjustment equations were developed based on target yield concept and accordingly nutrient doses were calculated. The standard package of practices was followed for growing rice crop variety Rajendra Shweta and intercultural operations were done at appropriate time. Rice crop was harvested at maturity and soil samples were collected for further analysis using standard procedure. The data generated from the field and laboratory studies were statistically analysed using the technique of Analysis of Variance for Randomized Block Design. Least Significant Difference (LSD) was computed at 5% probability level (Steel and Torrie, 1980). Pearson correlation matrix was also used to evaluate the relationship among different fractions of K.

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RESULTS

Fractions of K showed depletion in their content under farmers' practice and absolute control while all the fractions showed a build-up in their contents under STCR with IPNS approach. The content of different fractions of K statistically varied in the order, STCR with IPNS for high target yield>STCR without IPNS for high target yield> STCR with IPNS for medium target yield>STCR without IPNS for medium target yield> STCR with IPNS for low target yield> STCR without IPNS for low target yield> General fertilizer recommendation> Farmers' practice> Absolute control. Mean value of water soluble K ranged from 11.8 to 24.7 mg kg⁻¹, whereas exchangeable K found to be varying from 48.5 to 74.2 mg kg⁻¹, depicting its highest correlation with available K with about 98 per cent variation. Non- exchangeable K was found to be contributing towards water soluble K fraction with a range of value between 920 to 1051.2 mg kg⁻¹.

CONCLUSION

Application of inorganic fertilizers either alone or in conjunction with IPNS approach significantly influenced the water soluble K in soil. Its highest content was recorded under STCR (IPNS) treatment for high target yield which was statistically at par with STCR without IPNS for high target yield. The exchangeable K increased significantly with the application of inorganic fertilizers either alone or in combination with vermicompost (IPNS) over control plots. Highest content was recorded under STCR (IPNS) treatment for high target yield. Non- exchangeable K status of soil was slightly improved in treatments comprising of STCR approach. It was observed that all treatments were statistically at par except general recommended dose, farmers' practice and control treatments which show decline in their content.Mineralandtotal K under different treatments showed a non- significant result.Overall it can be concluded that STCR with IPNS for high target yield gave better results than rest other treatments.

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SPATIAL VARIABILITY OF MICRONUTRIENTS AND ITS PREDICTION MAP THROUGH ORDINARY KRIGGINGIN FLOOD PRONE AREAS OF PADDY GROWING SOIL

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During last few decades extensive use of mineral fertilizers mainly macronutrient has tremendously improved the crop productivity in India. But due to more emphasis towards supply of the macronutrients, the soil and plant system is now suffering from deficiency of micronutrients. At present, crops grown in the same field continuously are suffering from deficiencies of one or more micronutrients; even though the soils are sufficient of the respective elements in total natural pool. Similarly in rice fields, the prominent deficiency of zinc and other micronutrients has now been observed especially under waterlogged transplanted soil. Hence, the extent and nature of the micronutrient deficiency is particularly related to soil type, crop genotypes, management strategies and agroecological situations. There is limited information available on spatial variability of key micronutrients in flood prone areas of young alluvial plain which are vulnerable zone at wider scale. The main objective of this study is to understand the spatial variability and its distribution of micronutrients in paddy growing soils of middle Gangetic plain of India under prevalent conditions.

METHODOLOGY

Paddy growing soils in Supaul district, which is located in middle Gangetic plain of India, has been always suffered due to unprecedented food, and it's brought severe devastation, and deteriorates the soils properties. For the study, a total of 489 representative soils samples were collected from different flood prone areas across the block in Supaul district, during the months April to June between the years 2018-19which were mainly confined under soil order *Entisols*. The detailed sampling protocol, analytical techniques was followed given by Eze*et al.*, (2016). The descriptive statistics were evaluated to check the accuracy level of different soil properties along with micronutrients. Apart from that, semivarograms model was evaluated along with generation of prediction map to check the accuracy of geographical setting of different plant nutrients in the study areas, and main attributes of semivarograms model were nugget, sill and range which were obtained after cross validation of results.

RESULTS

The spatial variability of plant available micronutrients, likeextractableiron (Fe), manganese (Mn), zinc (Zn), copper (Cu) were evaluated through geostatistical methods, and its prediction map was generated based on their critical limit by using of ordinary kriging method, and develop the spatial relationship of micronutrient through with several soil properties. For each micronutrient, semivariograms were evaluated and their main attributes like nugget effect, sill and range wereobtained. The nugget/sill ratio values were 0.60, 0.37, 0.34 and 0.19 for extractable Zn, Fe, Cu and Mn, respectively. Available Fe, Zn, Mn and Cu deficiencies (including acute deficiencies) were observed in 28%, 15%, 14% and 13% of soil samples, respectively. The concentration of micronutrients might be varied because differences in management practices like tillage and fertilizer application in the different communities studied (Wade, 2017). While, discussing the correlation matrix of different plant nutrients, pH value shows negative correlation with Fe (r=-0.053), Mn (r=-0.210), and Zn (r=-0.263). However, EC



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value was shown negatively correlated with different plant nutrients except Zn. The predication maps generated could be used as guide site-specific micronutrient management at precise level in the study region.

CONCLUSION

The distribution of DTPA-extractable micronutrients showed wide variability after imposing the ordinary kriging method which enable to estimatedprediction at field as well as geographical setting. This technology is highly beneficial for better understanding the spatial variability and its potential for refining the agricultural management practices at wider scale.

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PLANTING TIME AND NITROGEN MANAGEMENT IN RICE-RICE RATOON SYSTEM FOR HIGHER PRODUCTIVITY

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Rice (Oryza sativa) is one of the most important food grain crops of the country. In North-Eastern India flood prone zone rice occupies nearly 2.25 million hectares area under rainfed shallow lowland rice ecosystem. Uncertainty of monsoon makes sowing time of rice become unpredictable during kharif season due to regular flash floods at end of July onwards. Being a major rainfed rice-growing area, Asom occupies a special place in the rainfed rice production system in the North-Eastern India by covering more than 10% of the total rice area and contributing 9% to the production (Pun et al. 2016). Low productivity and uncertainty of kharif rice diverted farmers to grow boro rice as productivity of boro rice under shallow lowland is higher (>5.0 t/ha) in North-Eastern States which is comparatively higher than that of the national average productivity of 3.27 t/ha (Singh et al. 2018). Boro rice is transplanted in February and harvested in May-June. This provide ample scope to extend growing season up to July by allowing ratoon crop to have second crop with minimum cost of production. Shallow lowland rice cultivation is about 14.4 million hectares, which accounts 32.4% of the total area of rice in the country. If rice ratoon managed properly could produce more than 50% of grain yield with 50-60% less labour, 32-42% low energy inputs, short duration and high production efficiency than main rice crop. Ratoon rice grain yield could be increased with the application of nitrogen. Not much study had been done on fertilizers management in ratoon rice in India, especially on nitrogen application after harvest of main rice. Naveen a high yielding rice variety was

identified by Regional Rainfed Lowland Rice Research Station, ICAR-NRRI, Gerua, Asom which can produce more than 50% grain yield of main rice crop of *Salis*eason. Therefore, to fulfil the knowledge gap, an experiment was conducted while using Naveen to assess the productivity and profitability of rice ratooning under different planting dates and nitrogen levels.

METHODOLOGY

A field experiments was conducted during 2014-15 and 2015-16 at Regional Rainfed Lowland Rice Research Station, ICAR-National Rice Research Institute, Gerua, Asom. Experiment was laid out in split plot design with three replications. The main boro rice crop was raised with three dates of transplanting (5^{th}) , 15th and 25th Feb.) in main plots and three nitrogen levels (0, 20 and 40 kg/ha N) in sub plots were imposed after harvesting of main rice to get better rice ratoon. 'Naveen' a high yielding variety of rice was taken for study. Staggered nurseries were raised and 45 days seedlings were transplanted at spacing of 20×15 cm and uniformly accommodating 34 hills (m²). Recommended dose of fertilizers, i.e. 80: 40: 40 kg/ha of N-P-K was applied to the main crop as urea, diammonium phosphate and muriate of potash respectively. Full dose of P, one-third of N and threefourths of Kwere applied basal at the time of transplanting. Remaining N was applied in 2 equal splits-at the maximum tillering and panicle-initiation stage, one-fourth of K was applied as top-dressing at panicle initiation. Rest agronomic practices were kept normal and uniform for all date of transplanting of main

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Table I: Productivit	у апо ргонарни	v от гисе -гисе гадоон	as affected by Diantif	ig linne and milrogen levels.

Treatment		Main ba	ororice						Rice rate	oon		
	Panicles (m ²)	Filled grains/ panicle	Straw yield (t/ha)	Grain yield (t/ha)	Dry matter at 45 days (g/hill)	Recovery of hills	Panicles (m ²) (m ²)	Filled grains/	Straw yield panicle	Grain yield (t/ha)	Net return ('/ha) (t/ha)	B:C ratio
Date of planting												
$5^{th}Feb$	224.7	108.0	5.66	5.33	65.0	28.1	215.9	67.5	2.79	2.11	24156	3.07
$15^{th}Feb$	252.1	124.2	6.54	6.04	73.0	29.4	229.5	79.3	3.10	2.33	27513	3.50
$25^{th}Feb$	268.4	112.7	6.38	5.85	68.4	30.3	223.9	68.1	3.08	1.99	22784	2.90
SEm±	10.11	1.59	0.14	0.11	2.79	0.48	6.89	1.81	0.05	0.07		
CD (P=0.05)	20.87	3.27	0.29	0.23	7.75	1.33	NS	5.03	0.14	0.19		
Nitrogen lev	els (kg/ha	.)										
0					64.4	27.67	208.0	63.3	2.62	1.87	21020	2.80
20					70.4	30.01	231.4	75.3	3.11	2.25	26415	3.36
40					71.6	30.11	229.9	76.3	3.24	2.31	27119	3.34
SEm±					2.55	0.25	4.27	2.31	0.10	0.09		
CD (P=0.05)					5.55	0.55	9.30	5.04	0.21	0.19		

crop. The main crop was harvested at 15 cm height between the last week of May and first week of June during both the years. Just after harvesting of the main crop 25 and 50% of recommended doses of N (i.e., 20 and 40 kg/ha N) were applied through urea to the allotted treatments of subplots. Crop parameters and grain yield were recorded at harvest. Pooled means average data of 2 years were analysed statistically using the F-test as per the standard procedure. LSD values at P=0.05 were used to determine the significance of difference between treatment means.

RESULTS

Growth and yield attributes of main crop as well as ratoon were significantly influenced by date of planting (Table 1). Results revealed that 15^{th} February planting turned in to significantly more productive for main rice (6.04 t/ha) as well as ratoon (2.33 t/ha) than the that of 5^{th} and 25^{th} February planting. It was mainly due to higher values obtained for growth and yield attributes like plant height, dry matter accumulation, tillers (m²), filled grains/panicle, panicle weight and length for main rice as well as ratoon crop from 15^{th} Feb. planting. Dry matter accumulation, panicles (m²) and filled grains/panicle1 of ratoon crop were significantly influenced by planting dates. However, straw yield was significantly higher with later date of transplanting i.e. 15th and 25th Feb. as compare to 5th Feb.Nitrogen application just after harvest of main rice mainly increased the recovery hills (m²), number of panicles (m²), and filled grains/panicle. It had been observed that nitrogen application increased the regeneration of hills around 90% which remained lowest with control around 80%. Nitrogen levels of 20 and 40 kg/ha produced significantly higher number of hills (m²), dry matter accumulation, panicles (m²) and filled grains/panicle which resulted in significantly higher grain and straw yield of ratoon rice over control but remained statistically at par with each other. The grain yield recovery in rice ratoon increased with increasing doses of nitrogen. However, both levels of N application recorded almost similar yield recovery whereas control recorded 6-7% less. Thus, 20 kg/ha N extra application was enough to get good rice ratoon crop and additional income of '26415/ha with 3.36 benefit cost ratio.



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CONCLUSION

With these findings 15th February is the optimum planting period for main *boro*rice and extra 20 kg/ha N is enough to get higher productivity and profitability from rice ratoon crop under shallow lowland rice ecology.

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Theme - II : Sustainable rice farming

COMBINED APPLICATION OF ORGANIC AND INORGANIC FERTILIZERS IN RICE IMPROVES ITS YIELD, PROFITABILITY AND SUSTAINABILITY UNDER INDIAN SUB-CONTINENT: A META-ANALYSIS STUDY

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Food security for rising population in limited resources has created tremendous pressure on current agriculture production system. To cope with this challengeinorganic fertilizers and other chemicals are overused which are worsening the soil health, causing environmental problems and ultimately decline in crop productivity. In this regard, innovative steps of soil managements are needed which can tackle these problems and optimize crop yield under sustainable environmental conditions. Nutrient management is one of the essential inputs for soil management to ensure higher yield within sustainable environments (Kumar et al., 2018; Sharma et al., 2019)However, the effect change of nutrient management practices in holistic manner on rice yield and soil carbon is poorly quantified under Indian subcontinent due to insufficient datasets. Hence, the present study was aimed to quantify the impact of nutrient management on rice yield and soil parameters in the Indian subcontinent through meta-analysis by using MetaWin 2.1.

METHODOLOGY

Data from different literatures pertaining to nutrient management in rice crop was collected during the period 1989-2016 from various fieldstudies of Indian subcontinent. After thorough review of the papers, those studies were selected whose data was comparatively quantified on following treatments- T_1 : control (No NPK); T_2 : use of organic fertilizer only; T_3 : 100% NPK inorganic fertilizerand T_4 : integrated nutrient management (INM). Rice yield, net return and soil properties related data were used in this study. Total 338 paired datasets were collected and analysis was done using MetaWin 2.1 and it was tested for significance at p < 0.05.

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RESULTS

Grain yield of ricewas found significantly (p < 0.05) higher in INM(T₄) treatment compared to other treatments irrespective of two soil types (clay and loam). Moreover, the net return in T₄ was also increased by 121% compared to control (T₁). The overall soil organic carbon improved by 23% and 35% in T₄ over the 100% NPK (T₃)(Figure 1) and T₁, respectively and among soil types, in loamy soils, it was increased by 27% and



Fig. 1.Effect of the treatment integrated nutrient management over the treatment 100% NPK inorganic fertilizer on grain yield and soil organic carbon (SOC) in rice crop. The error bars show 95% confidence intervals (CI) and the difference is significant if it does not pass zero. *indicates significant difference at p value is less than 0.05.



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51% in T_4 compared to T_3 and T_1 , respectively and clayey soils increased by 12% and 23% as compared to above mentioned treatments. The overall bulk density enhanced by 0.5% and 1.2% compared to T_3 and T_1 , respectively. In loamy soil, it was increased by 0.2% over T_1 and in clayey soil it was increased by 1.9% and 1.4% over the T_3 and T_1 , respectively. The total nitrogen, available phosphorus, available potassium and microbial biomass carbon showed significant positive effects indicating improvement in soil parameters in T_4 treatment than other nutrient management options.

CONCLUSIONS

The rice produce, net return and soil properties improved in the grated nutrient management treatment compared to different nutrient management alternatives, advocate integrated nutrient management as available nutrient management strategy for backing the crop production and generating less environmental pressure in rice crop of the Indian subcontinent. Reducing chemicals' usage could minimize greenhouse gases emissions by sequestering soil carbon and protecting the environment from their ill effects.

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Theme - II : Sustainable rice farming

IRC/TM-2/PP-20

Indian Rice

EVALUATION OF LIQUID BIOFERTILIZERS IN RICE AGAINST RECOMMENDED INORGANIC FERTILIZERS

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In rice, excessive use of inorganic fertilizers leads to increase in cost of cultivation and deterioration of soil health. After the introduction of chemical fertilizers in the last century, farmers were happy of getting increased yield in agriculture in the beginning. But slowly chemical fertilizers started displaying their ill-effects such as leaching out, and polluting water basins, destroying micro-organisms and friendly insects, making the crop more susceptible to the attack of diseases, reducing the soil fertility. Application of liquid bio fertilizers can mobilize the non labile form of nutrients like P and also fix atmospheric nitrogen thus making them available to plants. Thus liquid bio fertilisers can substitute the inorganic fertilizers. Hence, the present trail entitled "Evaluation of Liquid bio fertilizers in rice against recommended inorganic fertilizers" was conducted during kharif 2018-19 at KVK, Ghantasala with an objective to maintain eco-friendly and sustainable rice production.

METHODOLOGY:

The experiment was conducted in the micro farming situation of KE canal irrigation, Vertisols. The trial was conducted in six locations in the farmer's fields in Modumudi village, Avanigaddamandal, Inapuru, Pamidimukkalamandal, Kaza, Movvamandal, Velivolu, Challapallimandal and Pedaprolu, Mopidevimandal of Krishna district of Andhra Pradesh. Soils were neutral in reaction, non saline, low in nitrogen, high in phosphorus and potassium availability and medium in organic carbon content. Three treatments *viz;* T₁ -Farmers practice, T₂- RDF (Recommended dose of fertilizers) + Liquid biofertilisers and T₃-75% RDF + Liquid biofertilisers were tested. Recommended dose of fertilizers for kharif paddy used was 90-60-60 kg/ ha $N-P_2O_5-K_2O$. *Azospirillum, phosphobacteria* and potassium releasing bacteria were used as liquid biofertilisers @ 500 ml/ac each.

RESULTS:

Among the treatments tested, Application of RDF + Liquid biofertilisers (*Azospirillum* + *Phosphobacteria*+ Potassium releasing bacteria @ 500 ml per acre each) recorded highest yield, gross and net returns and B:C ratio compared to remaining treatments. Application of RDF + liquid biofertilisers (*Azospirillum* + *Phosphobacteria*+ Potassium releasing bacteria @ 500 ml per acre each) recorded 17.29 % more grain yield (67.80 q/ha) than farmers practice with net returns of Rs. 62,915 per ha, gross

Table 1 : Effect of Liquid bio fertilizers in rice againstrecommended inorganic fertilizers on yield, economics andpost harvestsoil properties

Parameter	Treatn	nents	
	T1 :	T2:	T3:
	Farmer's	RDF+LBF	75% RDF
	Practice		+LBF
Yield(q ha ⁻¹)	57.81	67.80	63.28
% increase in yield	-	17.29	9.46
Gross returns(Rsha ⁻¹)	1,04,058.00	1,22,040.00	1,13,904.00
Cost of cultivation(Rsha-1)	57,500.00	59,125.00	57,250.00
Net returns(Rs ha-1)	46,558.00	62,915.00	56,654.00
Benefit cost ratio	1.81:1	2.06:1	1.98:1
pН	8.00	7.70	7.90
EC(dS m ⁻¹)	0.80	0.78	0.77
Organic carbon (%)	0.69	0.82	0.75
Avail. N(kg ha ⁻¹)	220.00	242.00	236.00
Avail. P (kg ha ⁻¹)	82.00	118.00	96.00
Avail. K (kg ha-1)	308.00	385.00	343.00
RDF · Recommended dos	e of fertiliz	zers: LBF ·	Liquid bio

RDF : Recommended dose of fertilizers; LBF : Liquid bio fertilizers



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returns of Rs. 1,22,040 per hectare and B:C ratio of 2.06:1 and application of 75 % of RDF + liquid biofertilisers (Azospirillum + Phosphobacteria + Potassium releasing bacteria (2, 500 ml per acre each) recorded 9.46 % more grain yield (63.28 q/ha) than farmers practice with net returns of Rs. 56,654 per hectare, gross returns of Rs. 1,13,904 per hectare and B:C ratio of 1.98:1 while farmers practice resulted with grain yield of 57.81 q/ha, net returns of Rs. 46,558 per hectare, gross returns of Rs. 1,04,058 per hectare and B:C ratio of 1.81:1. (Table1). Banyo et al., (2012) reported that use of biofertilisers higher yields compared to chemical fertilisers alone. Nutrient status of available nitrogen, phosphorus, potassium and organic carbon in the post harvest soils was also more in T₂ where liquid biofertilisers along with recommended dose of fertilisers were applied followed by T3 where liquid biofertilisers along with 75 % of recommended dose of fertilisers were applied (Table 1). Increased yield with biofertilisers might be due to increased availability of nutrients. Biofertilisers are inoculants of live micro organisms capable of fixing atmospheric nitrogen,

soluble phosphate, stimulating plant growth through synthesis of growth promoting substances and adding considerable amount of organic matter to the soil increasing its fertility (Vessey, 2003).

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CONCLUSION:

Finally, to conclude that liquid biofertilisers along with recommended dose of fertilizers resulted in increase in yield, gross returns, net returns and B:C ratio besides improving soil fertility status. According to feed back from farmers also, it was noticed that yield of blackgram grown in rice fallows in liquid biofertilisers applied fields was improved.

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IRC/TM-2/PP-21

Indian Rice

YIELD OF DIRECT SEEDED UPLAND RICE AS INFLUENCED BY PRECISION NUTRIENT AND WEED MANAGEMENT

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The rainfed upland ecosystem of rice is the most ignored one but it helps in feeding a substantial numbers of poor farmers of India from its limited resources (Singh et al., 2011). The ecosystem spreads over an area of 7 mha across the states in the county. The DSR is gaining favours of the researchers as well as farmers due to its low input demand, rapidity and easiness in planting, shorter growing season of 7-10 days fitting well into the different intensive cropping system, lower methane emission and reduction of labour share on the total cost of cultivation. The opportunity of achieving higher yields under upland rice is often challenged by various biotic and abiotic stresses. Among these stresses, complexity of interactions among weeds and nutrient management are the main challenges. Therefore, exact combination of crop fertilization along with weed management at critical stages of growth for maintaining a proper balance between them is the key to achieve higher benefit.

METHODOLOGY

The field experiment was conducted in the plot no. E-15 of the Shankarpura Farm at NRRI-Central Rainfed Upland Rice Research Station (CRURRS) in the Hazaribaghdisctrict of Jharkhand. The field experiment was laid out in a split-plot design comprising 3 nutrient management practices in the main-plots and 5 weed management practices in the sub-plots, making a treatment combination of 15 with 3 replications. Separate randomization was executed for both mainplot and sub-plot. Main plot consist of Recommended dose of fertilizer (RDF), Nutrient Expert ® guided NPK and Leaf Colour Chart (LCC) guided N + Full P & K, while sub-plots were weed management, as Weedy check, Pre-emergence application of pendimethalin @ 1.0 kg/ha + post-emergence application of bispyribac-Na @ 25 g/ha at 25 DAS, Pre-emergence application of pendimethalin @ 1.0 kg/ha + one hand weeding at 25 DAS, Brown manuring of Dhanicha (*Sesbania aculeata*) at 25 DAS with bispyribac-Na @ 25 g/ha sown with a seed rate of 20 kg/ha and weed free.

RESULTS

Grain yield of direct seeded upland rice was significantly influenced by precision nutrient as well as weed management practices (Table 1). Among the nutrient management practices, Nutrient Expert ® guided NPK resulted in maximum grain yield (3.63 t/ ha), followed by Leaf Colour Chart (LCC) guided N + Full P & K (3.41 t/ha), which was significantly higher

Table 1 Yield and other yield parameters of direct seeded
upland rice as influenced by precision nutrient and weed
management

Treatments	Grain	Straw	Biological
	yield	yıeld	yield
	(t/ha)	(t/ha)	(t/ha)
Nutrient management practices			
Recommended dose of fertilizer			
(RDF)	3.03	4.98	8.01
Nutrient Expert ® guided NPK	3.63	5.64	9.27
Leaf Colour Chart (LCC) guided			
N + Full P & K	3.41	5.12	8.53
SEm±	0.11	0.19	0.24
LSD (p=0.05)	0.29	0.52	0.66
Weed management practices			
Weedy check	1.03	2.57	3.60
Pendimethalin fb hand weeding	4.09	6.05	10.15
Pendimethalin fb bispyribac-Na	3.79	5.81	9.60
Brown manuring	3.48	5.35	8.83
Weed free	4.39	6.45	10.85
SEm±	0.12	0.24	0.28
LSD (p=0.05)	0.24	0.49	0.57

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over RDF. Similar was the trend in straw and biological yield of upland rice for precision nutrient management. Weed management practices resulted in yield improvement under Pendimethalin fb hand weeding, Pendimethalin fb bispyribac-Na, Brown manuring and weed free teatments. Among the weed management Pendimethalin fb hand weeding, Pendimethalin fb bispyribac-Na were observed with significantly higher grain yield (4.09 and 3.79 t/ha) over brown manuring (3.48 t/ha) and weedy check. Maximum straw and biological yield were also observed under Pendimethalin fb hand weeding, Pendimethal

CONCLUSION

Grain yield of upland rice is significantly influenced by precision nutrient as well as weed

management practices.Nutrient management practices influenced the no. of tillers/m² and no. of panicles/m², no. of unfilled grain/panicle significantly but there was no impact on remaining yield attributes like 1000 grain weight, length of panicle and no. of filled grains per panicle. Thus leading to the increment of grain yield of upland DSR. Also keeping the field weed free during the critical period by weed management practices like Pendimethalin fb hand weeding, Pendimethalin fb bispyribac-Na and Brown manuring also give higher grain yield.

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IRC/TM-2/PP-22

ndian Rice

IMPACT OF DIRECT RICE-SOWING TECHNOLOGY WITH SEED DRILL ON RICE PRODUCERS' EARNINGS

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Rice contributes more than 40 per cent of the country's total food grain production. In Andhra Pradesh, rice is grown in all thirteen districts.Out of all these districts, Krishna district shares major part with an area of 2, 13,452 ha. In spite of difficultiesin agriculture viz., late release of water, late receipt of canal water in tail end regions, increased cost of cultivation with less profitability and increased labour migration to city areas due to industrialization causedseverelabour shortage and increased labour cost. In Paddy cultivation 25-30 per cent of cost of cultivation consumed by operations like nursery preparation, pulling out seedlings and transplanting. According to Das, 2003 raising of nursery and manual transplanting are both labour intensive and costly prepositions.For skipping these operations, direct sown paddy with seed drill is much great helpful to the farming community.Hence new innovations and initiatives are required to make rice production system more sustainable and economically profitable. Under these circumstances, direct sown paddy with seed drill appears to be a viable alternative for rice cultivation that saves expensive inputs, water and labour.Keeping view upon this, KrishiVigyan Kendra, Ghantasala has conducted the study with an objective to analyse the economic evaluation of the direct sown paddy over farmers traditional method of rice cultivation in terms of profitability in Krishna district of Andhra Pradesh

METHODOLOGY:

KrishiVigyan Kendra has conducted 100 demonstrations continuously for four years during

Kharif 2016-17, 2017-18 and 2018-19 on Direct Sown Paddy with Seed Drill in adopted villages in comparision with traditional method. All the farmers were selected for this study purpose and interviewed them with personal contact. Data was collected from the farmers by using schedule.

RESULTS:

To find out the economic performance of the technology, it is very important to find out the input cost of paddy under Direct Sown Paddy and Traditional method of paddy cultivation. Results showed that estimated input cost of paddy under direct sown was lower than Traditional method of paddy cultivation.

Table 1: Economic evaluation of paddy cultivation under Direct
Sown Paddy over Traditional method of cultivation at farmers
field of Krishna district, Andhra Pradesh

Particulars	Direct Sown Paddy	Traditional method of
		cultivation
Land Preparation (Rs.)	2400	2400
Nursery (Rs.)	900	2900
Transplanting (Rs.)		5000
Organic manures(Rs.)	1200	1200
Chemical manures (Rs.)	3500	3500
Weeding (Rs.)	1200	1200
Plant protection chemicals (Rs.)	1000	1500
Harvesting (Rs.)	8000	8000
Grain Yield (kg/ha)	5120	4806
Cost of cultivation (Rs/ha)	33,000	42,800
Gross returns (Rs.)	99,120	94,800
Net returns (Rs.)	61,200	57,600
Benefit cost ratio (B:C) 3.00 2.20	3.00	2.20



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Table shows the advantages of direct seeding with seed drill over traditional transplanting in terms of yield and net income besides reducing the duration of the variety. There is a difference in cost of cultivation which is nearly Rs.9000 to 10,000/ ha. The benefit cost ratio of 3.00 was also much higher than the Traditional method of planting (2.20). The lower net returns of Rs.57, 600 and low benefit cost ratio of 2.20 indicated nonprofitability of paddy cultivation under the Traditional method of planting method in Krishna district. Hence it could be recommended that wherever labour is scarce, costlier and for easy intercultural operations, direct seeding through seed drill may be advantageous for increasing the productivity and profitability of direct seeded rice.

CONCLUSION:

The study concludes that Direct Sown Paddy is a highly remunerative crop production method in paddy as compared to Traditional method of transplanting method in Krishna district. This method projected higher yield with low cost of cultivation over traditional method. Hence, the higher positive relationship between the grain yield and crop growth parameters resulted in increase in grain yield which leads to higher preference of farmers for adoption of direct sown paddy method of paddy cultivation over traditional method. Some of the factors are constraining the full adoption of the direct sown paddy are lack of land leveling, skill in operating seed drill, weed control and poor water control in the fields. If farmers overcome these constraints, this technique will make remarkable performance than the traditional method. This method gained a momentum in upscaling the paddy productivity which created a positive impact on farming community.

Indian Rice

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EFFICIENCY OF IRON COATED SEEDS UNDER DIFFERENT TIME OF SOWING INWET DIRECT SEEDED RICE

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Rice is a staple food crop in Asia and has been traditionally cultivated mainly by transplanting. Raising seedlings in nurseries, pulling and bundling, transporting to the field and transplanting are laborious and timeconsuming. Puddled soil is soft, which not only facilitates the transplanting work of farmers but also favours the growth of seedlings. Puddling controls weeds efficiently by killing them before planting and by suppressing the emergence of new weeds after planting. Labour shortages brought about by high economic growth prompted farmers to shift from transplanting method to direct seeding method. The area that shifted to direct seeding reached as much as 14% of all irrigated rice fields, but further expansion has been limited by inconsistent plant stands and the infestation of weeds that are difficult to control (Pandey and Velasco, 2005). The wet direct seeding technique, which aims to realize labour saving in paddy rice cultivation, has continued to gain popularity in recent years. Unlike the traditional transplantation method, in which young rice plants are first grown and then transplanted to a paddy field, wet direct seeding is a technique in which the seed rice is sown directly in a rice paddy, where it germinates and establishes, and the rice is harvested from the same paddy. Because the work of raising and transplanting seedlings can be omitted, wet direct seeding can make an important contribution to labour saving. When farmers use primed seeds, they do not need to pregerminate the seeds before planting. The use of Fe coated seeds prevents the occurrence of floating seedling in the water seeding of puddled soil. Integrating the preparation of primed and Fe- coated seeds make water seeding in puddled soil without soaking and incubation during the busy farm season feasible.

Because dry seeds are storable, Fe coated seeds could be prepared during the off season. In this context, this study is proposed to assess the impact of the iron coated seed on crop establishment and productivity with different time of sowing under direct seeded rice system.

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METHODOLOGY

A field experiment was conducted during Kharif, 2018 and 2019 at the Department of Rice, Tamil Nadu Agricultural University, Coimbatore, to study the productivity of direct seeded rice with iron coating under different rice ecologies. The experimental trial was laid out in split plot design with three replications. In main plot, 4 date of sowings with oneweek interval viz., M₁ - Ist week of August sowing, M₂ - IInd week of August sowing, M3 - IIIrd week of August sowing; M_4 - IVthweek of August sowing and five establishment methods in sub-plots viz., S₁- Iron coated seed broadcasting in 1-2 mm water level condition; S₂ - Iron coated seed broadcasting in wet condition; S₃ -Uncoated seed broadcasting in 1-2 mm water level condition; S_4 - Uncoated seed broadcasting in wet condition and S_5 – Normal method of transplanting. The variety chosen for this study was Swarna. Broadcasting of iron coated and uncoated seeds were done in an weekly interval to study the growth and yield performances. All the recorded data were analysed statistically as per the method suggested by Gomez and Gomez (1984).

RESULTS

Based on the two years of experimental study the result revealed that first fortnight of sowing during August resulted highest grain yield (5.27 t/ha) than those





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Table 1. Influence of treatments on grain yield (kg/ha) of rice

Treatments			Grain vield (kg	/ha)	
Treatments			Ofalli yielu (kg		
	I st sowing	II nd sowing	III rd sowing	IV th sowing	Mean
T_1 - Iron coated seed broadcasting in 1-2 mm					
water level condition	5517	5653	5043	4840	5263
T_2 - Iron coated seed broadcasting in wet					
condition	5340	5553	4890	4767	5138
T_3 - Un-coated seed broadcasting in 1-2 mm					
water level condition	4830	4737	4530	4377	4619
T_4 - Un-coated seed broadcasting in wet condition	4753	4667	4367	4203	4498
T_{5} - Normal transplanting method	5687	5763	5590	5347	5597
Mean	5225	5275	4884	4707	
		S.Ed		CD(0.05)	
М		23		64	
S		42		76	
M at S		68		144	
S at M		72		148	

of delayed sowing (Table 1). There was a significant reduction in grain yield due to a delay of one week from 2nd sowing. However, Fe coating significantly increased grain yield over non-coating. Fe coated seeds also exhibits higher growth and yield attributes when compared to uncoated seeds. There is a significant increase in grain yield due to iron coating of seeds which facilitated a better system of establishment and growth. Iron-coated rice seeds also exhibits high density, improved anchorage and resistance to sparrow attack and seed borne diseases. These iron coated seeds can be stored at room temperature for more than 1 year and can be sown without soaking or incubation.

CONCLUSION

In DSR method, Fe coated seeds broadcasting in 1-2 mm water level condition during first fortnight of August sowing resulted higher grain yield when compare to delayed second fortnight of August sowing. The Fe coating significantly increased grain yield over noncoating. This method has been successfully introduced in water seeding in puddled fields in an irrigated ecosystem by broadcasting, row and hill seeding. These iron coated seeds can be stored at room temperature for more than 1 year and can be sown without soaking or incubation.

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Indian Rice

ROLE OF ZINC FERTILIZERS ON YIELD AND QUALITY ENHANCEMENT IN RICE

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Zinc deficiency is one of the important abiotic factors limiting rice productivity worldwide and also a wide spread nutritional disorder affecting human health. Studies on zinc dynamics and management in rice soils is of great importance. Plants grown on soils low in available zinc generally produce low yield with poor nutritional quality (Welch and Graham 199). Field experiment was conducted at Regional Agricultural Research Station,Anakapalle with rice as test crop (variety RGL 2537) to study the effect of different levels of zinc fertilizers along with recommended dose of chemical fertilizers (NPK) on yield and nutrient enrichment of rice.

METHODOLOGY

The soils are neutral in reaction with normal conductivity. Soil organic carbon and available nitrogen status was low with medium available phosphorus and potassium and available zinc status was above critical limits (0.77 ppm). Experiment was conducted to study the effect of zinc fertilizers through different methods of application on crop productivity and zinc enrichment in rice. The treatments include T1 : Control (recommended dose of chemical fertilizers without zinc), T2 : T1 + 25 kg zinc sulphate ha-1 (soil application), T3 : T2 + zinc sulphate foliar spay at 21 days after transplanting (@2g lit-1), T4 : T2 + zinc sulphate foliar spay at 60 days after transplanting (@2g/lit, T5: T2+Foliar sprays of zinc sulphate at 21 and 60 days after transplanting, T6: T1 + 12.5 kg zinc sulphate/ha through soil application, T7: T6 + zinc sulphate foliar spray at 21 days after transplanting, T8 . 12.5 kg zinc sulphate/ ha as soil application + zinc sulphate foliar spray at 60 days after transplanting, T9

: 12.5 kg zinc sulphate/ha through soil application + Foliarsprays of zinc sulphate (21 & 60 days after transplanting), T10 : Foliar Spray (@ 2 g / lit) at 21 days after transplanting, T11 : Foliar Spray (@ 2 g / lit) at 60 days after transplanting and T12 : Foliar Sprays (@ 2 g / lit) at 21 & 60 days after transplanting. Recommended doses of nitrogen, phosphorus and potassium were applied uniformly to all the treatments in the form of urea, single super phosphate and muriate of potash.

RESULTS

Highest grain yield of rice (5.41 tha⁻¹) was recorded with application of 100 % chemical fertilizers + 12.5 kg zinc sulphate/ha as soil application + two foliar sprays of zinc sulphate at 21 and 60 days after transplanting, whereas, lowest grain yield of rice (4.71 tha-1) was recorded with control plots where no zinc application was done during entire experimentation period. Similar results were reported by Singh et al., 2011. However, this was on par with all the treatments which received zinc fertilizers through soil application and foliar sprays over foliar sprays alone. These results suggest that for better output and for balanced nutrition combined application which is also advocated by Depar et al 2011. Straw yield also followed the same trend as it was highest in the zinc applied treatments compared to control treatment. The significant increases in grain Zn concentration were found in the case of combined application of soil(25 kg zinc sulphate per ha) and foliar Zn fertilizers (0.2% foliar spray) that caused 6 to 15 % increase in grain Zn under different combinations and levels of zinc sulphate. Irrespective of soil Zn status, foliar Zn applications resulted in significant increasesin



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grain Zn, especially in the case of late-season foliar Zn application (Naik and Das, 2007).

CONCLUSION

In view of the above results, providing Zn to plants(for example, by applying Zn-fertilizers to soil and/ or to foliar) appears to be important to ensure success of breeding efforts for increasing Zn concentration in grain. Fertilizerstrategy could be a rapid solution to the problem and can be considered an important complementary approach to the on-going breeding programs.

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WEED DYNAMICS AND YIELD AS INFLUENCED BY LEAF COLOUR CHART BASED NITROGEN AND WEED MANAGEMENT TREATMENTS

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Direct seeded riceis an emerging production technology in India since requirement of water, labour and capital input are less initially. But direct seeded rice has problem of severe weed infestation (Chauhan, 2012). Various herbicides have been used for controlling weeds in DSR but efficiency of chemical methods based on single herbicide treatment may be unsatisfactory because of their narrow spectrum of weed control. Therefore, application of several herbicides in combination or in sequence can be more useful (Chauhan and Yadav, 2013). Nitrogen is the key nutrient for crops, which affects biomass production and partitioning into various plant parts, and plays a significant role in the competitive balance between weeds and crops. Gadgets such as the inexpensive leaf colour chart (LCC) and chlorophyll meter (Soil Plant Analysis Development) have proved quick and reliable tools to decide the time when N fertilizer should be applied to the crop.

METHODOLOGY

A field experiment was conducted during rainy (*Kharif*) season of 2016 and 2017 at Agricultural Research Farm, Department of Agronomy, Institute of Agricultural sciences, Banaras Hindu University, Varanasi, Uttar Pradesh. The soil was Gangetic alluvial having Sandy clay loam in texture with pH 7.80. It was moderately fertile, being low in available organic carbon (0.33%), available N (154.60 kg/ha), and medium in available P (12.10 kg/ha) and K (210.51 kg/ha). The experiment was laid out in split-plot design replicated thrice with four nitrogen management treatments and 5 weed management treatments (Table 1). Full dose of phosphorus and potash were applied as basal

application and nitrogen was applied as per treatment. The dry seed of 'HUR 105' variety of rice at 30 kg ha⁻¹ was sown manually with the help of spade at a row spacing of 20 cm. Weed samples were collected by placing a quadrate (50 x 50 cm) randomly at two places in each plot at 20, 40, 60, 80 DAS and at harvest.

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RESULTS

Application of nitrogen (a) LCC < 5 (N₄) recorded minimum weed density and weed dry matter might be due to the fact that in all LCC treatments equal and liberal amounts of nitrogen were applied with more number of splits at critical growth stages and made timely availability of nitrogen as per need of the plant. Under different leaf colour chart based nitrogen schedules, LCC < 5 (N₄) recorded highest weed control efficiency due to lower dry matter accumulation of weeds at all the stages of crop growth. Application of LCC $< 5 (N_{A})$ was recorded maximum grain and straw yield than other nitrogen treatments (Table 1). The increased grain and straw yield was perhaps as a result of better availability of nutrient as need based and reduced weed density, dry weight and better weed control efficiency.

Among weed management practices, maximum weed control efficiency, minimum total weed dry weight and weed density was recorded with pyrazosulfuron @ 20 g a.i ha⁻¹ (PE) *fb* bispyribac @ 25 g a.i ha⁻¹ at 15-20 DAS (W_4). Superior performance of herbicides in reducing the weed dry weight due to sequential application compared to alone application. The highest weed control efficiency might be due to the fact that the successive application of two herbicides at an interval of 20 days created an adverse reduction in total



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Table 1: Effect of Leaf colour chart based nitrogen and weed management on total density of weeds, dry weight and WCE of direct seeded rice

Treatments	Total weed density (No. m ⁻²)		Weed dry weight (g m ⁻²)		WCE (%)		Grain yield (kg ha ⁻¹)		Straw yield (kg ha ⁻¹)	
	2016	2017	2016	2017	2016	2017	2016	2017	2016	2017
Nitrogen management										
$N_1: RDN (120 \text{ kg N ha}^{-1})$	19.01 (367.26)	20.24 (416.17)	8.84 (78.74)	9.64 (94.04)	21.06	20.18	3515.15	3122.91	5471.86	5350.65
$N_2:LCC < 3$	18.68 (352.58)	20.06 (405.52)	8.60 (73.87)	9.35 (87.66)	25.94	25.60	3688.31	3316.02	5645.02	5428.57
N_3 : LCC < 4	17.66 (316.21)	19.10 (369.41)	8.14 (66.30)	8.64 (75.21)	33.53	36.17	3826.84	3696.97	5437.23	5423.84
N ₄ :LCC<5	16.42 (281.90)	18.12 (337.98)	7.91 (64.16)	8.34 (71.35)	35.68	39.44	4277.78	4025.97	6025.97	5922.08
SEm+	0.26	0.36	0.12	0.14			97.91	59.70	70.21	63.26
CD(P=0.05)	0.90	1.24	0.42	0.50			338.82	206.59	242.95	218.90
Weed management practices										
W ₀ : Weedy check	22.26 (495.89)	23.78 (565.39)	10.00 (99.75)	10.86 (117.82)	0.00	0.00	2532.47	2186.15	4956.71	4745.17
W ₁ : Two hand weedings at 20										
and 40 DAS	14.86 (224.51)	16.75 (283.33)	7.44 (55.71)	8.02 (64.29)	44.15	45.43	4827.75	4574.63	6093.07	6006.49
W ₂ : Pendimethalin @ 1 kg a.i ha ⁻¹ (PE) <i>fb</i> bispyribac @ 25 g a.i ha ⁻¹										
at 15-20 DAS	17.92 (321.85)	19.17 (368.13)	8.11 (65.65)	8.54 (73.13)	34.19	37.93	3733.77	3463.20	5692.64	5562.77
W ₃ : Flufenacet @ 120 g a.i ha ⁻¹ (PE) <i>fb</i> bispyribac @ 25 g a.i ha ⁻¹										
at 15-20 DAS	18.41 (340.27)	19.60 (384.90)	8.54 (72.58)	9.18 (84.87)	27.24	27.97	3387.45	3084.42	5422.08	5357.14
W ₄ : Pyrazosulfuron @ 20 g a.i ha ⁻¹ (PE) <i>fb</i> bispyribac @ 25 g a.i ha ⁻¹	l									
at 15-20 DAS	16.27 (264.92)	17.60 (309.60)	7.77 (60.15)	8.37 (70.23)	39.70	40.39	4653.68	4393.94	6060.61	5984.85
SEm+	0.21	0.12	0.11	0.08			76.89	70.45	68.19	54.23
CD(P=0.05)	0.60	0.34	0.31	0.24			221.49	202.94	196.42	156.22

Data were subjected to square root transformation x + 0.5. Figures in parenthesis are original values

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weed dry matter. Application of pyrazosulfuron @ 20 g a.i ha⁻¹ (PE) *fb* bispyribac @ 25 g a.i ha⁻¹ at 15-20 DAS resulted in significantly higher grain and straw yield. This might be due to prevalence of weed free crop growing environment might have enabled congenial conditions for production of higher growth stature and

better yield structure which might have eventually resulted in higher yields.

CONCLUSION

Thus, it may be concluded that, application of $LCC < 5 (N_4)$ recorded highest weed control efficiency,





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lower weed density and dry matter, highest grain and straw yield. Broad spectrum weed control with highest weed control efficiency, lower weed density and dry matter, higher grain and straw yield was achieved through sequential application of pyrazosulfuron 20 g/ ha(PE) *fb* bispyribac 25 g/ha at 15-20 DAS in *kharif* sown dry direct-seeded rice in Eastern Uttar Pradesh.

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MICROBIAL POPULATION DYNAMICS IN RICE FIELDS WITH THE APPLICATION OF BIOFERTILIZERS (*AZOSPIRILLUM* AND PHOSPOBACTERIA) IN VISAKHAPATNAM DISTRICT

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Bio-fertilizers are defined as biologically active products or microbial inoculants of bacteria, algae and fungi (separately or in combination), which possess the inborn ability either to fix or mobilize important nutrient elements from non-usable forms through biological process. In nutshell, it provides "ecofriendly" organic agro-input which has the ability to alter nutritionally important elements from unavailable to available form through biological processes (Vessey, 2003). So, it can be expected to reduce the use of chemical fertilizers and pesticides by introducing biofertilizers (Subashini*et al.*, 2007). It not only saves chemical fertilizers but also help in its effective utilization and results in higher yield rates.

Rice production needs huge amount of chemical fertilizer application, especially urea, which is

one of the causes of global warming and groundwater pollution. After nitrogen the second most important nutrient is phosphorus. It may prevail in the soil but may not be bio available to the plant. In this case, a group of microorganisms can help in Biological nitrogen fixation and solubilization of insoluble organic and inorganic phosphorus and simultaneously reduce use of chemical fertilizers. Biofertilizers are being produced at Regional Agricultural Research Station, Anakapalle and supplied directly to farmers and through Department of Agriculture and the effectiveness of the applied biofertilizers was not yet studied. Therefore, microbial population dynamics in rice fields with the application of biofertilizers was studied during Kharif 2018-19 to monitor the changes in the population of functional groups of microbes due to application of

Table 1: Microbial population counts of applied biofertilizers from Rice Fields in Visakhapatnam district.

Village	Mandal	Microbial population(X 10 ⁵ cfu/g soil)													
		05.10	0.18	(Tillering stage) 20.10.2018		(PI stage) 26.11.18				(After crop harvest) 05.01.2019					
		Initia	al	Inoculated Contro		rol	Inoculated		Control		Inoculated		Control		
		ASP	PSB	ASP	PSB	ASP	PSB	ASP	PSB	ASP	PSB	ASP	PSB	ASP	PSB
Gouripatnam	Chodavaram	-	-	10	9	3	2	2	1	1	1	1	1	1	1
V.R.peta	Chodavaram	1	1	5	7	2	1	3	1	1	1	2	1	1	1
Venkannapalem	Chodavaram	-	1	6	8	4	1	11	3	1	1	5	3	1	1
Venkannapalem	Kasimkota	1	-	6	5	3	1	9	4	1	2	5	3	1	1
Narsingabilli	Kasimkota	1	1	8	9	4	1	8	2	2	1	4	1	1	1
Shaiek Ali Palem	Kasimkota	-	-	9	4	6	2	4	3	1	1	3	2	1	-
Kokkirapalli	Yelamanchili	-	-	9	7	3	1	7	4	1	1	4	3	1	-
Somannapalem	Yelamanchili	-	-	9	9	2	1	3	3	1	1	2	1	1	1
Marripalem	Anakapalle	-	1	10	4	3	1	6	2	1	1	3	2	1	-
Sankaram	Anakapalle	1	-	10	5	2	1	6	3	2	2	4	2	1	1
Sivannapalem	Pendurthi	1	-	8	8	5	1	6	2	1	1	3	1	1	1
Dakamarri	Bheemili	-	1	11	10	1	1	5	5	1	1	3	2	-	1
Lakshmipuram	Bheemili	-	1	7	12	2	1	5	3	1	1	2	1	1	1

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biofertilizers (*Azospirillum* and Phospobacteria) to rice crop in Visakhapatnam district.

METHODOLOGY:

Collected initial rhizosphere soil samples from 7-10 days transplanted rice fields from 13 different villages in Visakhapatnam district. *Azospirillum* and Phospobacteria biofertilizers were applied to the field each at the rate of 5.0 Kg ha⁻¹. Rhizosphere soil samples were collected from both inoculated and un inoculated rice fields at three stages i.e. at tillering stage, panicle initiation stage and after crop harvest. *Azospirillum* and Phospobacteria population counts were recorded at microbiology laboratory.

RESULTS:

The data indicated that more number of colonies were recorded in inoculated rice fields compared uninoculated rice fields. Microbial population was recorded maximum at tillering stage in all the locations and the highest population was recorded *Azospirillum* (11X 10⁵cfu/g soil) and Phospobacteria (10X 10⁵cfu/ g soil) at Dakamarri, Bheemilimandal in inoculated rice field. However, reduction in the microbial population was observed after PI stage and minimum microbial population i.e. *Azospirillum* (5X 10⁵cfu/g soil) and Phospobacteria (3X 10⁵cfu/g soil) was recorded after crop harvest. Therefore, it is suggested to apply biofertilizers at least continuously for 3-4 seasons to establish sufficient microbial load in rice fields of Visakhapatnam district.

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NUTRIENT MANAGEMENT AND CROP ESTABLISHMENT METHODS OF RICE FOR HIGH ALTITUDE AND TRIBAL AREAS OF ANDHRA PRADESH

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Rice is the major staple food crop grown about 1 lakh hectares in high altitude and tribal areas of Andhra Pradesh. However the productivity is less than two tones per hectare with very less returns leaving the farmers poor. Adoption of improper and traditional agronomic practices, non application of fertilizers and manures as per the crop needs are the some of the reasons attributed. It is very high time to focus on escalation of crop productivity without hampering to their natural resource base. Farmers of this fragile ecosystem are also attracted towards the recent advancement in crop establishment methods and nutrient management practices adopted elsewhere. Therefore a field study was conducted involving improved methods of crop establishment with adequate

nutrition.

METHODOLOGY

A field experiment was conducted during *Kharif* 2013-14 at Agricultural Research Station, Seethampeta, Andhra Prtadesh, India. The soil was sandy clay loam having pH 6.8, organic carbon 0.71 %, available nitrogen 278 kg ha⁻¹, available P_2O_5 32.9 kg ha⁻¹ and K_2O 316 kg ha⁻¹. The trial was laid out in split plot Design with three replications with four main plots consists of crop establishment methods viz., Direct sowing, Drum seeding, modified SRI(Systems of rice intensification) and normal transplanting) and four nutrient management practices viz., 100% RDN (80 kg N through Green Manure+ FYM); 200% RDN (160 kg N through Green Manure+ FYM); 100%

Table 1. Effect of crop establishment methods and nutrient management on yield attributes and dry matter production at harvest in rice.

Treatment	No. of tillersm ⁻²	No. of panicles m ⁻²	No. of Filled grains/panicle	1000 grain wt (g)	Dry matter at harvest(Kg ha ⁻¹)
M ₁ – Direct sowing	557	452	126	22.43	11946
$M_2^{}$ – Drum seeding	529	445	121	22.37	11514
M ₃ – Modified SRI	511	437	149	23.48	12960
M_4 - Transplanting	502	415	137	23.31	12075
SEm+	12.79	11.05	4.07	0.22	235
CD at 0.05	44	38	14	0.68	807
S ₁ – 100% RDN (80 kg N through Green Manure+ FYM)	396	340	121	22.97	10845
$S_2 - 200\%$ RDN (160 kg N through Green					
Manure+FYM)	507	433	136	23.21	12410
$S_3 - 100\%$ RDF+ GM	574	468	142	23.43	12925
S ₄ - 100% RDF	493	422	133	22.67	11757
SEm+	15.52	12.19	4.85	0.31	243
CD at 0.05	45.32	35.59	14.16	0.91	710

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Table 7 Effect of crop ec	stablichment methods and	niitrient management o	n vield and	economics of rice
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Treatment	Grain yield (Kg ha ⁻¹)	Straw yield (Kg ha ⁻¹)	Gross Returns (Rs ha ⁻¹)	Net Returns (Rs ha ⁻¹)	B : C ratio
M ₁ – Direct sowing	5530	6418	78308	22808	1.41
M ₂ – Drum seeding	5182	6295	73661	15111	1.26
M ₃ – Modified SRI	6132	7333	87049	24524	1.39
M ₄ - Transplanting	5718	6725	81059	17809	1.28
SEm+	147	161	1081	241	0.022
CD at 0.05	506	554	3719	829	0.08
S ₁ – 100% RDN (80 kg N through Green Manure+ FYM)	4215	5309	60104	-396	0.99
$S_2 - 200\%$ RDN (160 kg N through Green					
Manure+FYM)	5035	6150	71605	8355	1.13
$S_3 - 100\%$ RDF+ GM	5325	6487	75712	15462	1.26
S ₄ - 100% RDF	5047	6030	71641	13091	1.22
SEm+	153	168	1056	267	0.023
CD at 0.05	447	491	3084	780	0.07

RDF+ GM; 100% RDF i.e., 80-50-40 kg N P K per hectare). Direct sowing was done using ferti-cum seed drill under irrigated dry conditions. 15 days old seedlings planted at a spacing of 30 cmX20 cm in case of modified SRI. Coimbatore drum seeding equipment was used for drum seeding. In case of manual transplanting 26 days old seedlings planted at a spacing of 20cmX15 cm during *Kharif*. MTU 1001 (140 days duration) was the test variety. Standard and recommended cultural and plant protection measures followed for respective establishment methods as per the treatments. Data were collected duly following standard procedure and analyzed using ANOVA and the significance was tested by Fisher's least significance difference (p=0.05).

RESULTS

Study revealed that, among crop establishment methods, direct sowing registered maximum number of tillers and panicles m^{-2} , whereas modified SRI recorded the higher number of filled grains/ panicle , 1000 grain weight, dry matter production at harvest , grain yield and straw yield followed by direct sown

rice. The grain yield in modified SRI was higher by 6.75% over transplanting and 15.49% higher over drum seeding. Optimum plant population and quick establishment of crop with modified SRI resulted in favourable yield structure which in turn leads to higher grain yield. Plant density plays a major role in determining the efficiency of solar energy conversion to plant product per unit of land area. Gross returns and net returns also higher with modified SRI Whereas B: C ratio was higher with direct sowing. Murthy et al., (2015) also reported similar findings of superior performance of alternate systems of rice establishment on productivity and returns of rice in north coastal Andhra Pradesh. With respect to nutrient management, application of 100% RDF along with green manuring showed superior performance followed by 200% RDN through organics. Application of 100% RDF along with green manuring recorded the highest growth, yield structure, dry matter, grain and straw yield, Gross returns, net returns and B: C ratio over rest of the nutrient management practices. Similar observations of superior performance of 100% RDF along with green



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manuring in rice was also reported by Rao *et al.*, (2016).

CONCLUSION

Modified SRI with of 100% RDF along with green manuring is the best crop establishment and nutrient management practice to improve yield and returns to rice farmers of high altitude and tribal areas of Andhra Pradesh.

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