ISSN 2319-3670

Journal of Rice Research

Volume 17, No. 2 December 2024

Society for Advancement of Rice Research

Society For Advancement of Rice Research

(Regd. No.2175/2004 of A.P. Society Regn. Act. 2001)

The Society for Advancement of Rice Research is a registered society started with main objective of providing a platform for exchange of information and knowledge related to latest developments in rice research.

Aims and Objectives

- To advance the cause of rice research and development in the country.
- To disseminate knowledge on latest developments in rice research through publications, seminars, lectures and training programmes.
- To provide consultancy in rice production and development.
- To facilitate research and industry collaboration and public private partnership at national level.
- To honour outstanding achievers in rice research and development.
- To cooperate with other organizations having similar aims and objectives.
- To promote any other scientific/professional activities conducive for the advancement of science of rice and rice improvement.

Executive Council (2019-2024)

President	:	Dr. RM Sundaram, Director, ICAR-IIRR, Hyderabad
Vice - Presidents	:	Dr. ON Singh, Vice-Chancellor, Birsa Agril. University, Ranchi
		Dr. Y Chandra Mohan, ARI, PJTSAU, Hyderabad
Secretary	:	Dr. R Mahender Kumar, ICAR-IIRR, Hyderabad
Joint Secretary	:	Dr. S Gopalakrishnan, ICAR-IARI, New Delhi
Treasurer	:	Dr. B Nirmala, ICAR-IIRR, Hyderabad
Zonal Councillors	:	Dr. VK Srivastava, BHU, Varanasi - North India
		Dr. PB Patel, Navsari Agril. University, Gujarat – West India
		Dr. Vijay Pal Bhadana, ICAR-IIAB, Ranchi – East India
		Dr. BNVSR Ravi Kumar, RARS, Maruteru, Andhra Pradesh – South India

Journal of Rice Research is an official publication of Society for Advancement of Rice Research (SARR), ICAR-Indian Institute of Rice Research, Hyderabad - 500030 and published twice a year i.e., June and December. All correspondence related to SARR should be addressed to secretary, Dr. R M Kumar (kumarrm213@gmail.com).

Membership: Membership of the Society is open to all persons interested in furthering the aims and objectives of the Society and in the opinion of the executive committee, have the necessary qualification and experience.

Membership and Journal Subscription fee w.e.f August 2019

	Subscription price	
Membership category	**Annual**	**Life**
A. Individual membership		
Indian (Rs.)	500 (300*)	3000 (2000*)
Foreigner (US $ or its equivalent)	50	300
B. Corporate members/Patrons-one time (Rs.)	----	20,000
C. Libraries and Institutions (Annual)		
Indian (Rs.)	2500	
Foreign (US $ or its equivalent)	550	

Admission fee of Rs. 100/- will be charged in addition to the above subscription fee; *For Students

All remittances should be made in favour of Society for Advancement of Rice Research, Hyderabad with a mail to treasurer, Dr. B Nirmala (treasurersarr@gmail.com).

ISSN 2319-3670

Journal of Rice Research

Volume 17, No. 2 December 2024

Society for Advancement of Rice Research

Journal of Rice Research

Volume 17: Issue No. 2 **December 2024**

REVIEW ARTICLE https://doi.org/10.58297/HPFZ4910

Understanding the Mechanism of Iron Metabolism and Bioavailability in Cereals towards Biofortification

Suman K, Jaldhani V, Sanjeeva Rao D, Aravind Kumar J, Sruthi K, Mangrauthia SK, Kalyani MB, Papa Rao Vaikuntapu, Sai Prasad SV, Sundaram RM and Neeraja CN*

ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad - 500 030

*Corresponding author Email: cnneeraja@gmail.com

Received: 11th July, 2024; Accepted: 5th October, 2024

Abstract

Iron (Fe) deficiency remains a critical global health issue, particularly affecting vulnerable populations such as children and pregnant women. Biofortification, the process of enhancing the micronutrients content in staple food crops, holds promise in addressing this challenge. This review aims to elucidate the mechanisms underlying Fe metabolism in cereals, thus focusing on strategies for Fe biofortification. Understanding the molecular mechanisms governing Fe uptake and transport in plants is essential for targeted breeding efforts to enhance the Fe content. Plants employ distinct strategies for Fe uptake from the soil, such as reduction-based and chelation-based approaches, influenced by environmental factors like soil pH. Long-distance Fe transport within plants involves intricate pathways mediated by transporter proteins and regulatory genes. Environmental factors, including soil properties and agricultural practices, influence Fe bioavailability in crops apart from Fe accumulation. Thus, strategies to enhance Fe absorption such as reducing phytic acid content are crucial for improving the nutritional quality of biofortified crops. Various *in vitro*, animal and human studies have assessed the bioavailability of Fe in biofortified crops, highlighting the potential for addressing Fe deficiency through dietary interventions. Combining genetic approaches with an understanding of physiological mechanisms can hasten grain Fe enrichment efforts, resulting in better outcomes through biofortification programmes.

Key words: Cereals, Biofortification, Fe metabolism, Bioavailability.

Introduction

The Green revolution has almost achieved food security across the world addressing the hunger through increasing the production of major staple foods including rice, wheat and other cereals. The prevalent reliance on carbohydrate-rich diets, coupled with restricted dietary diversity due to limited purchasing power in low or middle-income countries, is exacerbating hidden hunger, also known as micronutrient malnutrition (Black *et al.,* 2013). The significance of the nutritional quality of the diets has been underscored by United Nation's (UN) Sustainable Development Goal-2 targeting to eliminate hunger, accomplish food security and enhanced nutrition and promote sustainable agriculture (Lowe, 2021). According to the World Health Organization (WHO) estimates, around 40% of children below five years, 37% of pregnant women and 30% women between 15 to 49 years suffer Fe deficiency (https://www.who.int/). The requirements for Fe almost doubles between 1 and 6 years of age and also during adolescence/puberty, thus children, adolescents, women of gestation reproductive age and pregnant women are the most vulnerable to Fe deficiency (WHO, 2005; Abbaspour *et al.,* 2014). Almost 70% of the Fe in human body is

found in red blood cells (RBC) as haemoglobin and in muscles as in myoglobin facilitating the circulation and metabolism of oxygen among various tissues (McDowell, 1992; Hurrell, 1997). One-fourth of Fe is stored as ferritin to maintain Fe homeostasis and to support important cellular processes (Knovich *et al.,* 2009). For plants also, Fe is a critical essential element and deficiency of Fe is directly related to the reduction in crop productivity and quality (Grotz and Guerinot, 2006).

Increasing Fe content in food grains

Agronomic biofortification is the application of external Fe salts to the plant parts to increase Fe content in grains. However, it is simple and effective, additional cost required for the purchase of Fe salts and labour for the application hinders the wide adoption of agronomic biofortification. Genetic biofortification is a proven approach to enhance Fe content in cereals especially in pearl millet and wheat (Neeraja *et al*., 2022). Biofortification can be achieved through either traditional breeding or genetic engineering. The conventional breeding methodology is based on the existence or availability of genetic variability, crossing to combine the high Fe and yields, selection of desirable recombinants from the segregating material and their stabilization to be released as varieties (Vasconcelos *et al.,* 2017). For the use of marker assisted selection (MAS), several attempts were or being made to identify genomic regions and candidate genes associated with high Fe content in target edible tissues using approaches like QTL mapping, GWAS and genomic selection across crops (Srivastava *et al.,* 2020; Gupta *et al.,* 2021; Swamy *et al.,* 2021). Recent identification of ZmNAC78, a transcription factor associated with high Fe levels in maize appears to be promising for MAS (Yan *et al*., 2023). Genetic engineering approach has demonstrated its potential for enhancing Fe content in cereals, however its adoption is restrained by constraints of regulatory authorities worldwide (Garg *et al*., 2018). Using gene editing strategy, one or a few nucleotides can be changed, existing alleles can be replaced and new genes can be inserted precisely and can be inherited stably (Huang *et al.,* 2016). Genome editing for targeted gene editing through Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) involves Cas9/13, RNA-guided DNA endonucleases guided by a single guided RNA (sgRNA) resulting in a complex at the target site (Roy and Soni, 2021; Ahmad *et al.,* 2020). Gene editing of *OsNRAMP2* increased the grain Fe content in rice (Chang *et al*., 2022). Knocking out anti-nutrient genes responsible for accumulation of heavy metals and phytic acid can reduce the accumulation anti-nutrients. Disruption of inositol penta phosphate 2-kinase 1 (*IPK1*) gene increased grain Fe content in wheat (Aggarwal *et al.,* 2018). Supposed to be transgene free technology, the gene editing appears to be promising with supportive regulatory framework across the world. For targeted breeding efforts to increase Fe content in cereals, deciphering the molecular mechanism of Fe translocation and remobilization into grains is very critical. In the present review, we summarized the uptake and transport mechanisms of Fe and the associated genes in model plants and cereals.

Translocation of Fe from root to loading in grains

Available literature and bioinformatics resources focusing on candidate genes and gene families associated with the translocation of Fe from the roots to the grain-loading process in crops *viz.,* rice, wheat and maize are summarized below.

Fe uptake from soil to roots

Plants employ two distinct strategies for Fe uptake from the soil:

1. Strategy I, known as the reduction-based strategy, is activated by non-grass plants when they experience Fe deficiency.
2. Strategy II, referred to as the chelation-based strategy, is triggered in grasses (**Figure 1**).

Strategy I: Reduction-based strategy

The Strategy I (reduction-based strategy), is predominantly employed by non-graminaceous plants. This reduction-based strategy hinges on the activity of the Fe-regulated transporter 1 (*IRT1*). Here is how it works:

- In Strategy I, the available Fe^{3+} in the rhizosphere is first converted into Fe^{2+} through a reduction process by the plant before it can be taken up.
- When plants are under Fe-deficient conditions, they release protons (H^{+}) into the rhizosphere, which leads to a decrease in pH in the immediate root vicinity. This acidification process is facilitated by ATPases, which utilize ATP to pump protons into the rhizosphere (Kim and Guerinot, 2007).
- As the pH decreases in the rhizosphere, the solubility of ferric oxides (Fe^{3+}) increases.
- Furthermore, an enzyme called ferric reductase oxidase 2 (*FRO2*) aids in the reduction of ferric oxides (Fe^{3+}) to ferrous oxide (Fe^{2+}), using NADPH-dependent Fe^{3+} chelate reductase. This conversion makes Fe more soluble.
- Subsequently, the soluble ferrous oxide (Fe^{2+}) is transported from the rhizosphere to the roots, primarily through a transporter controlled by *IRT1* **(Figure 1)** (Ishimaru *et al.,* 2006).

Strategy II: chelation-based strategy

Strategy II (chelation-based strategy) is primarily employed by graminaceous plants *viz.,* maize, wheat and rice from the grass family for Fe uptake. Here is how it works:

- Strategy II transport activities are controlled by transporters known as mugineic acid (*TOM1*) and yellow stripe 1 (*YS1*).
- In Strategy II, ferric ions (Fe^{3+}) present in the rhizosphere are transported into the root cytosol with the help of soluble phyto-siderophores. These siderophores are natural Fe chelators with a high affinity for Fe^{3+} transport (Morrissey and Guerinot, 2009).
- Among these chelators, the mugineic acid (MA) belonging to family of phytosiderophores (PS) is particularly effective in binding to Fe^{3+}. Different plant species secrete various members of the MA family, depending on their specific needs. For instance, rice primarily releases 2′ deoxymugineic acid (DMA), while barley releases two different types of MAs, *viz.,* 3' epihydroxymugineic acid (epi HMA) and 3' epihydroxy 2′ deoxymugineic acid (epi HDMA), near the rhizosphere through the TOM1 transporter (Ishimaru *et al.,* 2006).
- These MAs efficiently form Fe^{3+}-MA complexes.
- The YS1 transporter then transported the formed complexes into the root (Schaff *et al.,* 2004 and Ishimaru *et al.,* 2006). This chelation-based strategy enhances the uptake of Fe in graminaceous plants.

Certain crops, including rice, are capable of employing a combination of both reduction based (Strategy I) and chelation based (Strategy II) strategies for Fe uptake from the rhizosphere into the roots. Here is how it works

- In this combined strategy, plants directly absorb the soluble ferrous oxide (Fe^{2+}) from the rhizosphere, which can be richer in Fe^{2+} compared to Fe^{3+}. This is facilitated through transporters like *IRT1* and/or *IRT2* (Kim and Guerinot, 2007; Sperotto *et al.,* 2012).
- Simultaneously, via Strategy II, Fe^{3+}-MA complexes are formed in the rhizosphere. These Fe^{3+}-MA complexes are then transported into the root's cytosol using transporters like Yellow stripe -like 15 (*YSL15*) (Ishimaru *et al.,* 2006).
- Instead of relying solely on direct Fe^{2+} uptake from the rhizosphere, rice successfully utilizes both reduction and chelation-based strategies, ensuring sufficient Fe is absorbed from the rhizosphere into the root cytosol through the Fe^{3+}-MA complexes (see **Figure 1**) (Ishimaru *et al.,* 2006).

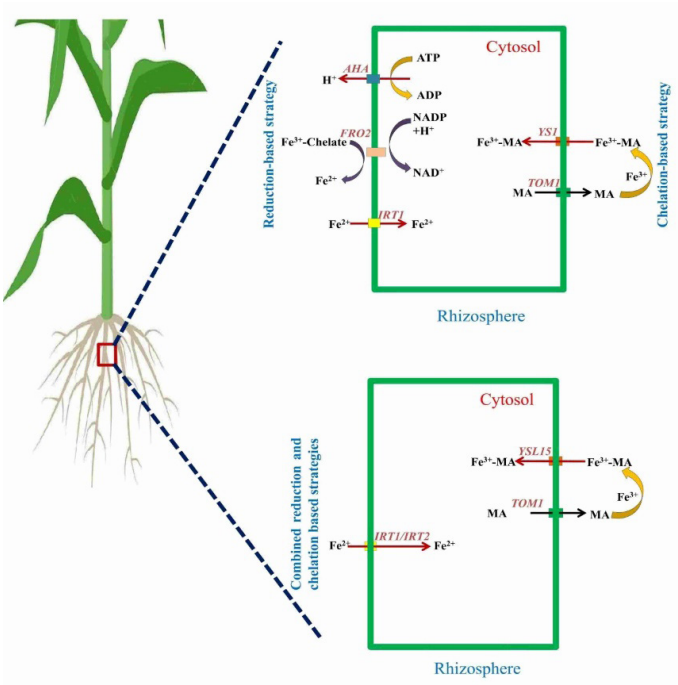


Figure 1: Fe uptake strategy I and II in plants

The expression of different sets of ferric reduction oxidase (*FRO)* genes in various locations suggests their role in Fe uptake in different plant tissues. *FRO2* corresponding gene to the yeast Fe (III) reductase 1 (*FRE1*) was identified in Arabidopsis based on its sequence similarity (Robinson *et al.,* 1999). *FRO2* is a primary *FER* expressed in the epidermal cells of Fe inadequate roots. In low Fe growth condition, the over expression of *FRO2* makes plants more resistant (Connolly *et al.,* 2003). Root specific FRO genes (*FRO2, FRO3* and *FRO5*) are expressed in roots, specifically FRO3 gene expressed in the vascular cylinder of roots. Shoot specific FRO genes (*FRO6, FRO7* and *FRO8*) are expressed in shoot (Feng *et al.,* 2006). The orthologs of *IRT1* gene have been identified which combines both Strategy I and II for Fe uptake in rice. Unlike Arabidopsis, the *LeIRT1* and *LeIRT2* genes are expressed in the roots of tomato in both the Fe deficient and sufficient roots, especially *LeIRT1*, shown induction under Fe deficiency (Eckhardt *et al.,* 2001). Ethylene is also associated in the stress adaptation like Fe deficiency in rice, although not in barley (Wu *et al.,* 2011). Additionally, Methylthioribose kinase (*MTK*) and S-adenosyl methionine synthetase (*SAM*) genes are expressed under Fe deficiency conditions in chelation-based strategy plants *viz.,* rice and maize (Liu *et al.,* 2015).

Several endogenous or housekeeping genes have been associated with grain Fe content in rice. For example, the ubiquitin activating enzyme (*UBA*), a small globular protein involved in the ubiquitination process, has shown a significant positive correlation with Fe concentration in rice grains. This suggests a potential role for *UBA* in Fe homeostasis, in addition to the reported ubiquitin-conjugating and ligase genes (Bej *et al.,* 2020). In both rice and Arabidopsis, genes related to acquisition, uptake and transport of Fe through both Strategies I and II have been identified and annotated. In Fe deficiency condition, six candidate genes have been associated with Fe in maize and these genes are associated in various aspects of Fe homeostasis, including Fe(III)-phytosiderophore transporter, Fe transport to vacuoles and transcriptional factors that regulate Fe-related gene expression (Curie *et al.,* 2001; Kobayashi *et al.,* 2014).

Long-distance Fe transport

Following the Fe transport from the rhizosphere into the root symplast, Fe is needed for chelating compounds. Then the Fe-chelator complexes are transported into the stele, following a diffusion gradient across intercellular connections. At this stage, Fe efflux is required to release Fe into the xylem vessels within the apoplastic space. However, the exact pathway of Fe efflux is not yet fully understood. In plants, especially Arabidopsis, three transporter proteins, known as Fe-regulated transporters (*IREGs*) or ferroportins (*FPTs*) are localized to the root epidermal cells. It is predicted that these transporters are involved in Fe-dependent nickel detoxification (Schaaf *et al.,* 2006). *AtIREG1/FPT1* is bound to the plasma membrane of stele cells, indicating a potential role in releasing Fe into the xylem tracheas (Kim and Guerinot, 2007). *FRD3* is a

citrate efflux long-distance Fe transporter associated to *MATE* family. *MATE* gene is expressed in the root pericycle and vascular cylinder, indicating its role in citrate efflux into the root pericycle and xylem vessels. However, in the xylem, the concentration of Fe is reduced and it accumulates in the shoot apoplast due to *FRD3's* involvement in bypassing long-distance Fe transport. This apoplastic movement of Fe, transfers it from cell to cell through intercellular spaces or walls, allowing Fe to move from the roots to the shoots and from the xylem to the phloem. This may compensate for Fe transport mediated by the xylem (Green and Rogers, 2004). Several genes play a role in the mechanism of Fe uptake from the xylem vessels into the plasma membrane of leaf cells. FRO and ZIP genes are expressed in shoots and the basal part of flowers, signifying their role in Fe uptake in aerial tissues (Vert *et al.,* 2002). The mechanism of Fe transport through the phloem is also noteworthy, as it provides a feasible means of Fe transport, particularly when the Fe levels are insufficient in developing tissues/organs *viz.,* apices, seeds and root tips if relying solely on xylem vessels. In phloem sap, the alkaline pH (>7) is favourable for maintaining Fe and Fe chelates in a soluble form. Phloem transport is also involved in the remobilization of Fe from older to younger leaves, where the alkaline pH in the phloem sap facilitates the binding of Fe to chelators to keep it soluble (Kim and Guerinot, 2007).

Chloronera (*chln*) is a mutant tomato that exhibits the role of nicotianamine in long-distance Fe transport. The *chln* gene encodes NAS in the mutant tomato and illustrates the role of nicotianamine in the transport of Fe over long distances. The *chln* gene was recognized due to the interveinal leaf chlorosis it caused in young leaves, although it led to increased Fe accumulation in roots. This phenomenon suggests that nicotianamine can act as a shuttle, chelating Fe^{2+} from Fe(III)-DMA during phloem loading and unloading, facilitating Fe^{2+}/Fe^{3+} transformation and specific Fe(II)-NA transport within the phloem. *OsYSL1* transporters, similar to maize YS1, play a key role in the transport of Fe (III)-PS and Fe (II)-NA complexes. In rice total 18 putative YSL genes are identified in its genome and *OsYSL2* is essential gene for transporting Fe(II)-NA and Mn(II)-NA (Koike *et al.,* 2004). The temporal and spatial expression of YSL family genes indicating their role in Fe uptake mechanisms. The expression of *AtYSL1* mRNA is increased in the vasculature of roots and shoots, specifically in the xylem tubes and is detected in young siliques and the chalazal zone of the embryo, indicating the role of YSLs in Fe loading of seeds. *AtYSL1* and *AtYSL3* shows a similar expression pattern in the vasculature of shoots and reproductive organs (Takahashi *et al.,* 2003). Over all in Strategy II plants, the YSL genes are important in the long-distance Fe transport mechanism. In maize, the *YS1* gene is expressed in both roots and shoots (Curie *et al.,* 2001). Several *OsYSL* genes *viz., OsYSL2* and *OsYSL13* being preferentially expressed in shoots particularly *OsYSL6, OsYSL14* and *OsYSL16* are over expressed in both roots and shoots (Koike *et al.,* 2004). *OsYSL2* is a crucial gene overexpressed in the vascular bundles of the panicle neck and the sieve element cells of the phloem in flowers and developing seeds.

Members of the NRAMP family genes are intermediaries in the uptake of divalent cations (Thomine *et al.,* 2003) and in mutant yeast, *AtNRAMP4* can complement the Fe uptake, indicating their role in Fe transport (Thomine *et al.,* 2003). In roots, *NRAMP1* is expressed to take up Fe from the soil and is induced by Fe deficiency. Under Fe-deficient conditions, *NRAMP1* targets the intracellular membrane and remobilizing the Fe into the cytosol (Thomine *et al.,* 2000). In tomato, *NRAMP1* and *NRAMP3* genes are localized to vacuolar, intracellular vesicle and plasma membrane (Bereczky *et al.,* 2003). In Arabidopsis, two *NRAMP* genes *viz., AtNRAMP3* and *AtNRAMP4* are localized to the vacuolar membrane (Lanquar *et al.,* 2005). The *NRAMP1, NRAMP3* and *NRAMP4*

genes are over expressed in response to Fe deficiency. When the *NRAMP3* gene is overexpressed in plants, the over-expression of Fe uptake genes, *viz., FRO2* and *IRT1*, is downregulated, indicating that *NRAMP3* remobilizes the vacuolar Fe into the cytosol (Thomine *et al.,* 2003). Fe is stored as ferritin in the plastid stroma of plant cells. Ferritin is a Fe storage protein capable of storing up to 4,500 Fe atoms. Arabidopsis has four genes (AtFer1-4) encoding ferritin. The transcript of AtFer1, 3 and 4 is expressed upon excess Fe treatment in both roots and leaves (Petit *et al.,* 2001). However, despite the abundance of Fe, the mechanism of Fe uptake into chloroplasts is not well understood. Studies of Fe uptake with isolated chloroplasts have suggested that the mechanism is light dependent and requires Fe (III) chelate reductase activity in barley (Bughio *et al.,* 1997).

Contribution of environmental factors

When the soils are aerobic or of higher pH, Fe is oxidized and fixed as insoluble ferric oxides and at the same time, as Fe is highly reactive, when it is present in excess it becomes toxic. Therefore, plants have developed a control system for Fe (Morrissey and Guerinot, 2009; Grillet *et al.,* 2014). Application of animal manure and plant residues modifies properties of the soils and reported to increase Fe and Zn availability, however foliar applications found to be more than soil nutrient application in increasing grain nutrient contents (Wei *et al.,* 2012; Prasad *et al.,* 2014; Velu *et al.,* 2015).

Bioavailability

Research on bioavailability of nutrients has received greater attention in the past decades. For improvement of Fe absorption, a ratio of phytic acid (PA): iron (Fe), <1:1, is requisite without any enhancers (Hurrell and Egli, 2010). Developing the biofortified crop with high nutritive content is not the only concern but also the bioavailability of the nutrients in human gut (Neeraja *et al.,* 2017). Antinutrient *viz.,* phytic acid inhibit absorption of minerals and hinder the bioavailability of Fe from the ingested food (Kumar *et al.,* 2017). Phytic acid represents 80% of the phosphorous in plants (Bohn *et al.,* 2008). However, variation in the phytic acid content is not attributed to the Fe bioavailability. In maize, by expressing a fungal phytase, 3-fold increase in bioavailable Fe and decrease in phytic acid is reported (Drakakaki *et al.,* 2005). Fe bioavailability is measured by *in vitro* methods *viz.,* Caco-2 cell model. The caco-2 cells are the colonic carcinoma cells that are morphologically and functionally similar to the epithelial cells lining the small intestine. Animal studies using rodent models have been used in bioavailability studies on Zn and carotenoids, but this model seems to be a poor choice to assess Fe bioavailability. High Fe bioavailability in biofortified food crops was observed using isotopic human studies, however they are time consuming and very expensive, which has limited their use (La Frano *et al.,* 2014). Around 23 articles evaluated the bioavailability in biofortified crops, of which eight were animal studies, seven were *in vitro* studies and eight were human studies. A combination of these *in vitro*, animal and human studies will be an effective approach for investigating the efficacy of biofortification programmes (Dias *et al.,* 2018).

Caco-2 cell bioassay was reported as the best approach to evaluate the nutritive quality of Fe biofortified beans (*Phaseolus vulgaris*) and these varieties have high absorption than normal bean variety. Caco-2 cell model can also disclose the effects of antinutrients like phytic acid. Fe absorption studies in 61 Rwandese women with low Fe status revealed no significant difference in the Fe absorption from Fe rich beans than normal beans, which might be due to high phytic acid and polyphenols in beans (Petry *et al.,* 2012). In Pea, phytic acid decrease by 60% has increased bioavailability of Fe in Caco-2 cell studies and improvement of Fe bioavailability by 50-100% was identified in *lpa* lines than in controls (Warkentin *et al.,* 2012; Liu *et al.,* 2015). Cognitive performance, especially the efficiency of search and the speed

of retrieval on memory tasks, was improved in 18-25 women tested by consuming the Fe biofortified beans (86.1 ppm) compared with the normal beans (Murray-Kolb *et al.,* 2017). High ferritin formation in the Caco-2 cells with digests having $FeSO_4$ and ascorbic acid than the digests with $FeSO_4$ and citric acid was reported by (Glahn *et al.,* 1998). The effects of Fe status by consuming the Fe-biofortified rice was tested in 191 women in Philippines which resulted in increase of Fe stores in the women (Haas *et al.,* 2005). Meta-analysis on Fe bioavailability in different types of millets, (*in vitro* and *in vivo*) showed variation in the Fe levels ranging from 2 to 8 mg/100 g and 13.2% significant increase in haemoglobin levels. Enhancement of Fe bioavailability by 3.4 to 2.2 times is noted in women by following traditional methods like fermentation and germination (Anitha *et al.,* 2021). Randomised efficacy trials in the Fe profiles like serum ferritin, soluble transferrin receptor, total body Fe etc. were conducted in the Philippines, India and Rwanda in different crops like rice, pearl millet and beans. Cognitive performance in attention and memory domains were significantly improved by Fe biofortified crops compared with conventional crops (Finkelstein *et al.,* 2019). When the Indian school children, between 12-16 years of age, fed with Fe biofortified pearl millet continuously for six months, showed increased light physical activity and decreased sedentary time in children (Pompano *et al.,* 2022). Decrease in pathogenic bacteria and increase in beneficial bacteria in the gut is reported by dietary intake of Fe biofortified foods (Gomes *et al.,* 2021). The bioavailability of Fe can be enhanced from 12.1 to 16.4 ppm by following different processing techniques like popping, malting etc. (Neeraja *et al.,* 2017). The Fe bioavailability can also be altered by different methods of cooking and digestion in the intestine. During heating, Fe^{2+} or Fe^{3+} are released from Fe (III) hydroxides in ferritin (Hoppler *et al.,* 2008) and in the food matrix they are chelated by phytic acid (Moore *et al.,* 2018; Perfecto *et al.,* 2018). Since, the primary inhibitors of Fe bioavailability in food crops are phytic acid and polyphenolic compounds, breeding low phytate genotypes is now being targeted in different crops.

Conclusion

With more than half of the world's women and children suffering from Fe deficiency, all the available strategies should be adopted for improving Fe status in food grains. Biofortification is one of the proven approaches for enhancing Fe content in cereals such as pearl millet and in other crops such as beans. Limited genetic variability for grain Fe content is a major constraint in cereals, thus extensive germplasm screening should be done. High throughput sequencing of germplasm accessions, genome wide association mapping and RNA seq analyses could lead to the candidate genes associated with high grain Fe content. Genome editing offers favorable opportunities to increase the grain Fe content by modifying known candidate genes for Fe metabolism. Converging the physiological and molecular mechanisms of Fe transport and translocation along with methods to improve bioavailability could pave way to the success Fe Biofortification targeting nutritional security.

References

Abbaspour N, Hurrell R and Kelishadi R. 2014. Review on iron and its importance for human health. *Journal of Research Medical Sciences,* 19(2): 164-174.

Aggarwal S, Kumar A, Bhati KK, Kaur G, Shukla V, Tiwari S and Pandey AK. 2018. RNAi-mediated downregulation of inositol pentakisphosphate kinase (IPK1) in wheat grains decreases phytic acid levels and increases Fe and Zn accumulation. *Frontiers in Plant Science*s, 9(256): 1-12.

Ahmad S, Wei X, Sheng Z, Hu P and Tang S. 2020. CRISPR/Cas9 for development of disease resistance in plants: recent progress, limitations and future prospects. *Briefing in Functional Genomics*, 19(1): 26-39.

Anitha S, Kane-Potaka J, Botha R, Givens DI, Sulaiman NLB, Upadhyay S, Vetriventhan M, Tsusaka TW, Parasannanavar DJ and Longvah T, Rajendran A, Subramaniam K and Bhandari RK. 2021. Millets Can Have a Major Impact on Improving Iron Status, Hemoglobin Level and in Reducing Iron Deficiency Anemia-A Systematic Review and Meta-Analysis. *Frontier in Nutrition*, 8(725529): 1-14.

Bej S, Neeraja CN, Kanth KT, Suman K, Barbadikar KM and Voleti SR. 2020. Correlation of expressional pattern of Ubiquitin activating gene with grain Fe content in rice. *ORYZA-An International Journal on Rice,* 57(3): 251-259.

Bereczky Z, Wang HY, Schubert V, Ganal M and Bauer P. 2003. Differential regulation of nramp and irt metal transporter genes in wild type and iron uptake mutants of tomato. *Journal of Biological Chemistry*, 278(27): 24697-24704.

Black RE, Victora CG, Walker SP, Bhutta ZA, Christian P, De Onis M, Ezzati M, Grantham-Mcgregor S, Katz J, Martorell R and Uauy R. 2013. Maternal and child undernutrition and overweight in low-income and middle-income countries. *The Lancet,* 382(9890): 427-451.

Bohn L, Meyer AS and Rasmussen SK. 2008. Phytate: impact on environment and human nutrition. A challenge for molecular breeding. *Journal of Zhejiang University -Sciences B*, 9(3): 165-191.

Bughio N, Takahashi M, Yoshimura E, Nishizawa NK and Mori S. 1997. Light-dependent iron transport into isolated barley chloroplasts. *Plant and Cell Physiology*, 38(1): 101-105.

Chang JD, Xie Y, Zhang H, Zhang S and Zhao FJ. 2022. The vacuolar transporter OsNRAMP2 mediates Fe remobilization during germination and affects Cd distribution to rice grain. *Plant Soil*, 476(1-2): 79-95.

Connolly EL, Campbell NH, Grotz N, Prichard CL and Guerinot ML. 2003. Overexpression of the FRO2 ferric chelate reductase confers tolerance to growth on low iron and uncovers posttranscriptional control. *Plant Physiology*, 133(3): 1102-1110.

Curie C, Panaviene Z, Loulergue C, Dellaporta SL, Briat JF and Walker EL. 2001. Maize yellow stripe1 encodes a membrane protein directly involved in Fe (III) uptake. *Nature*, 409(6818): 346-349.

Dias DM, Costa NMB, Nutti MR, Tako E and Martino HSD. 2018. Advantages and limitations of *in vitro* and in vivo methods of iron and zinc bioavailability evaluation in the assessment of biofortification program effectiveness. *Critical Review in Food Science Nutrition*, 58(13): 2136-2146.

Drakakaki G, Marcel S, Glahn RP, Lund EK, Pariagh S, Fischer R, Christou P and Stoger E. 2005. Endosperm-specific co-expression of recombinant soybean ferritin and Aspergillus phytase in maize results in significant increases in the levels of bioavailable iron. *Plant Molecular Biology*, 59(6): 869-880.

Eckhardt U, Mas Marques A and Buckhout TJ. 2001. Two iron-regulated cation transporters from tomato complement metal uptake-deficient yeast mutants. *Plant Molecular Biology*, 45: 437-448.

Feng YB, Qiu T, Shen CY and Li XY. 2006. Electromagnetic and absorption properties of carbonyl iron/rubber radar absorbing materials. *IEEE Transactions on Magnetics,* 42(3): 363-368.

Finkelstein JL, Fothergill A, Hackl LS, Haas JD and Mehta S. 2019. Iron biofortification interventions to improve iron status and functional outcomes. *Proceedings of Nutrition Society*, 78(2): 197-207.

Garg M, Sharma N, Sharma S, Kapoor P, Kumar A, Chunduri V and Arora P. 2018a. Biofortified Crops Generated by Breeding, Agronomy and Transgenic Approaches Are Improving Lives of Millions of People around the World. *Frontiers in Nutrition*, 5(12): 1-33.

Glahn RP, Lee OA, Yeung A, Goldman MI and Miller DD. 1998. Caco-2 cell ferritin formation predicts

nonradiolabeled food iron availability in an *in vitro* digestion/Caco-2 cell culture model. *Journal of Nutrition*, 128(9): 1555-1561.

Gomes MJC, Martino HSD and Tako E. 2021. Effects of Iron and Zinc Biofortified Foods on Gut Microbiota *In Vivo* (Gallus gallus): A Systematic Review. *Nutrients*, 13(1): 189.

Green LS and Rogers EE. 2004. FRD3 controls iron localization in Arabidopsis. *Plant physiology*, 136(1): 2523-2531.

Grillet L, Ouerdane L, Flis P, Hoang MTT, Isaure MP, Lobinski R, Curie C and Mari S. 2014. Ascorbate efflux as a new strategy for iron reduction and transport in plants. *Journal of Biological Chemistry*, 289(5): 2515-2525.

Grotz N and Guerinot ML. 2006. Molecular aspects of Cu, Fe and Zn homeostasis in plants. Biochim Biophys Acta - *Molecular Cell Research*, 1763(7): 595-608.

Gupta PK, Balyan HS, Sharma S and Kumar R. 2021. Biofortification and bioavailability of Zn, Fe and Se in wheat: present status and future prospects. *Theoretical and Applied Genetics*, 134:1-35.

Haas JD, Beard JL, Murray-Kolb LE, Del Mundo AM, Felix A and Gregorio GB. 2005. Iron-biofortified rice improves the iron stores of nonanemic filipino women. *Journal of Nutrition*, 135(12): 2823-2830.

Hoppler M, Schönbächler A, Meile L, Hurrell RF and Walczyk T. 2008. Ferritin-iron is released during boiling and *in vitro* gastric digestion. *Journal of Nutrition*, 138(5): 878-884.

Huang QN, Shi YF, Zhang XB, Song LX, Feng BH, Wang HM, Xu X, Li XH, Guo D and Wu JL. 2016. Single base substitution in OsCDC48 is responsible for premature senescence and death phenotype in rice. *Journal of Integrative Plant Biology*, 58(1): 12-28.

Hurrell R and Egli I. 2010. Iron bioavailability and dietary reference values. *Am Journal of Clinical Nutrition*, 91(5): 1461S-1467S.

Hurrell RF. 1997. Bioavailability of iron. *European Journal of Clinical Nutrition*, 51, pp.S4-S8.

Ishimaru Y, Suzuki M, Tsukamoto T, Suzuki K, Nakazono M, Kobayashi T, Wada Y, Watanabe S, Matsuhashi S, Takahashi M and Nakanishi H. 2006. Rice plants take up iron as an Fe3+-phytosiderophore and as Fe2+. *The Plant Journal,* 45(3): 335-346.

Kim SA and Guerinot ML. 2007. Mining iron: iron uptake and transport in plants. *FEBS letters*, 581(12): 2273-2280.

Knovich MA, Storey JA, Coffman LG, Torti SV and Torti FM. 2009. Ferritin for the clinician. *Blood Reviews*, 23(3): 95-104.

Kobayashi T, Nakanishi Itai R and Nishizawa NK. 2014. Iron deficiency responses in rice roots. *Rice*, 7(27): 1-11.

Koike S, Inoue H, Mizuno D, Takahashi M, Nakanishi H, Mori S and Nishizawa NK. 2004. OsYSL2 is a rice metal-nicotianamine transporter that is regulated by iron and expressed in the phloem. *The Plant Journal*, 39(3): 415-424.

Kumar A, Lal MK, Kar SS, Nayak L, Ngangkham U, Samantaray S and Sharma SG. 2017. Bioavailability of iron and zinc as affected by phytic acid content in rice grain. *Journal of Food Biochemistry*, 41(6): e2413.

La Frano MR, de Moura FF, Boy E, Lönnerdal B and Burri BJ. 2014. Bioavailability of iron, zinc and provitamin A carotenoids in biofortified staple crops. *Nutrition Review*, 72(5): 289-307.

Lanquar V, Lelièvre F, Bolte S, Hamès C, Alcon C, Neumann D, Vansuyt G, Curie C, Schröder A, Krämer U and Barbier-Brygoo H. 2005. Mobilization of vacuolar iron by AtNRAMP3 and AtNRAMP4 is essential for seed germination on low iron. *The EMBO Journal*, 24(23): 4041-4051.

Liu X, Glahn RP, Arganosa GC, Warkentin TD. 2015. Iron Bioavailability in Low Phytate Pea. *Crop Sciences*, 55(1): 320-330.

Lowe NM. 2021. The global challenge of hidden hunger: perspectives from the field. *Proceedings of the Nutrition Society*, 80(3): 283-289.

McDowell L. 1992. Minerals in animal and human nutrition. Academic Press, San Diego.

Moore KL, Rodríguez-Ramiro I, Jones ER, Jones EJ, Rodríguez-Celma J, Halsey K, Domoney C, Shewry PR, Fairweather-Tait S and Balk J. 2018. The stage of seed development influences iron bioavailability in pea (*Pisum sativum* L.). *Scientipic Reports*, 8(1): 6865.

Morrissey J and Guerinot ML. 2009. Iron uptake and transport in plants: the good, the bad and the ionome. *Chemical Reviews*, 109(10): 4553-4567.

Murray-Kolb LE, Wenger MJ, Scott SP, Rhoten SE, Lung'aho MG and Haas JD. 2017. Consumption of Iron-Biofortified Beans Positively Affects Cognitive Performance in 18 to 27 Year Old Rwandan Female College Students in an 18-Week Randomized Controlled Efficacy Trial. *Journal of Nutrition*, 147(11): 2109-2117.

Neeraja CN, Hossain F, Hariprasanna K, Ram S, Satyavathi CT, Longvah L, Raghu P, Voleti SR and Sundaram RM. 2022. Towards nutrition security of India with biofortified cereal varieties. *Current Science*, 271-277.

Neeraja CN, Ravindra Babu V, Ram S, Hossain F, Hariprasanna K, Rajpurohit BS, Prabhakar, Longvah T, Prasad KS, Sandhu JS and Datta SK. 2017. Biofortification in cereals: Progress and prospects. *Current Sciences*, 113(6): 1050-1057.

Perfecto A, Rodriguez-Ramiro I, Rodriguez-Celma J, Sharp P, Balk J and Fairweather-Tait S. 2018. Pea Ferritin Stability under Gastric pH Conditions Determines the Mechanism of Iron Uptake in Caco-2 Cells. *Journal of Nutrition*, 148(8): 1229-1235.

Petit JM, Briat JF, Lobréaux S. Structure and differential expression of the four members of the Arabidopsis thaliana ferritin gene family. 2001. *Biochemical Journal*, 359(3): 575-582.

Petry N, Egli I, Gahutu JB, Tugirimana PL, Boy E and Hurrell R. 2012. Stable iron isotope studies in Rwandese women indicate that the common bean has limited potential as a vehicle for iron biofortification. *Journal of Nutrition*, 142(3): 492-497.

Pompano LM, Udipi SA, Ghugre PS, Przybyszewski EM and Haas J. 2022. Iron-biofortified pearl millet consumption increases physical activity in Indian adolescent schoolchildren after a 6-month randomised feeding trial. *British Journal of Nutrition*, 127(7): 1018-1025.

Prasad R, Shivay YS and Kumar D. 2014. Agronomic Biofortification of Cereal Grains with Iron and Zinc. *Advance in Agronomy*, 125: 55-91.

Robinson NJ, Procter CM, Connolly EL and Guerinot ML. 1999. A ferric-chelate reductase for iron uptake from soils. *Nature*, 397(6721): 694-7.

Roy S and Soni P. 2021. Genome Editing for Biofortification of Rice. *Genome Engineering for Crop Improvement* : 297-313.

Schaaf G, Honsbein A, Meda AR, Kirchner S, Wipf D and von Wirén N. 2006. AtIREG2 encodes a tonoplast transport protein involved in iron-dependent nickel detoxification in Arabidopsis thaliana roots. *Journal of Biological Chemistry,* 281(35): 25532-25540.

Sperotto RA, Vasconcelos MW, Grusak MA and Fett JP. 2012. Effects of different Fe supplies on mineral partitioning and remobilization during the reproductive development of rice (*Oryza sativa* L.). *Rice*, 5(27): 1-11.

Srivastava RK, Singh RB, Pujarula VL, Bollam S, Pusuluri M, Chellapilla TS, Yadav RS and Gupta R. 2020. Genome-Wide Association Studies and Genomic Selection in Pearl Millet: Advances and Prospects. *Frontier in Genetics*, 10(1389): 1-9.

Swamy BPM, Marathi B, Ribeiro-Barros AIF, Calayugan MIC and Ricachenevsky FK. 2021. Iron Biofortification in Rice: An Update on Quantitative Trait Loci and Candidate Genes. *Frontier in Plant Sciences*, 12(647341): 1-11.

Takahashi M. 2003. Overcoming Fe deficiency by a transgenic approach in rice. *Plant Cell, Tissue and Organ Culture*, 72: 211-220.

Thomine S, Lelièvre F, Debarbieux E, Schroeder JI and Barbier-Brygoo H. 2003. AtNRAMP3, a multispecific vacuolar metal transporter involved in plant responses to iron deficiency. *The Plant Journal*, 34(5): 685-695.

Thomine S, Wang R, Ward JM, Crawford NM and Schroeder JI. 2000. Cadmium and iron transport by members of a plant metal transporter family in Arabidopsis with homology to Nramp genes. *Proceedings of the National Academy of Sciences*, 97(9): 4991-4996.

Vasconcelos MW, Gruissem W and Bhullar NK. 2017. Iron biofortification in the 21st century: setting realistic targets, overcoming obstacles and new strategies for healthy nutrition. *Current Opinion in Biotechnology*, 44: 8-15.

Velu G, Singh R, Balasubramaniam A, Mishra VK, Chand R, Tiwari C, Joshi A, Virk P, Cherian B and Pfeiffer W. 2015. Reaching out to farmers with high zinc wheat varieties through public-private partnerships: an experience from eastern-gangetic plains of India. *Advances in Food Technology and Nutritional Sciences*, 3(1): 73-75.

Vert G, Grotz N, Dédaldéchamp F, Gaymard F, Guerinot ML, Briat JF and Curie C. 2002. IRT1, an Arabidopsis transporter essential for iron uptake from the soil and for plant growth. *The Plant Cell*, 14(6): 1223-1233.

Warkentin TD, Delgerjav O, Arganosa G, Rehman AU, Bett KE, Anbessa Y, Rossnagel B and Raboy V. 2012. Development and characterization of low-phytate pea. *Crop Science*, 52(1): 74-78.

Wei Y, Shohag MJI, Yang X and Zhang Y. 2012. Effects of foliar iron application on iron concentration in polished rice grain and its bioavailability. *Journal of Agricultural Food Chemistry*, 60(45): 11433-11439.

Welch RM. 2002. Breeding strategies for biofortified staple plant foods to reduce micronutrient malnutrition globally. *The Journal of Nutrition,* 132(3): 495S-499S.

WHO (2005) World Health Organization. 2005. Fruit and vegetables for health: report of the Joint FAO/WHO Workshop on Fruit and Vegetables for Health, 1-3rd September 2004, Kobe, Japan. World Health Organization.

Wirth J, Poletti S, Aeschlimann B, Yakandawala N, Drosse B, Osorio S, Tohge T, Fernie AR, Günther D, Gruissem W and Sautter C. 2009. Rice endosperm iron biofortification by targeted and synergistic action of nicotianamine synthase and ferritin. *Plant Biotechnology Journal*, 7(7): 631-644.

Wu J, Wang C, Zheng L, Wang L, Chen Y, Whelan J and Shou H. 2011. Ethylene is involved in the regulation of iron homeostasis by regulating the expression of iron-acquisition-related genes in *Oryza sativa*. *Journal of Experimental Botany*, 62(2): 667-674.

Yan P, Du Q, Chen H, Guo Z, Wang Z, Tang J and Li WX. 2023. Biofortification of iron content by regulating a NAC transcription factor in maize. *Science*, 382(6675): 1159-1165.

RESEARCH ARTICLE https://doi.org/10.58297/OLXU5090

Genetic Variability for Yield Components, Iron and Zinc contents in Rice (*Oryza sativa* L.) Genotypes

Tukaram J Bhor[1*], Rohit K Jambhulkar[2] and Narendra V Kashid[1]

[1]Agricultural Research Station, Vadgaon Maval, Pune-412106, Maharashtra

[2] College of Agriculture, Pune-411005, Maharashtra

*Corresponding author Email: tjbhor1969@gmail.com

Received: 15th July, 2024; Accepted: 12th October, 2024

Abstract

The experiment was carried out for 11 characters in 41 rice genotypes during *kharif* 2022 at Agricultural Research Station, Vadgaon Maval, Pune. The highest value of GCV (32.111) and PCV (32.618) observed for grain yield per plant and followed by grain iron (Fe) content, GCV (31.137) and PCV (32.021), grain zinc (Zn) content GCV (27.039) and PCV (28.147), fertile spikelets per panicle GCV (20.462) and PCV (21.232), 1000 grain weight GCV (19.104) and PCV (20.094). The grain yield per plant was observed as the highest broad sense heritability (96.90%) followed by days to 50% flowering (95.60%) and grain iron (Fe) content (94.60%). The highest genetic advance as per cent of mean was observed for the traits grain yield per plant (65.121), grain iron content (62.373), grain zinc content (53.509) and fertile spikelets per panicle (40.625). The significant positive correlation was observed among grain yield per plant and days to 50% flowering (0.3171), panicle length (0.2974), fertile spikelets per panicle (0.5101), total spikelets per panicle (0.4519), spikelet fertility (0.4570), test weight (0.4378) and productive tillers per plant (0.5732). High heritability with high genetic advance observed for the trait grain yield per plant, grain iron (Fe) content, grain zinc (Zn) content, fertile spikelets per panicle and total spikelets per panicle indicated additive gene actions. The total spikelet per panicle (2.9940) was observed that had highest direct positive effect on grain yield per plant and followed by spikelet fertility % (0.7118), test weight (0.6805), productive tillers per plant (0.5068) and panicle length (0.1516).

Key words: Variability, heritability, genetic advance, correlation, direct effect

Introduction

The *Oryza sativa* (rice) species are commonly divided in to three subspecies namely; *Indica*, *Japonica* and *Javanica*. Rice (*Oryza sativa* L.) is one of the three leading cereals in the family Poaceae. It is cultivated during warm wet (*kharif*) and winter (*rabi*) seasons in the tropical and subtropical humid regions of the world. Rice is the staple food for a majority of the people of Asia, providing 50-60 per cent of the total calorie and 30 per cent of the total protein (Mackill *et al*., 2012).

According to the FAO (2003) and ICMR (2009), the recommended daily allowance (RDA) for zinc and iron is 10 mg for children and 12-15 mg for adults. Due to their effects on growth and development, as well as other physiological and neurophysiological processes, these micronutrients are important for health and medicine. According to estimates, 49 per cent of people worldwide fail to consume sufficient amounts of zinc. Micronutrients are necessary for both plants and animals to have a balanced diet. Additionally, micronutrients are essential for rice plants' ability to withstand abiotic stresses. From an agronomic perspective, zinc is important to rice for a number or reasons such as nitrogen assimilation and protein metabolism. Approximately 10% of proteins in plants require Zn for structural function and integrity. Low Zn supply limits the rice plant's ability to

convert amino acids to proteins. Iron (Fe) participates in several important metabolic processes such as photosynthesis, chloroplast development, chlorophyll biosynthesis, electron transport and redox reactions. The focus of the green revolution on increasing grain productivity resulted in a decrease in the amount of micronutrients available in a balanced diet. Most of the Iron and Zinc is found in rice bran-aleuronic layer and 80% of it gets removed in polishing. Hence it is essential to have genotypes with high Iron and Zinc content in endosperm.

The increase in rice production is crucial for providing food security. Understanding genetic variability in the experimental material offers a useful opportunity for selection (Singh *et al.,* 2020). Phenotypic variability is the differences between individuals in a population due to genetic composition and growing environment (Sumanth *et al.,* 2017). Planning and execution of any breeding program for improvement on quantitative traits depends on magnitude of genetic variability. Therefore, success on plant breeding activities entirely depends on the existence of genetic variability with respect to desired traits and selection skill of plant breeder (Adhikari *et al.,* 2018). Variability, genetic diversity, expected genetic advances and heritability of the traits are therefore key basis for genetic improvement of the trait.

The level of heritable variation in the traits studied is extremely useful in determining the genotype's potential for future breeding programs. Before planning an appropriate breeding strategy for genetic improvement, it is critical to assess variability for yield and its component characters (Singh *et al.,* 2011). For efficient crop development, understanding the nature and extent of genetic variation in quantitative traits such as yield and its components is critical. Heritability is the ratio of variation due to differences between genotypes to the total phenotypic variation for a trait in a population and shows the component of a character transmitted to future generations. Genetic advance shows the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance is more precise in predicting the genetic gain under selection than heritability alone. In addition relationship between yield and yield attributing traits is prime important for direct and indirect selection of traits which contributes to yield (Aditya and Bhartiya, 2013). Although there are thousands of distinguished genotypes in cultivation, the diverse material available will gives the scope to evolve the cultivars which are having potential for biotic and abiotic stresses along with good quality characters (Khan, 2018). The selected material from evaluations can be utilised for further hybridisation programme. Choosing high-yielding varieties purely on the basis of grain yield will be ineffective unless sufficient data on genetic characteristics is available to use them in hybridization programmes for the further improvement. In the selection process, information on character association, as well as the direct and indirect effects that each character has on yield, will be beneficial. The degree of the association between grain yield and its components, as well as the relative relevance of their direct and indirect effects, are revealed by correlation and path analysis, offering a comprehensive knowledge of their relationship with grain yield (Khan, 2018). About 176 million tons rice is required by 2035, which can be fulfilled by increasing yield potential from 10 to 12.3 tons per hectare (Khush, 2013).

Therefore, the present study was under taken to know information on variability, heritability, genetic advance and traits correlation in promising rice genotypes to develop a high yielding rice genotype. Information on genetic variability is essential for selection, which is the ultimate tool in plant breeding. However, the selection is challenging due to the masking effect of non-heritable variation. Therefore, partitioning of the total variation to understand the

role of the heritable component is very important, which helps the breeder to formulate a sound breeding programme. Correlation is very important factor for any election program. Success in selection depends on the knowledge of the association of component traits with grain yield. However, partitioning the correlation coefficients through path analysis is very important to understand the cause-effect relationship. This helps in understanding the relative importance of component characters for improvement in seed yield of rice. Finally, this type of research could aid the breeder in developing selection strategies to improve grain yield. Given the above scenario, the current investigation is carried out with the objectives of studying the genetic variability, character association and path coefficients in rice genotypes for yield improvement.

Materials and Methods

The present investigation was carried out during *kharif* 2022 at Agricultural Research Station, Vadgaon Maval, Pune. In the present study, forty-one genotypes were assessed to study the variability and genetic parameters for yield and its components, iron and zinc content. List of genotypes used in the present study is presented in **Table 1.** Each genotype was sown in three rows of 4 m length following a spacing of 20 cm between the rows and 15 cm between the plants in randomized block design (RBD) with three replications. Standard agronomic practices were performed uniformly for all the experimental units. Crop was raised following recommended package of practices. Phenological data for days to 50% flowering was recorded on plots basis for each genotype in each replication. At maturity five plants from each accession were selected randomly for recording data on grain yield per plant and yield component traits, namely, plant height, productive tillers per plant, panicle length, grains per panicle and test weight. In contrast, observations for test weight and iron and zinc content traits were obtained from a random grain sample drawn from each plot and replication using standard procedures. The statistical analysis was done by standard statistical method suggested by Panse and Sukhatme (1995). Mean performance of the genotypes were calculated and the genotypic (GCV) and phenotypic (PCV) coefficients of variation were estimated by using the formula given by Burton (1952). The estimates of PCV and GCV were classified as low (0-10%), moderate (10-20%) and high (>20%) according to Sivasubramanian and Madhavamenon (1973). Heritability in broad sense (h^2 b) was estimated according to the formula suggested by Johnson *et al.,* (1955) and Hanson *et al.,* (1956) and classified as low (0-30%), moderate (30-60%) and high (> 60%). Estimation of genetic advance was carried out following the formula given by Johnson *et al.,* (1955) and classified as low (< 10%), moderate (10-20%) and high (> 20%). The genotypic correlation coefficients were worked out by adopting the method described by Singh and Chaudhary (1977). Path coefficient analysis was done according to the procedure suggested by Dewey and Lu (1959).

Table 1: List of Rice genotypes used in the study

Sl. No	Entry	Source	Sl. No	Entry	Source	Sl. No	Entry	Source	Sl. No	Entry	Source
1	GNV 1905	AICRP Trial 2021	11	CSR HZR 17-42	AICRP Trial 2021	21	BRR-0184-1-IR 108194-9-1-2-1	AICRP Trial 2021	31	PDKV Red Rice-1	ARS, Sakoli
2	BPT 5204	AICRP Trial 2021	12	HURS 21-7-IR 105696-1-2-3-1-1-1-B	AICRP Trial 2021	22	NVSR 3148	AICRP Trial 2021	32	Phule Samruddhi	ARS, Vadgaon Maval
3	GNV 1906	AICRP Trial 2021	13	NVSR 526	AICRP Trial 2021	23	RP5401-JBB-B-622-3-1-1-1-1	AICRP Trial 2021	33	Indrayani	ARS, Vadgaon Maval
4	RP 6362-IR15M1298 (GID:4289666)	AICRP Trial 2021	14	RP 6195-MC/ RIL-A147	AICRP Trial 2021	24	CR 4365-1-IR 128768-7-2-2-5	AICRP Trial 2021	34	Pawana	ARS, Vadgaon Maval

Sl. No	Entry	Source	Sl. No	Entry	Source	Sl. No	Entry	Source	Sl. No	Entry	Source
5	DRR Dhan 45	AICRP Trial 2021	15	HURS21-6-IR 08195-3-1-1-2	AICRP Trial 2021	25	RP 6204-MB/ RIL-J65	AICRP Trial 2021	35	Phule Maval	ARS, Vadgaon Maval
6	IR-64	AICRP Trial 2021	16	RP 6204-MB/ RIL-J159	AICRP Trial 2021	26	RP 6196-PC/ RIL-B162	AICRP Trial 2021	36	Kundalika	ARS, Vadgaon Maval
7	Chittimutyalu	AICRP Trial 2021	17	R-RHZ-IA-99	AICRP Trial 2021	27	RP 6253-MV/RIL-MV 208	AICRP Trial 2021	37	Bhogawati	ARS, Radhanagari
8	HURS 17-6-IR 82475-110-2-2-1-2	AICRP Trial 2021	18	CSR HZR 23-1	AICRP Trial 2021	28	RP6514-IR128768-7-2-2-4	AICRP Trial 2021	38	VDN-1832	ARS, Vadgaon Maval
9	NVSR 522	AICRP Trial 2021	19	CSR HZR 17-8	AICRP Trial 2021	29	RP 4993-BC/ RIL-Z102	AICRP Trial 2021	39	Phule Radha	ARS, Radhanagari
10	RP 6211-PR/ RIL-Q181	AICRP Trial 2021	20	HURS-21-3-IR128773-4-4-2-3-B	AICRP Trial 2021	30	Karjat-4	RARS, Karjat	40	Ambemohar-157	ARS, Vadgaon
									41	IGP-13-12-19	ZARS, Igatpuri

Results and Discussions

The amount of genetic diversity in the crop is measured by the genotypic coefficient of variation (GCV) as it represents the heritable component of variability. Additionally, the difference between genotypic and phenotypic expression gives the role of environmental in expression of that particular trait. The genotypic differences were significant for almost all the traits studied indicated that there was considerable amount of variability present in genotypes **(Table 2)**. The estimates of genotypic coefficient of variation, range of variability and phenotypic coefficients of variation, the per centage of heritability in a broad sense and the genetic advance reported as a per centage of mean are given in **Table 3.** For each of the traits examined in the current analysis a significant range of variance was observed. In forty-one (41) genotypes, the total spikelets per panicle ranged from 109.00-221.50 followed by fertile spikelets per panicle (89.00-201.00), plant height (75.70-172.60 cm), grain zinc content (22.45-68.40 ppm), grain iron content (20.70-66.35 ppm), days to 50% flowering (82.00-116.50), grain yield per plant (9.95-33.50 g), spikelet fertility % (80.10-95.85), 1000 grain weight (11.25-23.65 g), panicle length (17.05-28.75 cm) and productive tillers per plant (6.25-9.85).This indicated that there was a large amount of variation for these traits (Maurya *et al.,* 2022 and Divya *et al.,* 2018).

Table 2: Analysis of variance for eleven different characters

Sl. No.	Characters	Mean sum of square		
		Replication (d.f.1)	Treatments (d.f.40)	Error (d.f.40)
1.	Days to 50% flowering	18.56	114.97**	2.57
2.	Plant height	1.97	525.29**	25.56
3.	Panicle length	2.74	13.87**	0.64
4.	Productive tillers/plant	1.19	2.09**	0.31
5.	Fertile spikelets/panicle	1705.80	1612.29**	59.50
6.	Total spikelets/panicle	1615.80	1798.75**	82.25
7.	Spikelet fertility %	16.70	33.83**	3.31
8.	1000 grain weight	1.01	28.53**	1.44
9.	Grain yield/plant	0.66	66.23**	1.04
10.	Grain iron (Fe) content	15.28	280.38**	7.84
11.	Grain zinc (Zn) content	2.70	326.48**	13.10

*Significant at 5% level; ** Significant at 1% level

For all characters, it was observed that the values for genotypic coefficients of variation (GCV) were lower than phenotypic coefficients of variation (PCV) **(Table 3)** indicated that these traits were considerably influenced by environments. The trait spikelet fertility exhibited the lowest GCV (4.474) as well as PCV (4.935), whereas grain yield per plant exhibited the highest GCV (32.111) and PCV (32.618). The broad difference between GCV and PCV were observed for productive tillers per plant indicated that the trait influenced more by environment whereas, days to 50% flowering, spikelet fertility and grain yield per plant recorded narrow difference that indicated less influence of environment. High GCV and PCV were observed for grain yield per plant followed by grain iron content, grain zinc content and fertile spikelets per panicle. Moderate GCV and PCV were observed for 1000 grain weight, total spikelets per panicle, plant height, productive tillers per plant and panicle length. The trait days to 50% flowering recorded low GCV and PCV. Roy *et al.,* (2021) and Maurya *et al.,* (2022) also reported high GCV and PCV for grain yield per plant and moderate GCV and PCV for 1000 grain weight, total spikelets per panicle, plant height and productive tillers per plant.

Table 3: Estimates of genetic variability parameters for 11 different characters of rice genotypes

Sl. No.	Name of the Character	Range	Mean	G.C.V. (%)	P.C.V. (%)	Heritability (h^2) (bs) %	GA as % of mean (at 5% K)
1.	Days to 50% flowering	82.00-116.50	96.50	7.76	7.94	95.60	15.64
2.	Plant height (cm)	75.70-172.60	100.02	15.80	16.59	90.70	31.00
3.	Panicle length (cm)	17.05-28.75	22.64	11.35	11.89	91.20	22.34
4.	Productive tillers/plant	6.25-9.85	7.69	12.28	14.26	74.10	21.78
5.	Fertile spikelets/panicle	89.00-201.00	136.17	20.46	21.23	92.90	40.62
6.	Total spikelets/panicle	109.00-221.50	155.59	18.82	19.71	91.30	37.05
7.	Spikelet fertility %	80.10-95.85	87.32	4.47	4.93	82.20	8.35
8.	1000 grain weight (g)	11.25-23.65	19.26	19.10	20.09	90.40	37.41
9.	Grain yield/plant (g)	9.95-33.50	17.78	32.11	32.61	96.90	65.12
10.	Grain iron (Fe) content (ppm)	20.70-66.35	37.49	31.13	32.02	94.60	62.37
11.	Grain zinc (Zn) content (ppm)	22.45-68.40	46.29	27.03	28.14	92.30	53.50

Genetic advance and heritability are recognised as important selection parameters. According to Burton (1952), combining genetic advance with heritability estimates, would provide a better idea for effective selection. Heritability is a reliable indicator that shows the transmission of parental values to their offspring. The plant breeder can pick superior traits from diverse genetic groups using the heritability estimates. The high heritability values were recorded for grain yield per plant (96.90%) followed by days to 50% flowering (95.60%), grain iron (Fe) content (94.60%), fertile spikelets per panicle (92.90%), grain zinc (Zn) content (92.30%), total spikelets per panicle (91.30%), panicle length (91.20%), plant height (90.70%), 1000 grain weight (90.40%), spikelet fertility % (82.20%) and productive tillers per plant (74.10%) character. High heritability estimates suggested that these characters were least influenced by the environment. Similar results were obtained by Divya *et al.,* (2018) for the characters number of productive tillers per plant, 1000 grain weight, number of grains per panicle and grain yield per plant and Shaili *et al.,* (2022) for grain

yield per plant, number of panicles, test weight and plant height.

The highest genetic advance (GA) as per cent of mean was observed for the trait grain yield per plant (65.121) followed by grain iron (Fe) content (62.373), grain zinc (Zn) content (53.509), fertile spikelets per panicle (40.625), 1000 grain weight (37.418), total spikelets per panicle (37.054) and plant height (31.009). The moderate genetic advance (GA) as per cent of mean was exhibited by the traits such as panicle length (22.342), productive tillers per plant (21.787) and days to 50% flowering (15.649). The low values were recorded by the trait spikelet fertility % (8.354). High heritability (h^2) with moderate genetic advance as per cent of mean showed for the characters fertile spikelets per panicle, total spikelets per panicle, 1000 grain weight and plant height suggested that both additive and non-additive gene effects were involved in the genetic regulation of these traits. High heritability (h^2) along with higher genetic advance (GA) as per cent of mean was recorded for the characters *viz.*, grain yield per plant, grain iron (Fe) content, grain zinc (Zn) content, fertile spikelets per panicle, 1000 grain weight, total spikelets per panicle, plant height and days to 50% flowering indicated that these traits were under control of additive gene action. The selection could be practised for these traits for improvement of genotype. Panigrahi *et al.,* (2018) reported additive gene action for 1000 grain weight and Shaili *et al.,* (2022) for test weight, grain yield and plant height.

Correlation studies

The genotypic correlation coefficient values between yield and its related characters are presented in **Table 4**. The highest and significant positive correlation of grain yield per plant was found with productive tillers per plant (0.5732) followed by fertile spikelets per panicle (0.5101), spikelet fertility (0.4570), total spikelets per panicle (0.4519), test weight (0.4378), days to 50% flowering (0.3171) and panicle length (0.2974). Plant height (0.1903) showed non-significant positive correlation with grain yield per plant. When making selections to improve yield, it is recommended that these characters be given top priority. Similar type of associations were reported earlier by Pachauri *et al.,* (2017) for days to 50% flowering, panicle length and number of productive tillers per plant. All the studied characters had a positive correlation with grain yield per plant.

Table 4: Genotypic correlation coefficients of 8 characters of 41 genotypes of rice on grain yield

Sl. No.	Days to 50% flowering	Plant height (cm)	Panicle Length (cm)	Productive tillers per plant	Fertile spikelets per panicle	Total spikelets per panicle	Spikelet Fertility %	Test weight (g)	Grain yield per plant (g)
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
1.	**1.0000**	0.3488**	0.1818	0.0555	0.5392**	0.4892**	0.4603**	-0.1501	0.3171**
2.		**1.0000**	0.4913**	-0.0603	0.2235*	0.2067	0.1771	0.0583	0.1903
3.			**1.0000**	-0.0471	-0.0523	-0.0697	0.0003	0.4095**	0.2974**
4.				**1.0000**	0.1982	0.1770	0.1280	-0.0642	0.5732**
5.					**1.0000**	0.9811**	0.4734**	-0.4045	0.5101**
6.						**1.0000**	0.2974**	-0.4441	0.4519**
7.							**1.0000**	0.0336	0.4570**
8.								**1.0000**	0.4378**
9.									**1.0000**

*, ** Significant at 5(0.2172) and 1(0.2829) per cent, respectively

Number of productive tillers per plant exhibit positive association with grain yield per plant, panicle length and number of productive tillers per plant, also exhibited high direct effect on yield. This result was in conformity with the earlier findings of Ramanjaneyulu *et al*., (2014). Correlation analysis of yield contributing characters shows that all the characters under study were significantly and positively correlated with grain yield per plant except, plant height. These results were agreement with Iqbal *et al.,* (2018). Kamana *et al*., (2019) reported positive direct effect of spikelet fertility, days to 50% flowering, plant height and 1000 grain weight on grain yield.

Path analysis: The path coefficient evaluation using genotypic correlation indicates the interrelationships between the characters, which are illustrated in **Table 5.** The character total spikelet per panicle (2.9940) showed highest direct positive effect on grain yield per plant followed by spikelet fertility % (0.7118), test weight (0.6805), productive tillers per plant (0.5068) and panicle length (0.1516). Hence, direct selection for these characters will be beneficial for yield improvement programme. The characters days to 50% flowering (-0.0340), plant height (-0.0563) and fertile spikelet per panicle (-2.5506) observed negative direct effect on grain yield per plant. Similar types of findings were reported by Singh and Ekka (2019). Days to 50 per cent flowering showed positive correlation with grain yield per plant (0.3171) but it showed negative indirect effect with plant height (-0.0119), panicle length (-0.0062), productive tillers per plant (-0.0019), fertile spikelet per panicle (-0.0183), total spikelet per panicle (-0.0166) and spikelet fertility % (-0.0157). Days to 50% flowering showed positive indirect effect with test weight (0.0051).

Table 5: Direct (diagonal) and indirect (above and below diagonal) path effects of different characters towards grain yield at genotypic level in rice

Sl. No.	Days to 50% flowering	Plant Height (cm)	Panicle length (cm)	Productive tillers per plant	Fertile spikelet per panicle	Total spikeletper panicle	Spikelet Fertility %	Test Weight (g)	Grain Yield per plant (g)
	1	2	3	4	5	6	7	8	9
1.	**-0.0340**	-0.0119	-0.0062	-0.0019	-0.0183	-0.0166	-0.0157	0.0051	0.3171**
2.	-0.0196	**-0.0563**	-0.0277	0.0034	-0.0126	-0.0116	-0.0100	-0.0033	0.1903
3.	0.0276	0.0745	**0.1516**	-0.0071	-0.0079	-0.0106	0.0001	0.0621	0.2974**
4.	0.0281	-0.0306	-0.0239	**0.5068****	0.1004	0.0897	0.0649	-0.0326	0.5732**
5.	-1.3752	-0.5701	0.1334	-0.5054	**-2.5506**	-2.5024	-1.2075	1.0318	0.5101**
6.	1.4646**	0.6189**	-0.2087	0.5300**	2.9374**	**2.9940****	0.8905**	-1.3297	0.4519**
7.	0.3277**	0.1261	0.0002	0.0911	0.3370**	0.2117	**0.7118****	0.0239	0.4570**
8.	-0.1021	0.0397	0.2787*	-0.0437	-0.2753	-0.3022	0.0229	**0.6805****	0.4378**

(Residual effect = 0.1035) *, ** Significant at 5 and 1 per cent, respectively

Productive tillers per plant showed significant positive correlation (0.5732) with grain yield, it also had the significantly positive direct effect (0.5068) on grain yield. The character influences the yield positively indirect effect with days to 50% flowering (0.0281), fertile spikelet per panicle (0.1004), total spikelet per panicle (0.0897), spikelet fertility % (0.0649). It also had negative indirect effect on grain yield with plant height (-0.0306), panicle length (- 0.0239) and test weight (-0.0326). Total spikelets per panicle had significant positive direct effect (2.9940) on grain yield per plant and indirect effect through days to

50% flowering (1.4646), plant height (0.6189), productive tillers per plant (0.5300), fertile spikelets per panicle (2.9374) and spikelet fertility (0.8905). It also observed that character had negative indirect effect like Panicle Length (- 0.2087) and Test weight (-1.3297). Test weight had positive direct effect (0.6805) on grain yield per plant and had positive significant correlation (0.4378) on grain yield. It had positive indirect effect through plant height (0.0397), panicle length (0.2787), spikelet fertility % (0.0229).

The residual effect determines how well the causal factors account for the variability of the dependent factors, in this case, the grain yield. The residual effect in the current study was relatively low (0.1035), indicating that the characters selected were sufficient for explaining variability in rice grain yield. The productive tillers per plant, total spikelet per panicle, spikelet fertility % and test weight identified as important components of rice grain yield. Similar type of association was recorded by Akinwale *et al*., (2011) for productive tillers per plant and test weight and, Hasan *et al*., (2011) for productive tillers per plant, spikelet fertility % and test weight and,

Conclusion

The trait grain yield per plant and grain iron content observed high magnitude of GCV and PCV this indicates that there is opportunity for improvement through selection. There was a high heritability with a high genetic advance as per cent of mean for the traits grain yield per plant, grain iron content, grain zinc content, fertile spikelets per panicle, 1000 grain weight, total spikelets per panicle, plant height and days to 50 per cent flowering indicated that these characters were primarily governed by additive gene action and selecting for these traits would be more effective in achieving desired genetic improvement. Grain yield per plant had significant and positive correlation with days to 50 per cent flowering, panicle length, fertile spikelets per panicle, total spikelets per panicle, spikelet fertility, test weight and productive tillers per plant. In the path analysis, highest and significant positive direct effect on grain yield per plant was recorded through total spikelet per panicle followed by spikelet fertility per cent, test weight, productive tillers per plant and panicle length. The direct selection of these traits will be beneficial for yield improvement programmes.

Acknowledgements

The authors are thankful to the Director, ICAR-IIRR, Hyderabad, Rice Specialist, RARS, Karjat, Officer In-charge, ARS, Radhnagari, ZARS, Igatpuri, ARS, Sakoli and ARS, Vadgaon Maval for supply of seed material.

References

Adhikari BN, Joshi BP, Shrestha J and Bhatta NR. 2018. Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (*Oryza sativa* L.). *Journal of Agriculture and Natural Resources*, 1(1): 149-160.

Aditya JP and Bhartiya A. 2013. Genetic variability, correlation and path analysis for quantitative characters in rainfed upland rice of Uttarakhand hills. *Journal of Rice Research*, 6(2): 24-34.

Akinwale MG, Gregorio NF, Akinyel BO, Ogunbaya SA and Odiyi C. 2011. Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *African Journal of Plant Science*, 5(3): 207-212.

Burton GW. 1952. Quantitative inheritance in grasses. In: Proceedings of 6th International Grassland Congress, Pennsylvania State College, USA. pp. 277-283.

Dewey DR and Lu K. 1959. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy journal*, 51(9): 515-518.

Divya J, Raju CD, Rao LS and Aparna K. 2018. Genetic Variability Studies in genetically diverse rice genotypes. *International Journal of Current Microbiology and Applied Science*, 7(4): 1169-1172.

Hanson GH, Robinson HF and Comstock RE. 1956. Biometrical studies of yield segregating

population of Korean lespedeza. *Agronomy Journal*, 48(6): 268-272.

Hasan MJ, Kulsum MU, Akter A, Masuduzzaman ASM and Ramesha MS. 2011. Genetic variability and character association for agronomic traits in hybrid rice (*Oryza sativa* L.). *Bangladesh Journal of Plant Breeding and Genetics*, 24(1): 45-51.

Iqbal T, Hussain I, Ahmad N, Nauman M, Ali M, Saeed S and Ali F. 2018. Regular article genetic variability, correlation and cluster analysis in elite lines of rice. *Journal of Scientific Agriculture*, 2: 85-91.

Johnson HW, Robinson HF and Comstock RE. 1955. Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, 47: 314-318.

Kamana B, Ankur P, Subarna S, Prasad KB and Koshraj U. 2019. Genetic variability, correlation and path analysis of rice genotypes in rainfed condition at Lamjung, Nepal. *Russian Journal of Agriculture Social and Economic Science*, 92(8): 274-280.

Khan M. 2018. Evaluation of various rice (*Oryza sativa* L.) genotypes for yield and yield characters under agro ecological conditions of Peshawar. *Advances in Plants and Agriculture Research*, 8(6): 491-494.

Khush GS. 2013. Strategies for increasing the yield potential of cereals: case of rice as an example. *Plant Breeding*, 132(5): 433-436.

Mackill DJ, Ismail AM, Singh US, Labios RV and Paris TR. 2012. Development and rapid adoption of submergence-tolerant (Sub1) rice varieties. *Advances in Agronomy,* 115: 299-350.

Maurya RK, Dwivedi DK, Khan NA, Giri SP and Dixit S. 2022. Genetic variability studies for qualitative and quantitative traits in rice (*Oryza sativa* L.). *The Pharma Innovation Journal*, 11(5): 1140-1143.

Pachauri A, Sarawgi AK, Bhandarkar S and Ojha GC. 2017. Genetic variability and association study for yield contributing traits of promising core rice germplasm accessions (*Oryza sativa* L.). *Research on Crops*, 18(1): 133-138.

Panigrahi AK, Bharathi M and Kumaravadivel N. 2018. Genetic variability and character association studies in advanced backcross generation of rice (*Oryza sativa* L.). *Journal of pharmacognosy and Phytochemistry*, 7(1): 2397-2400.

Panse VG and Sukhatme PV. (1995). Statistical Methods for Agricultural Workers. ICAR, New Delhi.

Ramanjaneyulu AV, Gouri Shankar V, Neelima T and Shashibhusahn D. 2014. Genetic analysis of rice (*Oryza sativa* L.) genotypes in aerobic conditions on alfisols. *SABRAO Journal of Breeding and Genetics*, 46 (1): 99-111.

Roy A, Hijam L and Roy SK. 2021. Genetic variability and character association studies for quality attributing traits in rice (*Oryza Sativa* L.). *Electronic Journal of Plant Breeding*, 12(4): 1201-1208.

Shaili MR, Kumar GV, Lal GM and Lavanya GR. 2022. Assessment of genetic diversity in rice (*Oryza sativa* L.) Genotypes for grain yield characters. *International Journal of Environment and Climate Change,* 12(11): 1113-1122.

Singh RK and Chaudhary BD. (1977) Biometrical methods in quantitative genetic analysis. *Kalyani Publishers*, New Delhi.

Singh A and Ekka RE. 2019. Correlation and path analysis in aromatic and pigmented genotypes of rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Science*, 8(4): 1832-1837.

Singh SK, Singh CM and Lal GM. 2011. Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). *Research in Plant Biology*, 1(4): 73-76.

Singh SK, Pandey V, Mounika K, Singh DK, Khaire AR, Habde S and Majhi PK. 2020. Study of genetic divergence in rice (*Oryza sativa* L.) genotypes with high grain zinc using Mahalanobis' D^2 analysis. *Electronic Journal of Plant Breeding,* 11(02): 367-72.

Sivasubramanian S and Madhavamenon P. 1973. Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*, 60(9/13): 1093-1096.

Sumanth V, Suresh BG, Ram BJ and Srujana G. 2017. Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.). *Journal of Pharmacognosy and Phytochemistry,* 6(4): 1437-1439.

RESEARCH ARTICLE https://doi.org/10.58297/NDBN4905

Genetic Variability Studies in Rice Genotypes

Jyothsna B[1], Roja V [2*], Krishnaveni B[1], Prasanna kumari V[3] and Pranaya J[1]

[1]Department of Genetics and Plant Breeding, ANGRAU, Maruteru

[2]Department of Molecular Biology and Biotechnology, ANGRAU, Maruteru

[3]Department of Plant Pathology, Acharya N.G. Ranga Agricultural University

*Corresponding author Email: v.roja@angrau.ac.in

Received : 29th July, 2024; Accepted: 30th September, 2024

Abstract

Seventy-four rice genotypes were evaluated to assess their genetic variability, heritability and genetic advance as per cent of mean. The analysis of variance revealed significant differences for all the characters under the study except number of productive tillers per plant, indicating the presence of high genetic variability among the genotypes. The genotypes per se performance revealed BPT 3130, BPT 3164, BPT 3264, BPT 3092, BPT 3275, BPT 2824, BPT 2954, BPT 3276, BPT 3095 and BPT 3178 exhibiting significant superiority over the check Samba Mahsuri for the characters *viz.*, grain yield per plant, test weight and panicle length. The high estimates of GCV and PCV were observed for grain yield per plant. High heritability coupled with high expected genetic advance as per cent of mean was observed for test weight and grain yield per plant suggesting that selection for the improvement of these traits may be rewarding.

Keywords: Analysis of variance, GCV, PCV, heritability, genetic advance as per cent of mean

Introduction

Rice (*Oryza sativa*, 2n=2x=24) occupies a notable position among food grains by directly feeding the majority of people more than any other crop. The demand for rice production is increasing day by day because of the increase in the number of rice consumers. To meet this demand, it is necessary to enhance the production and productivity of rice cultivars. The success of any breeding programme depends on the degree of variability present in the germplasm. Before initiating any breeding programme, knowledge on the nature and magnitude of genetic variation governing the inheritance of characters and as well as adopting appropriate selection techniques is essential for genetic improvement. Genetic parameters such as Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) are useful in detecting the amount of variability present in the population (Idris *et al.,* 2012). It is very difficult to judge whether detected variability is heritable or not. Heritability indicates the extent of transmissibility of a character into future generations. Heritability can be either broad sense or narrow sense. Broad sense heritability is the relative magnitude of genotypic and phenotypic variances for the traits and has a predictive role in selection procedures (Allard, 1960). This gives an idea of total variation ascribed to genotypic effects, which are the exploitable portion of variation (Mba and Dixon, 1995). The magnitude of variation due to the heritable component is very important because it would be a guide for the selection of parents for crop improvement (Dutta *et al.,* 2013) and also plays a vital role to plan an efficient breeding program for the genetic improvement of quantitative traits (Seyoum *et al.,* 2012). The estimate of heritability alone is

not very much useful because it includes the effect of both additive and non-additive genes. The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population (Vanniarajan *et al.,*1996).

Identification of effective selection criteria is very important in any breeding programme for effective yield improvement. The present investigation was undertaken in this context to elucidate information on variability, heritability and genetic advance in rice genotypes for utilization in the further breeding programme.

Materials and Methods

The material for the present study consists of 74 rice genotypes including yield check Samba Mahsuri. These genotypes were evaluated in an augmented randomized complete block design during *kharif,* 2021 at Agricultural College Farm, Bapatla and Andhra Pradesh. Observations were recorded for the characters, plant height (cm), number of productive tillers per plant, panicle length (cm), spikelet fertility (%), test weight (g), grain yield per plant (g) and days to 50 per cent flowering.

Statistical analysis

The mean data of all the characters were subjected to analysis of variance (ANOVA) based on the model proposed by Federer (1956) using Windostat Version 9.3. Different genetic parameters such as genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean were estimated by using the following formula.

Estimation of genotypic and phenotypic variances

The genotypic and phenotype variances were calculated as per the formulae proposed by Burton and Devane (1953).

Phenotypic standard deviation (σp) =	$\sqrt{\sigma^2 p} = \sqrt{\sigma^2 g} + \sqrt{\sigma^2 e}$

$$GCV = \frac{\text{Genotypic standard deviation } (\sigma g)}{(\text{General mean } (\bar{x})} \text{ X } 100$$

$$PCV = \frac{\text{Phenotypic standard deviation } (\sigma p)}{(\text{General mean } (\bar{x})} \text{ X } 100$$

GCV and PCV values were categorized as low (<10%), moderate (10-20%) and high (>20%) (Subramaniam and Menon, 1973).

Estimation of heritability (broad sense)

Heritability in broad sense (h^2) was computed and categorized as per the suggestions of Hanson *et al.,* (1956) and Johnson *et al.,* (1955) respectively.

$$GCV = \frac{\text{Genotypic variance } (\sigma 2g)}{(\text{Phenotypic variance } (\sigma 2p)} \text{ X } 100$$

Heritability was classified as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson *et al.,* (1955).

Estimation of genetic advance

From the heritability estimates, the genetic advance (GA) was calculated by the following formula given by Lush (1940) and Johnson *et al.,* (1955).

Genetic Advance (GA) = $K \times \sigma_p \times h^2_{(b)}$

Where,

K=Selection differential at 5% selection intensity which accounts to a constant value of 2.06

$h^2_{(b)}$ = Heritability in broad sense.

σ_p= Phenotypic standard deviation.

Estimation of Genetic advance as per cent of mean (GAM)

Genetic advance as per cent of mean was calculated as per the formula

$$GAM = \frac{\text{Genetic advance}}{\text{General mean } (\bar{x})} \text{ X } 100$$

The degree of genetic advance as per cent of mean was classified as suggested by Johnson *et al.,* (1955) as low (<10%), moderate (10-20%) and high (>20%).

Results and Discussions

Analysis of variance

The ANOVA results indicated significant variability among the genotypes for all the characters studied except for the trait number of productive tillers per plant. Similar results were reported by Chandramohan *et al.,* (2016). Analysis of variance for the yield and yield component traits was furnished in **Table 1**.

Table 1: Analysis of variance for yield and yield component traits

Sources of variation	d. f	DFF	PH	NPT	PL	SF	TW	GYP
		Mean sum of squares						
Blocks	4	3.576	20.401	1.175	0.376	4.09	0.066	1.591
Entries	73	94.345 **	143.158 **	4.296	4.262 **	26.372 **	9.456 **	45.571 **
Genotypes	69	49.023 **	82.952 **	3.962	3.952 **	24.139 **	5.014 **	45.524 **
Checks	3	797.333 **	1138.847 **	6.467	3.729 *	47.576 **	110.531 **	53.010 **
Checks vs Genotypes	1	1112.584 **	1310.292 **	20.829 *	27.280 **	116.870 **	12.714 **	26.518 *
Error	12	3.375	8.573	2.342	1.05	4.944	0.089	3.421

*Significant at 5% level; **Significant at 1% level; DFF: Days to 50% flowering; PH: Plant hieght; NPT No. of productive tillers; PL: Panicle length; SF: Spikelet fertility %; TW: Test weight; GYP: Grain yield for plot.

Mean performance

Mean values of the seventy-four genotypes along with the standard yield check Samba Mahsuri for the studied seven quantitative characters were presented in **Table 2**. Genotype TN1 was found earliest in flowering (85 days) suggesting that this genotype can be used as a donor in the hybridization programme for evolving short-duration rice variety. Genotype Samba Mahsuri and BPT 3068 were recorded as the shortest and tallest, respectively. The highest mean performance for productive tillers per plant was observed in BPT 2808 (15 tillers) followed by BPT 2824 (13 tillers). Genotype BPT 3137 (29.80 cm) exhibited the highest mean performance for panicle length. The maximum grain yield per plant was observed 41.71 g by BPT 2854 indicating that these genotypes can be used in a hybridization programme to achieve a desirable increment in yield. A critical analysis on the mean performance of the genotypes studied revealed that BPT 3130, BPT 3164, BPT 3264, BPT 3092, BPT 3275, BPT 2824, BPT 2954, BPT 3276, BPT 3095, BPT 3178 exhibited significant superiority over the check Samba Mahsuri for the characters grain yield per plant, test weight, panicle length and were also on par for spikelet fertility and productive tillers per plant.

Table 2: Mean performance of rice genotypes for yield and yield components

Sl. No	Genotypes	DFF	PH	NPT	PL	SF	TW	GYP
1	BPT 1235	90	101.90	7	24.04	88.47	18.83	24.30
2	BPT 2231	116	98.40	10	25.30	93.21	19.39	26.81
3	BPT 2295	122	109.80	12	22.26	88.54	15.13	30.55
4	BPT 2411	113	116.00	8	25.25	79.69	19.56	23.01
5	BPT 2595	121	102.20	8	22.88	92.42	14.81	18.25
6	BPT 2620	102	108.40	7	23.10	90.07	16.01	20.88
7	BPT 2677	98	103.00	8	24.90	85.97	21.44	25.62
8	BPT 2764	121	105.80	8	23.50	88.72	16.48	15.54

Sl. No	Genotypes	DFF	PH	NPT	PL	SF	TW	GYP
9	BPT 2766	110	104.40	8	22.10	89.75	14.93	19.61
10	BPT 2776	116	107.80	10	22.90	94.39	16.03	27.05
11	BPT 2782	114	95.80	8	20.88	96.23	15.14	20.75
12	BPT 2808	112	101.00	15	21.80	87.82	15.81	30.52
13	BPT 2824	110	109.80	13	23.88	86.76	16.17	34.82
14	BPT 2846	111	101.40	6	22.30	84.45	15.28	32.12
15	BPT 2848	109	117.80	8	20.04	87.79	14.38	24.65
16	BPT 2849	111	111.00	8	24.28	79.60	19.38	16.12
17	BPT 2854	112	111.20	12	21.00	92.61	20.28	41.71
18	BPT 2863	114	105.00	9	23.40	91.82	16.35	29.08
19	BPT 2950	110	115.60	5	22.00	86.63	19.80	13.65
20	BPT 2954	96	130.80	9	22.90	93.65	18.68	34.48
21	BPT 2958	108	105.60	7	20.90	82.92	19.53	23.50
22	BPT 3032	101	104.40	8	22.20	91.08	22.19	22.61
23	BPT 3033	115	106.00	10	20.50	86.10	15.00	20.14
24	BPT 3061	110	117.60	8	24.20	94.60	15.57	19.34
25	BPT 3068	110	137.20	9	26.30	93.02	16.93	19.72
26	BPT 3074	95	114.80	9	21.90	92.94	16.94	30.51
27	BPT 3081	106	103.00	6	20.50	90.09	16.26	18.33
28	BPT 3086	110	122.20	5	28.70	86.29	16.57	16.86
29	BPT 3092	90	125.40	10	24.70	93.14	22.28	36.89
30	BPT 3095	114	118.80	8	24.80	96.32	21.19	34.04
31	BPT 3111	106	110.00	8	24.80	88.21	19.08	27.29
32	BPT 3113	107	104.20	9	26.50	84.07	18.13	32.16
33	BPT 3114	110	117.80	9	23.90	93.59	15.84	20.92
34	BPT 3115	110	97.60	12	21.70	94.67	14.58	30.71
35	BPT 3118	111	98.20	11	21.80	79.31	14.61	30.28
36	BPT 3120	110	93.60	9	21.40	86.53	20.02	23.50
37	BPT 3121	106	101.00	11	22.25	88.29	15.61	28.62
38	BPT 3129	110	109.40	7	22.38	81.92	16.55	24.04
39	BPT 3130	110	111.60	11	23.70	91.74	17.04	41.02
40	BPT 3133	109	115.40	10	22.80	94.07	15.78	27.01
41	BPT 3135	102	128.00	8	24.30	91.68	16.96	27.94
42	BPT 3136	107	116.20	7	24.10	87.02	17.85	26.95
43	BPT 3137	114	132.40	6	29.80	79.31	14.59	22.32
44	BPT 3145	119	107.60	7	25.10	91.73	23.61	20.33
45	BPT 3147	114	116.60	9	22.20	85.71	14.60	24.97
46	BPT 3148	110	109.60	6	21.90	85.40	19.60	28.08
47	BPT 3150	110	102.80	7	25.40	89.78	18.02	23.06
48	BPT 3151	101	106.80	9	22.30	76.74	16.06	32.93

Sl. No	Genotypes	DFF	PH	NPT	PL	SF	TW	GYP
49	BPT 3159	114	112.80	10	25.10	91.97	18.53	29.28
50	BPT 3164	105	105.20	12	22.75	87.87	20.40	40.86
51	BPT 3168	110	116.40	7	22.63	85.29	16.92	18.54
52	BPT 3170	106	114.20	7	22.60	85.54	19.32	23.61
53	BPT 3172	96	104.20	7	21.30	88.86	14.34	20.33
54	BPT 3178	106	100.60	11	24.20	91.53	18.90	33.56
55	BPT 3208	108	107.40	8	21.60	93.59	17.29	21.48
56	BPT 3244	105	108.60	10	22.60	90.76	15.54	27.54
57	BPT 3260	111	112.40	11	25.00	76.82	16.99	31.80
58	BPT 3261	113	111.40	6	26.83	85.70	19.30	15.91
59	BPT 3262	98	122.60	6	26.50	89.62	21.03	18.20
60	BPT 3263	112	126.00	9	25.70	90.80	17.68	23.03
61	BPT 3264	96	115.00	11	23.60	91.85	17.03	37.25
62	BPT 3269	98	109.40	8	21.70	95.64	14.69	20.36
63	BPT 3270	118	118.20	8	28.60	87.02	17.85	22.92
64	BPT 3274	118	116.00	6	25.30	88.73	18.89	27.61
65	BPT 3275	119	114.40	8	22.20	76.85	15.63	36.32
66	BPT 3276	113	116.40	7	23.60	94.13	19.19	34.25
67	BPT 3277	108	100.60	7	21.20	82.35	17.79	20.09
68	BPT 3279	106	108.20	10	24.20	93.41	16.42	25.33
69	BPT 3291	110	101.00	7	22.90	89.78	16.35	21.21
70	BPT 4358	117	93.50	7	23.00	82.38	13.64	12.87
71	Improved Samba Mahsuri	96	92.06	9	21.84	87.42	13.99	19.87
72	Krishnaveni	108	97.56	8	22.82	90.14	19.29	24.83
73	TN 1	85	123.46	10	22.86	92.60	24.43	25.87
74	Samba Mahsuri (Yield Check)	113	91.66	11	21.06	94.23	15.45	27.40
	Min	85	91.66	5	20.04	76.74	13.64	12.87
	Max	122	137.20	15	29.80	96.32	24.43	41.71
	Mean	**108**	**109.87**	**9**	**23.40**	**88.65**	**17.46**	**25.73**
	CV %	**6.99**	**8.62**	**13.60**	**8.70**	**5.61**	**13.64**	**15.68**
	C.D. (0.05)	**2.53**	**4.03**	**2.11**	**1.41**	**3.06**	**0.41**	**2.55**

Variability, Heritability and Genetic advance as per cent of mean

The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance as per cent of mean (GAM) are presented in **Table 3** and **Figures 1 and 2**. The results are discussed here under. GCV and PCV are high for grain yield per plant (22.66% and 23.77%) indicating the existence of sufficient variation among the genotypes for potential yield improvement through selection. High GCV,

PCV for grain yield per plant were also observed in the findings of Nithya *et al.,* (2020), Bhargava *et al.,* (2021), Chamar *et al.,* (2021), Gupta *et al.,* (2021) and Priyanka *et al.,* (2023). The traits like days to 50% flowering (5.84% and 5.59%), plant height (7.52% and 7.04%), panicle length (7.86% and 6.54%), spikelet fertility (5.12% and 4.46%) exhibited low phenotypic and genotypic coefficient of variation indicating the presence of less genetic variability as a result of which there is less scope for selection. Similar results were observed by Mohan *et al.,* (2016), Jan *et al.,* (2017), Adhikari *et al.,* (2018), Nithya *et al.,* (2020), Bhargava *et al.,* (2021) and Teja *et al.,* (2023).

High estimates of heritability combined with high genetic advance was observed for test weight (97.83%, 23.40) and grain yield per plant (90.90%, 44.51) provides evidence that this was under the control of additive gene effects and selection may be effective. Similar results were also reported earlier by Anyaoha *et al.,* (2018), Nithya *et al.,* (2020), Chamar *et al.,* (2021), Bhargava *et al.,* (2021), Gupta *et al.,* (2021) and Priyanka *et al.,* (2023). Similarly high heritability coupled with moderate genetic advance was observed for days to 50% flowering (91.65%, 11.03), plant height (87.57%, 13.57), panicle length (69.17%, 11.20) indicating the preponderance of additive and non-additive gene actions in the expression of this trait. The results were in conformity with Gampala *et al.,* (2015), Mohan *et al.,* (2016), Adhikari *et al.,* (2018) and Bhargava *et al.,* (2021) whereas spikelet fertility (75.91%, 8.01) had exhibited high heritability combined with low genetic advance as per cent of mean due to the favourable influence of environment rather than the genotype, indicating the possibility of improvement of the trait through heterosis breeding rather than simple selection. High heritability coupled with low genetic advance as per cent of mean for spikelet fertility was reported by Parimala *et al.,* (2021).

Conclusion

In a nutshell, based on the results obtained, the studied rice genotypes showed adequate variability. High PCV and GCV were recorded for grain yield per plant indicating the existence of large variation among the genotypes for potential yield improvement through selection. High heritability coupled with high genetic advance as per cent of mean was observed for the traits test weight and grain yield per plant revealing that these traits are governed by additive gene action and therefore selection can be practiced based on phenotypic performance.

Table 3: Variability, heritability and genetic advance as per cent of mean for yield and yield component traits

S. No.	Character	Coefficient of variation		Heritability (%)	Genetic advance as Per cent of mean
		PCV (%)	GCV (%)		
1	Days to 50 per cent flowering	5.84	5.59	91.65	11.03
2	Plant height	7.52	7.04	87.57	13.57
3	Number of productive tillers	22.39	13.43	35.97	16.58
4	Panicle length	7.86	6.54	69.17	11.20
5	Spikelet fertility	5.12	4.46	75.91	8.01
6	Test weight	11.61	11.49	97.83	23.40
7	Grain yield per plant	23.77	22.66	90.90	44.51

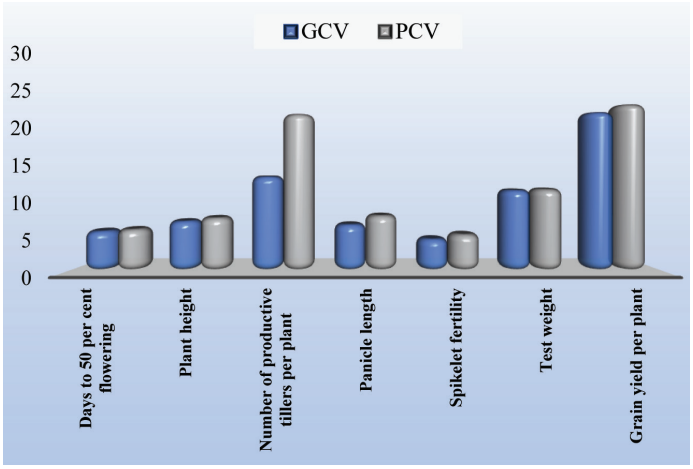


Figure 1: Variability parameters for yield and yield component traits

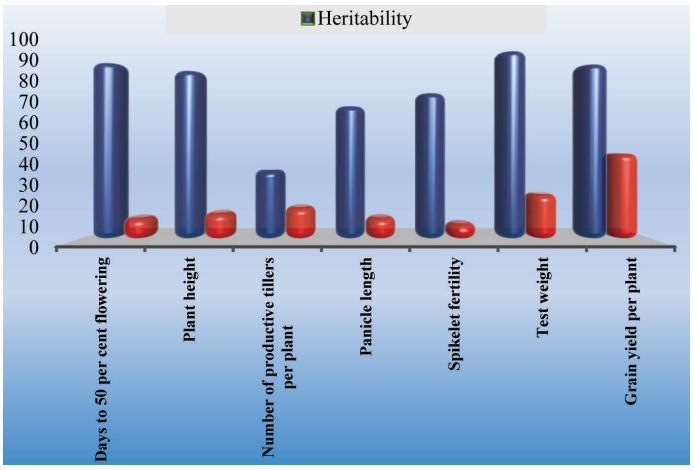


Figure 2: Heritability and Genetic advance as per cent mean for yield and yield component traits

References

Adhikari BN, Joshi BJ, Shrestha J and Bhatta NR. 2018. Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (*Oryza sativa* L.). *Journal of Agriculture and Natural Resources*, 1(1): 149-160.

Allard RW. 1960. Principles of Plant Breeding. John Wiley and Sons, Inc. New York, p. 485.

Anyaoha C, Adegbehingbe F, Uba U, Popoola B, Gracen V, Mande S, Onotugoma E and Fofana M. 2018. Genetic diversity of selected upland rice genotypes (*Oryza sativa* L.) for grain yield and related traits. *International Journal of Plant and Soil Science,* 22(5): 1-9.

Bhargava K, Shivani D, Pushpavalli SNCVL, Sundaram RM, Beulah P and Senguttuvel P. 2021. Genetic variability, correlation and path coefficient analysis in segregation population of rice. *Electronic Journal of Plant Breading,* 12(2): 549-555.

Burton GW and Devane EM. 1953. Estimating heritability in tall Fescue (*Festuca arundinaceae*) from replicated clonal material. *Agronomy Journal*, 51: 515-518.

Chamar JP, Joshi RP, Katkani D, Sahu D and Patel V. 2021. Genetic variability, heritability and correlation coefficient analysis in rice (*Oryza sativa* L.) germplasm. *The Pharma Innovation Journal*, 10(5): 763-769.

Chandramohan Y, Srinivas B, Thippeswamy S and Padmaja D. 2016. Diversity and variability analysis for yield parameters in rice (*Oryza sativa* L.) genotypes. *Indian Journal of Agricultural Research*, 50(6): 609-613.

Dutta P, Dutta PN and Borua PK. 2013. Morphological Traits as Selection Indices in Rice: A Statistical View. *University Journal Agricultural Res*earch, 1(3): 85-96.

Federer WT 1956. Augmented designs. *Hawaiian Planter's Record*, 55: 191-208.

Gampala S, Vikram JS, Pathak SK, Srivastava N, Kaushik SK and Rangare NR. 2015. Estimation of genetic variability for yield and quality traits in rice (*Oryza sativa* L.) genotypes. *Environment and Ecology*, 33(1a): 303-305.

Gupta S, Gauraha D, Sao A and Chaudhary PR. 2021. Assessment of genetic variability, heritability and genetic advance in accessions of rice (*Oryza sativa* L.). *The Pharma Innovation Journal*, 10(6): 1231-1233.

Hanson CH, Robinson HF and Comstock RE. 1956. Biometrical studies of yield in segregating populations of Korean lespedza. *Agronomy Journal*, 48(6): 268-272.

Idris AE, Justin FJ, Dagash YMI. and Abduli AI. 2012. Genetic variability and inter relationship between yield and yield components in some rice genotypes, *American Journal of Experimental Agriculture*, 2(2): 233-239.

Jan N, Lal EP, Kashyap SC and Arpit G. 2017. Genetic variability, character association and path analysis studies for grain yield and contributing traits in rice (*Oryza sativa* L.) under temperate conditions of Kashmir. *Vegetos*, 30(2): 1-7.

Johnson HW, Robinson HF and Comstock RE. 1955. Estimation of genetic and environmental variability in soybean. *Agronomy Journal*, 47(7): 314-318.

Lush JL. 1940. Intra-sire correlation on regression of off-spring on dams as a method of estimating heritability of characters. *Proceedings of American Society of Animal Production*, 33: 292-301.

Mba REC and Dixon AGO. 1995. Genotype by environment interaction, phenotypic stability of cassava yields and heritability estimates for production and pest resistance traits in Nigeria. Proceeding of the *6th Triennial Symposium of the International Society for Tropical Root Crops-AB Lilonge*, Malawi, 22-28 October,1995. pp. 255-261.

Mohan VC, Srinivas B, Thippeswamy S and Padmaja D. 2016. Diversity and variability analysis for yield parameters in rice (*Oryza sativa* L.) genotypes. *Indian Journal of Agricultural Research*, 50(6): 609-613

Nithya N, Beena R, Stephen R, Abida PS, Jayalekshmi VG, Viji MM and Manju RV. 2020. Genetic variability, heritability, correlation coefficient and path analysis of morphophysiological and yield related traits of rice under drought stress. *Chemical Science Review and Letters*, 9(33): 48-54.

Parimala K, Raju CHS, Kumar SS and Reddy SN. 2021.Genetic variability, correlation and path analysis in rice (*Oryza sativa* L.). *International Journal of Ecology and Environmental Science,* 3(1): 385-387.

Priyanka K, Krishna Veni B, Roja V and Jayalalitha K. 2023. Genetic Parameters and Association Studies for Morphological, Physiological and Grain Quality Parameters in Rice (*Oryza sativa* L.). *Journal of Rice Research*, 16(1): 48-56.

Seyoum M, Alamerew S and Bantte K. 2012. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). *Journal of Plant Science,* 7(1): 13-22.

Subramaniam S and Menon M. 1973. Inheritance of short stature in rice. *Madras Agriculture Journal*, 60(12): 1129-1133.

Teja DS, Divya B, Sonali K, Salam JL, Singh DP, Kumar AP, Swamy AVSR and Rao LVS. 2023. Genetic variability and correlation studies in high-yielding varieties of rice (*Oryza sativa* L.). *Journal of Rice Research,* 16(2): 22-30.

Vanniarajan C, Rangasamy P, Ramalingam J, Nadarajan N and Arumugampillai M. 1996. Studies on genetic variability in hybrid rice derivatives. *Crop Research*, 12(1): 24- 27.

RESEARCH ARTICLE HTTPS://DOI.ORG/10.58297/NPDI3188

Genetic Diversity Analysis of Rice Germplasm (*Oryza sativa* L.) Using Morphological Markers

Sudarshana Negi, Neelam Bhardwaj* Kajal Bhardwaj and Deepika Sud

Department of Genetics and Plant Breeding, CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur-176062

*Corresponding author Email: neenabhardwaj@gmail.com

Received : 15th July, 2024; Accepted: 3rd October, 2024

Abstract

The present investigation was carried out to assess the genetic diversity among 35 rice germplasm lines for 19 different traits including quantitative and grain quality traits. The genotypes were grouped into 8 clusters and out of these maximum number of genotypes were placed in cluster I (25 genotypes) followed by Cluster II (4 genotypes). The highest intra-cluster distance was observed for cluster I whereas, highest inter-cluster distance was recorded between cluster VII and cluster VIII. Cluster III, cluster V and cluster VIII showed the highest cluster mean values for most of the traits studied. The maximum contribution towards the genetic divergence was exhibited by spikelets per panicle followed by 1000 grain weight, days to 75% maturity and plant height. These traits, hence could be focused for selection improving grain yield. The germplasm lines falling in different clusters with high mean for grain yield and other component traits can be utilized for hybridization programme to obtain elite segregants.

Keywords: Rice germplasm, Markers, Genetic diversity, Cluster analysis

Introduction

Rice is the staple food for more than half the world's population of 7.8 billion people and plays a pivotal role in food security of many countries. More than 90% of the global production and consumption of rice is in Asia. It is the primary food source for more than one-third of the world's population and is grown on 11% of the world's cultivated area. It provides minerals, vitamins and fiber. To meet the challenge of producing more rice from limited available lands, we need varieties or hybrids which grow better under adverse conditions and possess high yield potential. Genetic diversity is the pre-requisite for any crop improvement programme because it helps in the development of superior recombinants, through selection of parents having wider variability for different characters. Since, the last few centuries, rice has faced loss in diversity due to replacement of native varieties with high yielding varieties (Choudhary *et al.,* 2013). Genetic divergence analysis evaluates the genetical distance among the selected genotypes and shows the relative contribution of specific traits towards the total divergence. A higher heterosis could be achieved from crosses between genetically distant parents (Falconer, 1960). Therefore, the present investigation is aimed to assess the nature and magnitude of genetic divergence present in the 35 germplasm lines of basmati rice and to select suitable diverse genotypes as parents for further utilization in crop improvement programmes.

Materials and Methods

Experimental Material and Plan

Experiment was conducted during *kharif,* 2022 at Chaudhary Sarwan Kumar Himachal Pradesh Krishi

Vishvavidyalaya Rice and Wheat Research Centre, Malan. The experimental material comprised of 35 germplasm lines of rice. The nursery was sown on 28th May and 21 days old seedlings were transplanted in the field in Randomized block design with three replications. Standard agronomic practices and plant protection measures were taken as per schedule. Each germplasm line was raised in a 3 rowed plot of 3 m length with a spacing of 20 × 15 cm respectively.

Morphological Markers

Observations were recorded on five randomly selected plants per replication for different quantitative traits: days to 50 per cent flowering (DF), days to maturity (DM), total tillers per plant (TT), effective tillers per plant (ET), plant height (PH), panicle length (PL), spikelets per panicle (SPP), grains per panicle (TG), spikelet fertility per centage (SFP), 1000- grain weight (TW) biological yield per plant (g), harvest index per cent and grain yield per plant (GYPP); four quality traits: grain length (GL), grain breadth (GB), L/B ratio (LB) and amylose content (AC).

Statistical analysis

Genetic divergence was estimated by Mahalanobis' D^2 statistics (1936). The germplasms lines were grouped into a number of clusters by Tocher's method described by Rao (1952). Each character was ranked on the basis of values in all the combination of genotype for estimation of contribution of individual characters towards divergence.

Results and Discussions

Cluster distances and composition

It is the task of grouping a set of genotypes in which accessions falling in the same group are more similar to each other than to those in other groups or clusters which is very helpful in diversity analysis. In the present investigation with nonhierarchical Euclidean cluster analysis, 35 rice germplasm lines were grouped into eight different clusters based on the *inter se* genetic distances. Out of eight clusters two clusters were polygenotypic while six were monogenotypic based on genetic divergence. Maximum number of genotypes were placed in cluster I (25 genotypes) followed by cluster II (4 genotypes), cluster III (1 genotype) and cluster IV (1 genotype), cluster V (1genotype), cluster VI (1 genotype), cluster VII (1 genotype), cluster VIII (1genotype). Genotypes falling under each cluster are presented in **Table 1** which indicates cluster 1 represent maximum genotypes. Similar studies were taken up by Chakravorty *et al.,* (2013) who assessed genetic divergence among 51 rice genotypes and grouped them into 11 clusters using D^2 analysis and Akhter *et al.,* (2022) who assessed genetic divergence among rice genotypes and grouped them into different clusters using D^2 analysis. Rao *et al.,* (2018) conducted diversity analysis in rice germplasm and divided the genotypes into 8 clusters. Tushara *et al.,* (2022) also conducted similar studies on grouping of rice germplasm into different clusters.

Table 1: Grouping of rice genotypes into different clusters on the basis of Mahalanobis D^2 -analysis

Clusters	No. of genotype	Genotypes
Cluster 1	25	HPR-5021, HPR-5024, HPR-2612, HPR-5022, HPR-5007, HPR-5015, HPR-5008, PB-1509, HPR-3221,Kasturi,HPR-5020, HPR-2750, HPR-5023, HPR-5016, HPR-5001, HPR-5018, HPR5017, HPR-5003, HPR5012, HPR-5009, HPR-5013, HPR-5026,HPR- 2749,HPR-5019, HPR-5025
Cluster 2	4	HPR-5004,HPR-5005, HPR-5002, HPR-5006
Cluster 3	1	HPR-2696
Cluster 4	1	HPR-5014
Cluster 5	1	HPR-5010
Cluster 6	1	HPR-3225
Cluster 7	1	HPR-5011
Cluster 8	1	HPR-5027

The average intra and inter-cluster distances are presented in **Table 2**. The highest intra-cluster distance is observed for cluster I (18.31), followed by cluster II (12.62) and no intra-cluster distance is observed for cluster III, cluster IV, cluster V, cluster VI, cluster VII and cluster VIII as these clusters possess only one genotype each. Presence of high intra-cluster distances revealed that genotypes within the same cluster were quite diverse; hence the selection of parents within the cluster would be effective. The highest inter-cluster distance was 42.92, which was observed between clusters VII and cluster VIII followed by VI and VII (39.80), V and VIII (35.02) ,V and VI (34.53), IV and VIII (34.17), II and VIII (33.01), I and VIII (32.02) and III and V (31.71) indicating that, hybridization between the most diverse genotypes would yield desirable segregants with the accumulation of favorable genes in the segregating generations, while, least inter cluster distance was observed between cluster V and VII (18.48) indicating that the genotypes belonging to these clusters were comparatively less diverse. Similar studies were also conducted by Kishore *et al.,* (2018), Vennila *et al.,* (2011), Chakravorty *et al.,* (2013) and Devi *et al.,* (2015).

Table 2: Average intra and inter-cluster distance

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	**18.31**	21.67	22.78	22.39	23.19	23.65	22.93	32.03
Cluster II	0	12.62	26.43	26.38	24.48	30.09	30.18	33.01
Cluster III		0	0	29.97	31.78	21.17	30.99	28.55
Cluster IV				0	21.95	25.22	22.87	34.17
Cluster V					0	34.53	18.48	35.02
Cluster VI						0	26.14	39.80
Cluster VII							0	**42.92**
Cluster VII								0

Cluster means for different characters:

The cluster means of rice genotypes falling under different clusters are presented in **Table 3**. Analysis of cluster means indicates existence of considerable differences in the mean values of different traits. The highest values of total tillers per plant, effective tillers per plant, biological yield per plant and amylose content were observed in cluster III. Cluster V showed highest value for plant height, flag leaf length, 1000-grain weight and grain breadth. Cluster VIII showed highest value for days to 50% flowering, days to 75% maturity, harvest index and grain yield per plant Cluster IV showed highest values for flag leaf breadth, grain length, L/B ratio. Cluster VI showed highest value for panicle length and spikelets per plant and cluster VII showed highest value for spikelet fertility and grains per panicle. The cluster IV exhibited minimum values for most of the traits *viz.*, days to 75% maturity, flag leaf length, total tillers per plant, effective tillers per plant, spikelet fertility, biological yield per plant and grain yield per plant while, cluster VI showed minimum values for plant height, grain length and grain breadth. Thus, various traits contribute to the total divergence in cluster, III, V and VII and the genotypes comprising these clusters seem to be quiet promising for many of the traits under study. Similar studies in rice were also done by Sharma *et al.,* (2011), Chakravorty *et al.,* (2013), Kumar (2015) and Amudha and Ariharasutharsan (2021).

Table 3: Cluster means of eight clusters for yield and yield related traits of rice genotypes

Cluster/ Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Mean	Min	Max
Days to 50% flowering	87.78	88.58	94.00	82.33	87.00	86.00	80.00	108.00	89.21	80.00*	108.00**
Days to 75% maturity	121.01	120.75	118.00	108.00	122.67	119.33	122.00	124.67	119.55	108.00*	124.67**
Plant height (cm)	120.69	128.74	108.13	122.20	146.87	85.93	112.53	134.93	120.00	85.93*	146.87**
Flag leaf Length (cm)	36.05	36.48	33.83	29.53	37.30	30.20	32.77	34.37	33.82	29.53*	37.30**
Flag leaf width (cm)	1.48	1.48	1.53	1.87	1.73	1.50	1.73	1.43	1.59	1.43*	1.87**
Total tillers per plant	8.39	8.02	11.47	6.60	8.53	11.30	9.27	7.60	8.90	6.60*	11.47**
Effective tillers per plant	7.93	7.34	10.47	6.47	8.13	10.40	8.47	7.47	8.34	6.47*	10.47**
Panicle length (cm)	25.64	25.42	24.30	24.97	24.07	26.70	23.80	23.13	24.75	23.13*	26.70**
Spikelets per plant	180.87	136.27	182.90	193.73	182.47	199.40	195.67	172.40	180.46	136.27 *	199.4 0**
Spikelet fertility (%)	91.96	94.29	94.57	76.23	97.10	78.07	98.17	96.03	90.80	76.23 *	98.17**
Grains per panicle	166.29	128.31	172.93	147.73	177.13	155.63	192.00	165.60	163.20	128.31*	192.00**
1000 grain weight (g)	23.73	23.23	20.63	26.20	31.13	22.73	30.17	26.23	25.51	20.63*	31.13**
Harvest index (%)	34.95	34.45	26.07	37.83	25.90	34.30	37.37	40.17	33.88	25.90*	40.17
Biological yield per plant (g)	43.82	37.13	58.63	33.23	55.27	40.6	39.6	44.93	44.15	33.23*	58.63**
Grain length (mm)	6.33	5.63	5.70	7.17	6.60	5.13	6.50	6.63	6.21	5.13*	7.17 **
Grain breadth (mm)	1.82	1.82	1.93	1.73	2.20	1.60	2.13	1.97	1.90	1.60*	2.20**
L/B ratio	3.52	3.12	2.96	4.15	3.00	3.22	3.06	3.39	3.30	2.96*	4.15**
Amylose content (%)	23.31	22.04	25.89	24.85	22.99	24.50	25.40	21.53	23.81	21.53*	25.89**
Grain yield per plant (g)	15.23	12.66	15.30	12.60	14.33	13.97	14.40	17.73	14.53	12.60*	17.73**

Trait contribution towards the divergence

A comparison of contribution of different traits towards genetic diversity was estimated based on ranking method. Contribution of different traits to total divergence is presented in **Table 4**. The maximum contribution towards the genetic divergence was exhibited by spikelets per panicle followed by 1000 grain weight, days to 75% maturity, plant height, days to 50% flowering, spikelet fertility, grain yield per plant, amylose content, grains per panicle, flag leaf length, grain length, flag leaf width, grain breadth, L/B ratio, harvest index and biological yield. Hence, spikelets per panicle, 1000 grain weight, plant height and days to 50% flowering, were found to be potential contributors to genetic divergence. The results are supported by the earlier findings of Devi *et al.,* (2015) and Rachappanavar (2017) who revealed similar findings.

Table 4: Relative contribution of individual trait towards divergence among rice genotypes

Traits	Rank	Contribution
Days to 50% flowering	48	7.62%
Days to 75% maturity	74	11.75%
Plant height	74	11.75%
Flag leaf Length	22	3.49%
Flag leaf width	8	1.27%
Total tillers	0	0.00%
Effective tillers	0	0.00%
Panicle length	0	0.00%
Spikelets per panicle	**185**	**29.37%**
spikelet fertility	31	4.92%
Grains per panicle	24	3.81%
1000 grain weight	88	13.97%
Harvest index	2	0.32%
Biological yield	1	0.16%
Grain length	10	1.59%
Grain breadth	6	0.95%
L/B ratio	5	0.79%
Amylose content	25	3.97%
Grain yield per plant	27	4.29%

Conclusion

A significant range of variation is evident among thirty-five rice genotypes evaluated in the present study. The thirty-five rice genotypes were grouped into eight clusters which was in consonance with the clustering pattern obtained by Mahalanobis D^2 statistics. The parents for hybridization program should be selected on the basis of magnitude of genetic distance, contribution of different characters towards the total divergence and magnitude of cluster means for different characters performance having maximum heterosis. Genetic diversity studies revealed that maximum number of genotypes were placed in cluster I. The highest intra-cluster distance was observed for cluster I, whereas, highest inter-cluster distance was recorded between cluster VII and cluster VIII followed by V and VII, IV and VIII, II and VIII, I and VIII and III. Hence, crosses between the genotypes of these clusters are expected to manifest high heterosis along with, accumulation of favorable genes in subsequent segregating generations.

References

Akhter MB, Mosab-Bin A, Kamruzzaman M, Reflinur R, Nahar N, Rana MS, Hoque MI and Islam MS. 2022. Morpho-molecular diversity study of rice cultivars in Bangladesh. *Czech Journal of Genetics and Plant Breeding,* 58(2): 64-72.

Alagappan P and Bhardwaj N. 2022. Morphological characterization of red rice germplasm of Himachal Pradesh and identification of potential genotype for yield and biotic stress tolerance. *Journal of Cereal Research,*14(1): 63-75.

Amudha K and Ariharasutharsan G. 2021. Genetic diversity analysis for yield and yield components in rice. *Journal of Rice Research*, 14(2): 18-26.

Chakravorty A and Ghosh PD. 2013. Genetic divergence analysis of traditional rice cultivars of West Bengal, India. *Electronic Journal of Plant Breeding*, 4(2): 1155-1160.

Choudhary G, Ranjitkumar N, Surapanen M, Deborah DA, Vipparla A and Anuradha G. 2013. Molecular genetic diversity of major Indian rice cultivars over decadal period. *PLoS One,* 8(6): e66197

Devi GN, Ravindrababu VR, Padmavathi G and Sunitha T. 2015. Genetic diversity in grain quality traits of rice genotypes. *Journal of Rice Research,* 8(1): 6-14.

Falconer S. 1960. Introduction to Quantitative Genetics. The Ronald Press, New York.

Kishore C, Kumar A, Pal AK, Kumar V, Prasad BD and Kumar A. 2018. Character association and path analysis for yield components in traditional rice (*Oryza sativa* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences*, 7(3): 283-291.

Kumar V. 2015. Genetic diversity and character association studies for some economic traits in rice (*Oryza sativa* L.). *The Bioscan*, 10(2): 899-904.

Mahalanobis PC. 1936. On the generalized distance in statistics. Proceedings of National Institute of Science. India, 1, Park Street and printed by P. Knight, Baptist Mension, Press 41A, Loar Circle Road: 12-49.

Rachappanavar V. 2017. Morphological and molecular characterization of traditional and improved germplasm of paddy cultivated in Himachal Pradesh. M.Sc. Thesis, Department of Genetics and Plant Breeding, CSK Himachal Pradesh Krishi Vishwavidyalaya, Palampur, India.

Rao Eswar R, Krishna Veni B, Rama Kumar P V and Srinivasa Rao V. 2018. Morphological and molecular diversity in rice (*Oryza sativa* L.) genotypes. *Journal of Rice Research*, 11(1): 1-6.

Rao CR. 1952. Advanced statistical methods in biometric research. Wiley, Oxford, England, 17(3): 390.

Sharma SK, Nandan R, Singh SK, Sharma AK, Kumar S, Sharma PK, Singh MK and Kumar V. 2011. Genetic divergence in rice (*Oryza sativa* L.) genotypes under irrigated condition. *Indian Journal of Agriculture,* 11(2): 321-325,

Tushara M, Krishna Veni B and Sambasiva Rao N 2022. Morphological characterization of advanced coloured rice genotypes. *Journal of Rice Research*, 15(2): 94-103.

Vennila S, Anbuselvam Y and Palaniraja K. 2011. D^2 analysis of rice germplasm for some quantitative and quality traits. *Electronic Journal of Plant Breeding*, 2(3): 392-403.

RESEARCH ARTICLE https://doi.org/10.58297/RIRZ5171

Unveiling Genetic Variation in Rice Hybrids Through Hierarchical Clustering and Principal Component Analysis

Vijay Kumar Reddy C, Amarnath K and Ravi Kumar BNVSR*

Acharya N. G. Ranga Agricultural University, Regional Agricultural Research Station, Nandyal, Andhra Pradesh

*Corresponding author Email: bnvsr.ravikumar@angrau.ac.in

Received: 13th August, 2024; Accepted 20th October, 2024

Abstract

The present investigation was carried out with 67 rice hybrids along with eight checks (four varietal and four hybrid checks) to ascertain the extent of genetic diversity for yield and yield associated traits through multivariate techniques like hierarchical clustering and principal component analysis (PCA). By using Wards method of clustering, 67 rice hybrids along with eight checks were aggregated into eight clusters based on different traits in which cluster VI comprised of 15 hybrids is the largest one followed by cluster III and IV with 12 hybrids. The hybrids in cluster I and II had highest values for test weight and effective bearing tillers /m^2 respectively. Similarly, the hybrids in cluster III recorded maximum values for plant height and Grain yield. In PCA, the total variation was bisected into 10 major principal components (PCs) in which PC1, PC2, PC3 and PC4 with eigen values more than one describing 24.76%, 23.26%, 14.54 and 13.22%, respectively attributing for overall variation of 75.80%. From the present study, the hybrids *viz*., NRH 24, NRH 46, NRH 40, NRH 38, NRH 53, NRH 2; Hybrid checks HC2 (US 314), HC4 (HRI 174) and varietal check VC1 (BPT 5204) were identified to be genetically potential for commercial exploitation to enhance yield and its attributing traits in rice.

Keywords: Rice, Genetic diversity, Cluster analysis, Principal component analysis

Introduction

Rice (*Oryza sativa* L.), a global food grain and an important staple food crop for half of the global population. Globally, India holds second place in rice production next to China. The major rice producing states in India include West Bengal, UP, Andhra Pradesh, Punjab, Telangana and Tamil Nadu. Besides, West Bengal and Uttar Pradesh produce 30% of total quantity of rice produced in the country. In India, the rice crop reported a production of 203.6 million tonnes from 47.8 million ha with average productivity of 4259 Kg/ha (https://ipad.fas.usda.gov/countrysummary/Default.aspx?id=IN&crop=Rice). In Andhra Pradesh, the crop is cultivated in total area of 2.13 million ha with production of 12.63 million tonnes and productivity of 5932 million tonnes (Agricultural statistics at a glance, 2022-23, Directorate of Economics and Statistics, Government of Andhra Pradesh, 2022-23). In the present national scenario, the population growth rate is reached to 1.58% and the requirement of rice was estimated to be around 140.7 million tonnes by 2025 (http://worldfood.apionet.or.jp). In order to make India self-sufficient in rice, enhancement of rice productivity to larger extent is a prime requisite (Hossain, 1996; Mishra, 2002). Despite this, task is quite challenging for breeders as the options available are very limited. Hence, breeders need to identify genetically diverse and potential hybrids for their inclusion in crop

improvement programme by divergence studies for yield and its attributing traits.

Although yield is a complex and challenging trait which depends mainly on environment and other different variables. For an efficient selection, breeder can reduce the number of characteristics and this can be made possible by using a method known as PCA. PCA is one of the multivariate techniques utilized in data analysis that converts data into a series of new orthogonal variables called principal components by linearly combining the variables that account for majority of variance in the original variables (Abdi and Williams, 2010) and it comprehends non-parametric strategy from a complicated set of data (Tiwari *et al.,* 2022). The main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only (Mohammadi, 2002). The cluster analysis is a pertinent method for concluding relationship among hybrids and amount of genetic distance from each other (Mellingers, 1972). Divergence analysis using PCA and hierarchical cluster analysis has been shown to be effective in determining potential hybrids useful for hybridization (Chaudhary *et al*., 2015). The prime objective of this investigation was to unveil genetic diversity and identify the best divergent hybrids for their inclusion in commercial rice improvement programme.

Materials and Methods

The experimental material consisted of 67 rice hybrids along with eight checks (four varietal and four hybrid checks) which were evaluated at Regional Agricultural Research Station (RARS), Nandyal, Andhra Pradesh, India during *kharif*, 2023. All the hybrids were evaluated in Augmented Block Design with plot size of 10 m^2 per hybrid with a spacing of 20 cm x 15 cm. All the agronomic practices recommended by Acharya N.G. Ranga Agricultural University were followed to raise a healthy crop. Data was collected from five competitive and randomly selected plants for recording yield and yield attributes *viz*., Days to 50% flowering (DFF), Days to maturity (DM), Plant height (cm) (PH), Effective bearing tillers/m^2 (EBT/m^2), Panicle length (cm) (PL), Filled Grains per panicle (FGP), Unfilled grains per panicle (UFGP), Total grains per panicle (TGP), Spikelet fertility % (SF %), Test weight (g) (TW) and grain yield (Kg/m^2)(GY) whereas DFF and DM data was recorded on plot basis. PCA (Hotelling, 1936) and cluster analysis were used to identify the most contributing traits for variation and diversity among hybrids, respectively (Peeters and Martinelli, 1989). The data generated by evaluation of hybrids s forwarded to statistical analysis to estimate genetic diversity through PCA and hierarchical clustering using JMP 17.0 statistical software (SAS Institute Inc., Cary, NC, USA).

Results and Discussions

The performance of 67 rice hybrids together with eight checks evaluated for eleven yield and yield attributes is presented in **Table 1**. The hybrid NRH 3 was found to be early flowering (81 days), while VC2(MTU 1262) was identified as late flowering (114 days). DM ranged from 109 days (NRH2) to 144 days (NRH 51). NRH 36 was found as taller (123 cm) whereas VC1 (BPT 5204) noticed as shorter (87.70 cm) with an average of 106.98 cm. The hybrid NRH 43 was found to bear a greater number of effective tillers (726 / m^2), while least number of effective tillers (238 / m^2) was displayed by hybrid, NRH 8. The mean value of PL was found to be 25.19 cm with range of 21.22 cm (HC2) to 27.86 cm (NRH 55). The TGP ranges from 160 (HC 2) to 599 (NRH 40) with mean value of 337. The mean SF % was recorded as 84.55% in which NRH 34 topped the list with 93.64% and NRH 17 occupied the bottom position with 60.06%. The TW ranged from 11.27 g (NRH 40) to 23.27 g (NRH 11) with average TW value of 15.98 g. The mean GY was recorded as 1.27Kg/m^2 with ranges from 0.612 Kg/m^2 (NRH 26) to 2.152 Kg/m^2 (NRH 5) among the studied hybrids. Vasudeva Reddy *et al*., (2023) reported same kind of experimental results while evaluating hybrids for yield and its component traits in rice.

Table 1. *Per se* performance of 67 hybrids along with eight hybrids for yield and its component traits

S. No.	Entry	Cross Combination	DFF	DM	PH (cm)	EBT/m²	PL(cm)	FGP	UFGP	TG/P	SF %	TW (G)	GY (kg/sq.m)	Heterosis %
1	NRH 1	IR 58025A /RTCNP 67	92	120	103.8	389	24.90	193	50	243	79.57	20.24	1.246	-13.24
2	NRH 2	IR 68888 A / AE 1325	82	109	95.3	310	24.90	296	22	318	92.96	15.20	0.870	-39.42
3	NRH 3	IR 79156 A / AE 1305	81	110	97.2	277	25.90	301	21	322	93.60	16.52	1.002	-30.22
4	NRH 4	APMS 6A / M 652	82	110	92.3	277	24.34	298	33	331	90.02	14.23	1.152	-19.78
5	NRH 5	APMS 6A / RTCNP 103	97	125	109.4	442	26.06	239	19	258	92.56	16.23	2.152	**49.89**
6	NRH 6	APMS 6A / RTCNP 152	88	115	106.5	422	23.94	240	25	265	90.55	17.29	1.304	-9.17
7	NRH 7	APMS 6A / RTCNP 67	85	113	96.9	479	25.40	336	42	377	88.98	14.47	1.542	7.35
8	NRH 8	APMS 6A / SN 698	87	125	95.5	238	24.90	307	26	333	92.30	16.21	1.354	-5.71
9	NRH 9	APMS 9A / BM 559	96	125	96.8	403	25.70	270	26	296	91.14	13.80	1.020	-28.97
10	NRH 10	APMS 9A / RTCNP 151	99	128	114.6	432	27.80	294	50	344	85.53	19.36	1.631	**13.61**
11	NRH 11	APMS 9A / RTCNP 167	97	125	105.1	640	25.08	296	43	339	87.32	23.27	1.782	**24.09**
12	NRH 12	APMS 9A / RTCNP 168	99	126	111.2	353	25.68	245	66	310	78.80	20.95	1.186	-17.39
13	NRH 13	APMS 9A / RTCNP 67	101	130	103.7	653	25.94	204	45	249	81.90	16.23	0.963	-32.94
14	NRH 14	PMS 3A / RTCNP 66	102	129	109.0	317	24.70	271	82	353	76.68	15.83	1.846	**28.54**
15	NRH 15	CMS 23A / BPT 2782	95	124	113.4	370	26.50	315	37	352	89.49	18.20	1.470	2.37
16	NRH 16	APMS 11A / AM 925	87	116	103.4	436	25.76	277	26	303	91.55	18.30	1.752	**22.01**
17	NRH 17	APMS 11A / RTCNP 152	90	116	109.9	376	26.52	206	137	343	60.06	19.35	0.881	-38.68
18	NRH 18	APMS 11A / RTCNP 167	101	133	103.5	386	26.22	214	37	251	85.26	15.50	1.709	**19.02**
19	NRH 19	APMS 11A / RTCNP 170	95	125	110.6	389	26.64	197	63	260	75.67	18.77	1.201	-16.39
20	NRH 20	APMS 11A / RTCNP 176	98	128	105.9	574	25.40	201	32	233	86.27	16.77	1.494	4.04
21	NRH 21	APMS 11A / RTCNP 66	95	123	115.3	686	25.04	216	52	268	80.60	19.45	1.134	-21.03
22	NRH 22	APMS 11A / RTCNP 67	97	125	106.5	614	25.48	257	41	298	86.25	18.93	1.422	-0.97
23	NRH 23	APMS 11A / RTCNP 99	99	128	99.1	548	26.14	248	52	300	82.67	17.74	1.368	-4.74
24	NRH 24	APMS 14A / RTCNP 167	111	137	104.7	409	24.18	189	76	265	71.42	17.32	0.695	-51.61
25	NRH 25	APMS 15A / BM 563	90	117	106.1	389	26.50	370	26	396	93.39	15.54	0.987	-31.27
26	NRH 26	APMS 15A / CM 458	92	117	98.5	330	25.30	336	53	388	86.45	15.55	0.612	-57.38
27	NRH 27	APMS 15A / NICRA P3	83	112	106.3	350	26.46	340	39	380	89.63	17.74	1.674	**16.57**
28	NRH 28	APMS 15A / RTCNP 133	86	116	106.3	429	25.00	335	42	377	88.76	16.30	1.602	11.56
29	NRH 29	APMS 15A / RTCNP 169	107	136	108.7	393	24.32	218	83	301	72.38	15.86	1.220	-15.03
30	NRH 30	APMS 15A / RTCNP 67	102	130	114.9	541	26.70	301	41	342	88.00	14.21	1.467	2.16
31	NRH 31	APMS 15A / SN 698	88	118	102.6	396	26.00	324	27	350	92.40	14.26	0.828	-42.34
32	NRH 32	APMS 16A / RTCNP 150	94	124	88.9	488	24.10	197	52	249	79.12	13.24	1.035	-27.92
33	NRH 33	APMS 16A / RTCNP 170	105	135	114.1	409	24.96	250	85	336	74.57	16.22	1.040	-27.58
34	NRH 34	APMS 16A / RTCNP 37	95	124	119.1	703	25.70	324	22	346	93.64	13.93	1.233	-14.14
35	NRH 35	APMS 16A / RTCNP 66	99	128	106.1	568	24.56	224	43	267	83.92	14.52	1.233	-14.14
36	NRH 36	APMS 16A / RTCNP 67	100	128	123.0	535	25.66	260	28	288	90.29	15.64	1.693	**17.90**
37	NRH 37	APMS 16A / SN 698	96	125	100.5	422	26.40	339	77	415	81.51	11.51	0.906	-36.91
38	NRH 38	APMS 17A / CM 449	90	118	92.4	350	22.40	422	105	528	80.06	13.30	0.690	-51.95
39	NRH 39	APMS 17A / CM 454	97	127	101.7	376	24.20	352	57	409	86.05	15.40	1.521	5.92
40	NRH 40	APMS 17A / NICRA P3	96	125	106.4	403	26.90	485	114	599	80.93	11.27	1.122	-21.87
41	NRH 41	APMS 17A / RTCNP 168	94	123	102.7	416	25.84	361	48	409	88.21	17.54	1.170	-18.52

S. No.	Entry	Cross Combination	DFF	DM	PH (cm)	EBT/m²	PL(cm)	FGP	UFGP	TG/P	SF %	TW (G)	GY (kg/sq.m)	Heterosis %
42	NRH 42	APMS 17A / RTCNP 66	102	130	114.6	673	24.40	198	42	240	82.50	14.75	1.242	-13.51
43	NRH 43	APMS 17A / RTCNP 67	97	125	101.5	726	24.80	277	48	325	85.21	14.28	1.341	-6.62
44	NRH 44	APMS 18A / CM 460	97	127	108	409	25.10	496	72	568	87.26	13.84	1.038	-27.72
45	NRH 45	APMS 18A / RTCNP 145	98	127	106	528	26.46	356	51	407	87.47	14.18	1.146	-20.19
46	NRH 46	APMS 18A / RTCNP 166	106	133	111.9	449	27.10	286	132	418	68.49	15.69	1.366	-4.89
47	NRH 47	APMS 18A / RTCNP 172	97	125	108.9	380	24.90	212	87	298	70.96	17.96	1.673	**16.52**
48	NRH 48	APMS 18A / RTCNP 176	99	130	114.7	373	25.04	301	103	404	74.48	14.83	1.293	-9.99
49	NRH 49	APMS 18A / RTCNP 66	93	120	118.3	475	25.50	273	36	309	88.33	16.61	0.99	-31.06
50	NRH 50	APMS 18A / RTCNP 84	104	128	107.2	350	24.68	320	74	394	81.17	16.30	0.958	-33.30
51	NRH 51	APMS 18A / RTCNP 97	105	134	115.8	413	25.74	318	86	404	78.77	16.42	1.304	-9.17
52	NRH 52	APMS 18A / RTCNP 99	104	132	105.9	370	26.00	394	67	462	85.40	14.41	1.643	14.38
53	NRH 53	APMS 19A / BM 563	91	119	108.7	403	25.42	469	61	531	88.47	15.11	0.840	-41.50
54	NRH 54	APMS 19A / BM 571	98	127	105.1	422	24.78	394	35	430	91.76	12.19	1.512	5.29
55	NRH 55	APMS 19A / RTCNP 103	97	126	113.4	383	27.86	392	66	458	85.64	14.90	1.278	-11.00
56	NRH 56	APMS 19A / RTCNP 133	99	129	112.5	462	25.34	478	78	556	85.98	16.64	1.506	4.87
57	NRH 57	APMS 19A / RTCNP 167	93	120	109.7	502	24.56	194	32	226	85.84	11.89	1.381	-3.83
58	NRH 58	APMS 19A / RTCNP 171	94	124	111.1	363	22.10	205	89	294	69.75	14.76	1.019	-29.03
59	NRH 59	APMS 19A / RTCNP 172	94	127	110.1	383	25.28	263	76	338	77.66	17.20	1.418	-1.24
60	NRH 60	APMS 19A / RTCNP 173	100	130	109.7	399	25.08	296	59	355	83.33	17.56	1.361	-5.20
61	NRH 61	APMS 19A / RTCNP 174	98	127	111.1	396	22.58	286	23	309	92.49	17.67	1.471	2.45
62	NRH 62	APMS 19A / RTCNP 175	99	129	113.3	389	24.46	198	41	239	82.69	18.33	1.116	-22.28
63	NRH 63	APMS 19A / RTCNP 176	98	130	115.3	373	25.68	310	76	386	80.37	13.63	1.480	3.05
64	NRH 64	APMS 19A / RTCNP 66	95	124	119.9	455	25.70	247	33	280	88.21	15.03	1.412	-1.67
65	NRH 65	APMS 19A / RTCNP 67	90	118	121.4	561	24.30	236	25	261	90.41	15.68	1.386	-3.48
66	NRH 66	APMS 19A / RTCNP 97	98	128	106.1	406	26.44	299	71	370	80.78	14.89	1.339	-6.73
67	NRH 67	APMS 19A / RTCNP 99	106	132	110.8	380	24.50	325	71	396	82.04	11.60	1.417	-1.30
68	VC1	BPT 5204	111	140	87.7	502	23.04	175	22	197	88.73	14.30	1.160	
69	VC2	MTU 1262	114	144	106.9	386	24.76	363	42	405	89.62	12.57	0.990	
70	VC3	NDLR 7	100	129	97.4	360	23.72	250	22	272	91.77	13.19	1.315	
71	VC4	NDLR 8	96	126	103.9	432	23.96	175	30	205	85.19	15.59	1.366	
72	HC1	US 312	96	125	107.2	393	26.48	296	37	333	88.88	18.16	0.831	
73	HC2	US 314	85	115	106.6	452	23.92	143	18	160	89.03	20.43	1.250	
74	HC3	27 P 63	96	126	108.9	403	21.22	267	38	305	87.54	14.98	1.356	
75	HC4	HRI 174	101	130	106.6	386	24.28	165	30	195	84.72	20.49	1.436	
Mean			96	125	106.9	435	25.19	285	52	337	84.55	15.98	1.27	
Maximum			114	144	123	726	27.86	496	137	599	93.64	23.27	2.15	
Minimum			81	109	87.7	238	21.22	143	18	160	60.06	11.27	0.61	
SD			6.74	6.82	7.22	100.35	1.20	77.44	26.81	87.90	6.78	2.36	0.29	
SE			0.778	0.788	0.834	11.588	0.139	8.942	3.096	10.150	0.783	0.274	0.034	

DFF-days to 50% flowering, DM-days to maturity, PH-plant height, EBT/m²- Effective bearing tillers/m², PL-panicle length, FGP-filled grains per panicle, UFGP-unfilled grains per panicle, TGP-total grains per panicle, SF %- spikelet fertility %, TW-test weight, GY- grain yield

Hierarchical cluster analysis was conducted with 67 rice hybrids along with eight checks using Wards method which provides the best result to get the finest possible classification. The cluster analysis revealed the aggregation of hybrids into eight clusters **(Table 2 and Figure 1)**. The cluster means computed for eleven major yield attributing characters revealed the existence of ample amount of variation among the clusters **(Table 3)**. The highest and lowest cluster means were recorded for the traits EBT/m^2 (631.4) and GY (1.00), respectively. Maximum cluster mean of overall traits was noticed in cluster VII (174.60) followed by cluster VIII (154.20). In contrast, the least cluster mean was displayed by cluster I (121.70). This clearly infers the existence of ample amount of genetic divergence in the hybrids of these clusters. Further, among the eight divergent clusters, the highest numbers of hybrids were grouped in cluster VI with 15 hybrids followed by 12 hybrids in cluster III and IV. The hybrids in cluster IV showed highest mean values for DFF, DM, PH, EBT/m^2 and SF %. The hybrids of cluster III and cluster VIII showed maximum value for GY. Ravikumar *et al., (*2015), Tejaswani *et al., (*2016), Tejaswini *et al., (*2018), Muthuramu and Sakthivel (2018), Dhakal *et al., (*2020), Kusuma Kumari *et al., (*2021) and Amudha and Ariharasutharsan (2021) also documented same kind of clustering of accessions into distinct clusters.

Table 2: Grouping of different hybrids into different clusters

Cluster	No. of hybrids	Hybrids
I	5	NRH 1, NRH 12, NRH 19, NRH 62,HC4
II	9	NRH 11, NRH 13, NRH 35, NRH 42, NRH 43, NRH 20, NRH 22, NRH 23, NRH 21
III	12	NRH 5, NRH 18, NRH 10, NRH 15, NRH 30, NRH 45, NRH 55, NRH 34, NRH 36, NRH 64, NRH 49, NRH 65
IV	12	NRH 2, NRH 3, NRH 4, NRH 25, NRH 31, NRH 26, NRH 41, HC1, NRH 7, NRH 28, NRH 16, NRH 27
V	11	NRH 6, HC2, NRH 61, HC3, NRH 8, NRH 9, VC3, NRH 32, NRH 57, VC4, VC 1
VI	15	NRH 14, NRH 47, NRH 48, NRH 63, NRH 51, NRH 50, NRH 59, NRH 60, NRH 66, NRH 46, NRH 24, NRH 29, NRH 33, NRH 58, NRH 17
VII	6	NRH 37, NRH 40, NRH 44, NRH 53, NRH 56, NRH 38
VIII	5	NRH 39, NRH 54, NRH 52, NRH 67,VC2

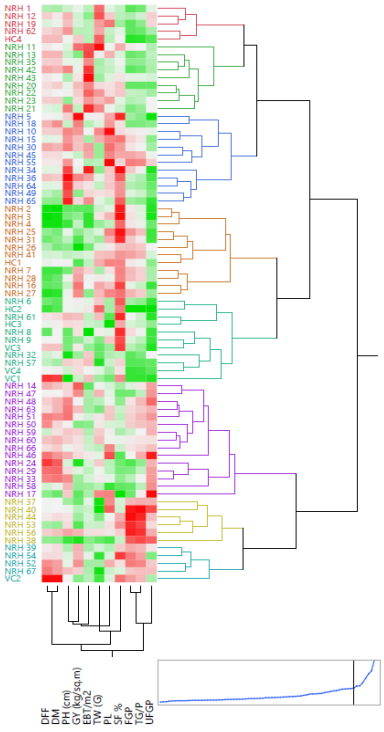


Figure 1: Dendrogram showing clustering by Wards method

DFF-days to 50% flowering, DM-days to maturity, PH-plant height, EBT/m^2- Effective bearing tillers/ m^2, PL-panicle length, FGP-filled grains per panicle, UFGP-unfilled grains per panicle, TGP-total grains per panicle, SF %- spikelet fertility %, TW-test weight, GY- grain yield

Table 3: Cluster means of various characters of rice hybrids under study

Cluster No.	DFF	DM	PH	EBT/m²	PL	FGP	UFGP	TGP	SF %	TW	GY	Mean
Cluster I	96.9	125.7	109.1	381.5	25.2	**199.5**	50.0	**249.4**	80.3	**19.8**	1.2	**121.7**
Cluster II	98.3	126.9	106.4	**631.4**	25.2	235.6	44.2	279.9	84.1	17.3	1.3	150.1
Cluster III	96.8	125.5	**114.7**	484.3	**26.2**	287.6	37.1	324.7	88.7	15.8	**1.5**	145.7
Cluster IV	**87.1**	**115.5**	**101.2**	**373.5**	25.7	322.4	34.6	357.1	**90.4**	16.2	1.2	138.6
Cluster V	94.8	124.5	**101.2**	417.9	**23.8**	227.5	**28.6**	256.1	88.5	15.3	1.3	125.4
Cluster VI	100.5	129.3	110.5	386.1	25.1	263.0	**87.7**	350.7	**74.7**	16.3	1.3	140.5
Cluster VII	94.8	123.8	104.8	408.1	25.3	**448.2**	84.6	**532.8**	84.0	13.6	**1.0**	**174.6**
Cluster VIII	**103.7**	**132.2**	106.1	386.8	24.8	365.7	54.6	420.3	87.0	**13.2**	1.4	154.2
Mean values	96.6	125.4	106.7	433.7	25.2	293.7	52.7	346.4	84.7	15.9	1.3	

Bold figures indicate maximum and minimum values in each character. DFF-days to 50% flowering, DM-days to maturity, PH-plant height, EBT/m²- Effective bearing tillers/m², PL-panicle length, FGP-filled grains per panicle, UFGP-unfilled grains per panicle, TGP-total grains per panicle, SF %- spikelet fertility %, TW-test weight, GY- grain yield

The constellation plot based on Wards method **(Figure 2)** depicts relationship among the 67 hybrids together with eight checks. The hybrids are grouped as end points and every cluster join as a new point with lines drawn will act as membership in constellation plot. The plot divided the total hybrids into 8 clusters with membership of 5,9,12,12,11,15,6 and 5. The Clustering pattern divulged that majority of hybrids congregated in cluster VI (15), followed by Cluster III (12) and Cluster IV (12). The hybrids with longer line representing greater genetic distance between the clusters. Further, the identified hybrids with maximum genetic distance are considered as superior and exploited commercially in yield improvement programme in rice.

The PCA an authentic tool utilized for successful selection of divergent genotypes in crop improvement programme. The results of PCA revealed the significance of first four PCs in discriminating 67 rice hybrids along with eight checks. The first four PCs, PC1, PC2 PC3 and PC4 exhibited eigen value greater than one explaining 75.80% of total variation. The eigen values and total cumulative per centage of variances explained by PCs is furnished in **Table 4**. PC1 with eigen value of 2.724 contribute 24.76% of the total variability, PC2, PC3 and PC4 with eigen value of 2.559, 1.604 and 1.455 attributed 23.62%, 14.54% and 13.22% of the total variability, respectively. The first PC displayed high positive weight to UFGP (0.850), DFF (0.645), TGP (0.624) and DM (0.622). The second PC displayed highest positive loading to DFF (0.569), DM (0.563) and EBT (0.438). Likewise, the third and fourth PCs gave positive loading to GY (0.588) and TW (0.661), respectively **(Table 5)**.

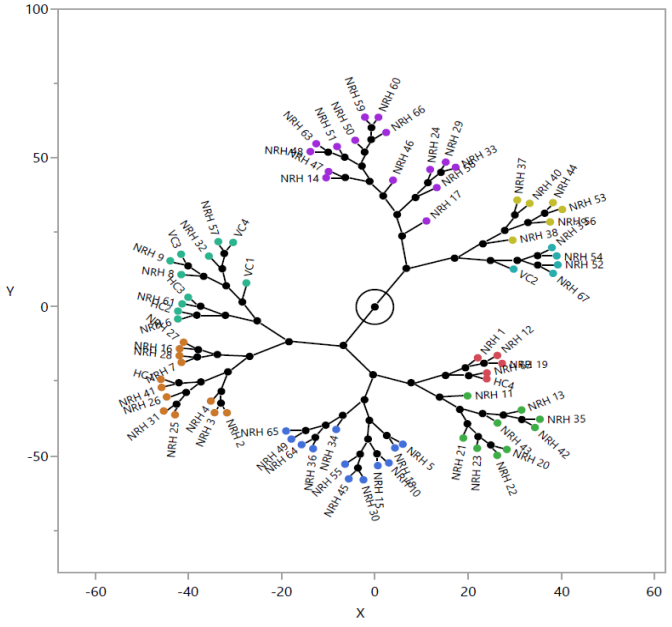


Figure 2: Constellation plot of 67 hybrids along with eight checks into Eight clusters based on Euclidean distance

Table 4: Total variances explained by different principal components in rice hybrids

Components	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
Eigen values	**2.724**	**2.559**	**1.604**	**1.455**	0.862	0.682	0.56	0.506	0.033	0.012
Proportion variance %	24.76	23.262	14.547	13.229	7.83	6.21	5.14	4.60	0.30	0.11
Cumulative variance %	24.76	48.03	62.577	75.806	83.65	89.86	94.99	99.59	99.89	100.00

Table 5: Factor loading of different characters with respect to different principal factor in rice hybrids

Principal Components	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10
DFF	0.645	0.569	0.150	-0.402	0.075	0.184	0.106	0.076	0.129	-0.007
DM	0.622	0.563	0.164	-0.420	0.154	0.193	0.095	0.060	-0.126	0.008
PH (cm)	0.283	0.344	0.509	0.379	-0.095	-0.398	0.403	-0.257	-0.002	0.0007
EBT/m2	-0.115	0.438	0.435	-0.120	-0.654	-0.161	-0.273	0.247	-0.007	0.0007
PL	0.219	-0.201	0.500	0.480	-0.182	0.571	-0.119	-0.234	-0.000	-0.0001
FGP	0.414	-0.807	0.336	-0.087	0.029	-0.064	0.076	0.209	-0.006	-0.0320
UFGP	0.850	-0.034	-0.321	0.338	-0.023	-0.130	-0.184	0.035	0.010	0.0741
TGP	0.624	-0.722	0.198	0.026	0.018	-0.096	0.011	0.195	-0.002	-0.0056
SF %	-0.629	-0.389	0.500	-0.383	0.055	0.079	0.190	0.050	0.014	0.0740
TW (G)	-0.292	0.384	-0.021	0.661	0.128	0.168	0.235	0.477	-0.001	0.0029
GY (Kg/sq.m)	-0.145	0.277	0.588	0.149	0.581	-0.186	-0.400	0.010	0.007	-0.0034

DFF-days to 50% flowering, DM-days to maturity, PH-plant height, EBT/m^2- Effective bearing tillers/m^2, PL-panicle length, FGP-filled grains per panicle, UFGP-unfilled grains per panicle, TGP-total grains per panicle, SF %- spikelet fertility %, TW-test weight, GY- grain yield

The greater portion of the variance (24.76%) was noticed in PC1and was strongly convinced DFF, DM, PH, PL, FGP, UFGP, TGP. Similarly, PC2 was influenced by DFF, DM, PH, EBT/m^2, TW and GY. Likewise, PC3 and PC4 are primarily influenced by UFGP, TW and DFF, DM, EBT/m^2, FGP, SF, respectively. Similar kind of results are in agreement with findings of Nachimuthu *et al*., (2014), Allam *et al.,* (2017), Riaz *et al.,* (2018), Umadevi *et al., (*2019), Sudeepthi *et al.,* (2020), Singh *et al.,* (2020), Pushpa *et al.,* (2021), Christina *et al.,* (2021), Dhanuja *et al.,* (2021), Venkata Ratnam *et al.,* (2022), Lakshmi *et al.,* (2022), Mushtaq and Kumar (2023), Nayak *et al.,* (2023), in rice.

The interaction between the characters and the genotypes that perform better for the traits are depicted in the biplot diagram. The length of the vector for each trait represents its offering to total divergence, longer the vector length, more is the contribution of concerned traits. The biplot depicted the relationship of 67 rice hybrids along with eight checks for 11 traits **(Figure 3)**. The trait TG/P displayed greater vector length implying its contribution to the total divergence followed by DFF, SF %and FGP. These results are in congruence with the research findings of Lakshmi *et al.,* (2022), Tiwari *et al.,* (2022) and Gayathridevi *et al.,* (2023).

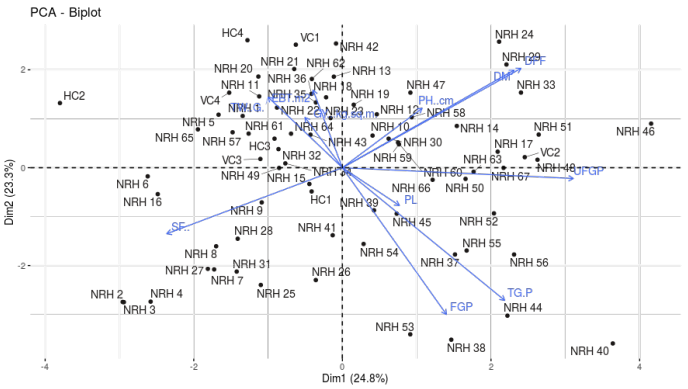


Figure 3: Biplot comprising of 67 rice hybrids along with eight hybrids studied for eleven yield and yield attributing traits

DFF-days to 50% flowering, DM-days to maturity, PH-plant height, EBT/m^2- Effective bearing tillers/ m^2, PL-panicle length, FGP-filled grains per panicle, UFGP-unfilled grains per panicle, TGP-total grains per panicle, SF %- spikelet fertility %, TW-test weight, GY- grain yield

The angle formed by the vectors of the traits indicates the association between the traits. A right angle (90º) between the vectors denotes no correlation, while an obtuse angle (>90º) denotes a negative correlation and an acute angle (<90º) between vectors suggests a positive correlation. All the traits studied displayed positive correlation with grain yield per plant except UFGP which noticed no correlation. From the biplots, the 11 yield and yield attributing traits were divulged into four groups. GY, TW and EBT were grouped in same cluster. DFF, DM and PH were grouped in same cluster. The traits UFGP, PL, TGP and FGP were grouped in another cluster. Whereas, SF % alone grouped as one cluster. The selection of hybrids with desirable highest score (0.588) for grain yield in PC3 will be desirable for developing high grain yielders in rice. The study showed that NRH 24, NRH 46, NRH 40, NRH 38, NRH 53, NRH 2; Hybrid checks HC2 (US 314), HC4 (HRI 174) and varietal check VC1 (BPT 5204) were located at extreme ends of distinct quadrants of the plot. Hence, theses hybrids and checks were recognized as highly divergent and found to be potential for exploitation in hybridization programme to enhance heterotic potential in rice crop. These results are in congruence with findings of Rahimi *et al., (*2013), Pandit *et al., (*2016), Sharafi *et al., (*2018), Divya *et al.,* (2022), in rice.

Conclusion

PCA concluded that the first four PCs with eigen values more than one describing 24.76%, 23.26%, 14.54 and 13.22%, respectively attributed 75.80% of total variation. The cluster analysis exhibited high genetic diversity, indicating a great chance for crop improvement by employing hybrids from other clusters. NRH 24, NRH 46, NRH 40, NRH 38, NRH 53, NRH 2 were identified as promising hybrids and can be used in developing diverse and heterotic inbred lines. Besides, the hybrids *viz.*, NRH 5 (49.89%), NRH 14 (28.54%), NRH 11(24.09%), NRH 16 (22.01%), NRH 18 (19.02%), NRH 36 (17.90%), NRH 27 (16.57%), NRH 47 (16.52%) were recognized as best heterotic hybrids for yield over best hybrid check HC4 (HRI 174) that governed by dominant genes and hence these hybrids can be advanced to evaluate under multi-location trails and further forwarded for commercial exploitation.

Acknowledgements

The authors thank to Acharya N. G. Ranga Agricultural University, Regional Agricultural Research Station, Nandyal for providing the required experimental material for the study and also thankful to Consortium Research Platform on Hybrid Technology (Rice hybrids) for providing financial support for the conduct of experiment.

References

Abdi H and Williams LJ. 2010. Principal component analysis. Wiley interdisciplinary reviews: *Computational Statistics*, 2(4): 433-459.

Allam CR, Qamar A, Prakash J and Jaiswal HK. 2017. Multivariate approach to analyse genetic diversity in some basmati rice genotypes (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 8(1): 269-278.

Amudha K and Ariharasutharsan G. 2021. Genetic diversity analysis for yield and yield components in rice. *Journal of Rice Research*, 14(2): 18:26

Chaudhary S, Sagar P, Hooda BK and Arya RK. 2015. Multivariate analysis of pearl millet data to delineate genetic variation. *Forage Research*, 40(4): 201-208.

Christina GR, Thirumurugan T, Jeyaprakash P and Rajanbabu V. 2021. Principal component analysis of yield and yield related traits in rice (*Oryza sativa* L.) landraces. *Electronic Journal of Plant Breeding*, 12(3): 907-911.

Dhakal A, Pokhrel A, Sharma S and Poudel A. 2020. Multivariate analysis of phenotypic diversity of rice (*Oryza sativa* L.) landraces from Lamjung and Tanahun Districts, Nepal. *International Journal of Agronomy*, 867961: 1-8.

Dhanuja N, Ganesamurthy K, Pushpam R, Amudha K and Uma D. 2021. Studies on genetic diversity in selected rice (*Oryza sativa* L.) landraces of Tamil Nadu. *Electronic Journal of Plant Breeding*, 12(3): 990-997.

Divya M, Singh PK, Rabiya P, Sareeta N and Mankesh K. 2022. Estimation of Genetic Diversity by Principal Component Analysis of Yield Attributing Traits in Katarni Derived Lines. *Journal of Rice Research*, 15(2): 63-69.

Gayathridevi G, Shanthi P, Suresh R, Manonmani S, Geetha S, Sathyabama K and Geetha P. 2023. Genetic variability, association and multivariate analysis for yield and yield parameters in rice (*Oryza sativa* L.) landraces. *Electronic Journal of Plant Breeding*, 14(3): 991-999.

Hossain M. (1996). Economic prosperity in Asia: Implications for Rice Research. In: Khush, G.S. (ed) *Rice Genetics* III. IRRI, Manila, Philippines. pp. 3-16.

Hotelling H. (1936). Relations between two sets of varieties. *Biometrica*, 28(3-4): 321-377.

Kumari BK, Kumar BR, Jyothula DPB and Rao NM. 2021. Diversity analysis in rice breeding lines for yield and its components using principal component analysis. *Journal of Pharmacognosy and Phytochemistry*, 10(1): 905-909.

Lakshmi M, Shanmuganathan M, Jeyaprakash P and Ramesh T. 2022. Genetic variability and diversity analysis in selected rice (*Oryza sativa* L.) varieties. *Electronic Journal of Plant Breeding*, 13(3): 959-966.

Mellingers JS. 1972. "Measures of genetic similarity and genetic distance studies in genetics". VII Univ Tex Publ. 27(13): 145-153.

Mishra M. (2002). Rice in India. *Agrolook*, 3:10-15.

Mohammadi SA. 2002. Statistical Methods in Genetics. Paper presented at the 6th International Conference of Statistics, University of Tarbiatmodares.

Mushtaq D and Kumar B. 2022. Multivariate analysis among advanced breeding lines of rice (*Oryza sativa* L.) Under sub-tropical ecology of Jammu region of Jammu and Kashmir. *Electronic Journal of Plant Breeding*, 13(4): 1387-1394.

Muthuramu S and Sakthivel S. 2018. Genetic diversity analysis for yield traits in upland rice (*Oryza sativa* L.) *Journal of Rice Research*, 10(1): 40-43.

Nachimuthu VV, Robin S, Sudhakar D, Raveendran M, Rajeswari S and Manonmani S. 2014. Evaluation of rice genetic diversity and variability in a population panel by principal component analysis. *Indian Journal of Science and Technology*, 7(10): 1555-1562.

Nayak G, Vaidya N, Parida M, Lal J, Katara PC, Samantaray S and Chaudhari P. 2023. Assessment of variability and principal component analysis in rice (*Oryza sativa* L.). *The Pharma Innovation Journal*, 2(9): 1985-1989.

Pandit E, Barik SR, Mohanty SP., Mohanty DP, Das L, Singh ON and Pradhan SK. 2016. Principal component analysis for selection of heterotic hybrids for yield component traits in mid and mid-early duration rice genotypes. *ORYZA-An International Journal on Rice*, 53(3): 255-261.

Peeters JP and Martinelli JA. 1989. Hierarchical cluster analysis as a tool to manage variation in germplasm collections. *Theoretical and Applied Genetics,*78(1): 42-48.

Pushpa R, Sasikumar D, Suresh R and Iyanar K. 2022. Evaluation of nutritional and grain quality diversity in rice (*Oryza sativa* L.) germplasm based on multivariate analysis. *Electronic Journal of Plant Breeding*, 13(4): 1187-1197.

Rahimi M, Dehghani H, Rabiei B and Tarang AR. 2013. Evaluation of rice segregating population based on drought tolerance criteria and biplot analysis. *International Journal of Agriculture and Crop Sciences*, 5(3): 194-199

Ratnam TV, Kumar BR, Subba Rao LV, Srinivas T and Kumar AA. 2022. Principal component analysis of yield and quality traits in Zinc rich landraces of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 13(4): 1162-1169.

Ravikumar BNVSR, Kumari PN, Rao PVR, Rani MG, Satyanarayana PV, Chamundeswari N, Vishnuvardhan KM, Suryanarayana Y, Bharathalakshmi M and Reddy AV. 2015. Principal component analysis and character association for yield components in rice (*Oryza sativa* L.) cultivars suitable for irrigated ecosystem. *Current Biotica*, 9(1): 25-35.

Riaz A, Bibi T, Raza Q, Sabar M and Akhter M. 2018. Evaluation of rice (*Oryza sativa* L.) advance uniform lines using multivariate analysis. *African Journal of Plant Science*, 12(11): 284-289.

Sharifi P and Ebadi AA. 2018. Relationships of rice yield and quality based on genotype by trait (GT) biplot. *Anais da Academia Brasileira de Ciencias*, 90(1): 343-356.

Singh KS, Suneetha Y, Raja DS and Srinivas T. 2020. Principal component analysis for yield and quality traits of coloured rice (*Oryza sativa* L.). *The Pharma Innovation Journal*, 9(7): 456-462.

Sudeepthi K, Srinivas T, Kumar, BNVSRR, Jyothula, DPB and Umar SN. 2020. Genetic divergence studies for anaerobic germination traits in rice (*Oryza sativa* L.). *Current Journal of Applied Science and Technology*, 39(1): 71-78.

Tejaswini KLY, Manukonda S and Rao PR. 2018. Genetic divergence and cluster analysis studies in rice (*Oryza sativa* L.) using D^2 statistics. *Journal of Pharmacognosy and Phytochemistry*, 7(4S): 108-116.

Tejaswini KLY, Manukonda S, Rao PR, Kumar BR, Mohammad LA and Raju SK. 2016. Cluster analysis studies in rice (*Oryza sativa* L.) using wards minimum variance method. *Journal of Agricultural and Crop Research*, 4(9): 129-139.

Tiwari DN, Tripathi SR, Tripathi MP, Khatri N and Bastola BR. 2019. Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. *Advances in Agriculture*, 2019(1): 1-9.

Tiwari S, Singh Y, Upadhyay PK and Koutu GK. 2022. Principal component analysis and genetic divergence studies for yield and quality-related attributes of rice restorer lines. *Indian Journal of Genetics and Plant Breeding,* 82(1): 94-98.

Umadevi M, Shanthi P and Saraswathi R. 2019. Characterization of rice landraces of Tamil Nadu by multivariate analysis. *Electronic Journal of Plant Breeding*, 10(3): 1185-1193.

Vasudeva Reddy D, Suneetha Y, Ravi Kumar BNVSR and Ramesh D. 2023. Evaluation of experimental hybrids for yield and yield component traits in rice (*Oryza sativa* L.). *The Andhra Agricultural Journal,* 70(1): 050-061.

RESEARCH ARTICLE https://doi.org/10.58297/NHMB6165

Estimates of Heterosis, Inbreeding Depression and Transgressive Segregation in Rice (*Oryza sativa* L.) Under Sodic Soil

Shiv Prakash Shrivastav[1]*, Verma OP[1] and Kuldeep Srivastava[2]

[1]Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya -224 229 (UP), India.

[2]ICAR-Indian Institute of Vegetable Research, Varanasi (UP), India.

*Corresponding author Email: ms.shiv92@gmail.com

Received :18th August, 2024; Accepted: 9th October, 2024

Abstract

The present investigation was carried out at the Main Experimental Station of Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) India. A field experiment was conducted by using a line x tester set of 63 F_1s and 63 F_2s derived by crossing 21 rice genotypes/varieties as lines (females) with three testers (males) *viz.,* Narendra Usar Dhan 3, CSR 23 and IR 28 with 2 check varieties (Jaya and CSR 43) of rice (*Oryza sativa* L.) in randomized complete block design with three replications to work out the heterosis, transgressive segregation and inbreeding depression effects for various attributes under the sodic soil condition. Among these, F_1s *viz*., NDRK 5037 x Narendra Usar Dhan 3, NDRK 5062 x IR 28, NDRK 5062 x CSR 23, NDRK 5037 x CSR 23 and NDRK 5040 x Narendra Usar Dhan 3 were showed significant positive standard heterosis for grain yield per plant over SV_1 and SV_2. All these crosses also had highly significant inbreeding depression for grain yield per plant in F_2 generation. Inspite of grain yield of these F_1s had significant heterosis and inbreeding depression for some of the other yield contributing characters also. This study indicated the presence of non additive gene action in the inheritance of grain yield per plant and some of the other yield contributing characters. Tolerant breeding populations showed similar banding pattern whereas susceptible exhibited similar banding pattern but possesses wide variations between tolerant and susceptible. At 35 kDa the medium to dark bands were present in parents, F_1s, F_2s, transgressive segregants and checks while in highly inbreeding depressed cross combinations, variable range of the bands were observed *viz.,* absence of bands, light, medium and dark bands. The data offer a valuable resource for advancing the understanding and facilitating the utilization of additive and non-additive information for rice improvement.

Keywords: Rice, heterosis, transgressive segregation, inbreeding depression, SDS PAGE, protein profiling, breeding populations and sodic soil.

Introduction

Rice (*Oryza sativa* L.), is a staple food for more than 50% of the world population (Jiang *et al*., 2020, Shrivastav *et al.,* 2023). It forms the breath of life '*prana*' for the human being. Rice is a high caloric food, which contain 75% starch, 6-7% protein, 2-2.5% fat, 0.8% cellulose and 5-9% ash. India has the largest area of 46.38 million hectare constituting 28.26% of the land under rice in the world and rank second in total production 130.29 million tonnes next to China with an average productivity of 2809 Kg/ha (DAC and FW, 2021-2022). It showed that the average productivity of rice is very low in our country. Therefore, there is immence need to develop high yielding, multiple resistance and wider adoptive

hybrid varieties. Taking the above points under consideration the present investigation was carried out to sort out the best heterotic hybrids for yield and its component characters. Heterosis is a common phenomenon in which an F_1 hybrid performs better than either inbred parent (Shrivastav *et al*., 2022, Modunshim *et al.,* 2022).

Heterosis or hybrid vigor refers to the phenomenon that the heterozygous first filial generation (F_1) performs better than its parental inbred lines in target traits. With the development of the first commercial hybrid maize variety in the 1930s (Ayalneh 2020) and the development of rice hybrid varieties in the early 1970s in China, exploitation of heterosis in crop plants has achieved remarkable yield advantages over inbred lines and remains a crucial approach to increase agricultural production for global food demand in response to rapidly increasing global population and changing climate (Gu *et al.,* 2023).

In crop genetic research, the mechanism of heterosis has always been a key topic and several hypotheses have been proposed the dominance hypothesis, which proposes the masking of deleterious recessive parental alleles in the hybrid; the overdominance hypothesis, which attributes heterosis to the superiority of heterozygotes over parental homozygotes at individual loci; and the epistatic hypothesis, which postulates the contribution of positive epistatic interactions between non-allelic genes. However, there are no reports explaining the genetic mechanisms responsible for heterosis of rice grain quality traits (You *et al.,* 2022).

Inbreeding depression and heterosis are related phenomena of fundamental importance to evolutionary biology and applied genetics. Inbreeding depression refers to reduced fitness of progenies resulting from inbreeding (Stebbins 1958; Wright 1977). In contrast, heterosis, or hybrid vigor, is defined as the superiority of an F_1 hybrid over its parents (Stuber, 1994). Both heterosis and inbreeding depression are widely observed in both animal and plant kingdoms. In evolution, inbreeding depression may contribute to formation of reproductive barriers between species and populations, while heterosis may be an important force in maintenance of genetic variation in populations. In applied genetics, exploitation of heterosis has played a major role in the genetic improvement of many crop plants and animals (Falconer, 1981; Stuber, 1994). Heterosis and inbreeding depression are considered two aspects of the same phenomenon (Falconer, 1981; Mather and Jinks, 1982). Heterosis is clearly related to heterozygosity, but it has long been debated how heterozygosity results in heterosis. Two predominant theories were proposed as the genetic basis of heterosis. The overdominance hypothesis (Shull, 1908; East, 1936) states that heterozygosity at single loci confers properties that are superior to either homozygote. In contrast, the dominance hypothesis (Bruce, 1910; Keeble and Pellew, 1910; Jones, 1917) proposed that dominant factors from either parent mask deleterious recessive mutations from the other parent in the heterozygous F_1. In both cases, the inbreeding depression is due to segregation and expression of deleterious recessive mutations in inbred progenies (Allard, 1960; Simmonds, 1979). A third, less widely embraced hypothesis suggests that heterosis may arise from epistasis between alleles at different loci (Stuber, 1994; Goodnight, 1999).

Transgressive segregation is common in plant breeding populations, where small minority of recombinants are outliers relative to parental phenotypes. While this phenomenon has been attributed to complementation and epistatic effects, the physiological, biochemical and molecular bases have not been fully illuminated. The phenomenon of transgressive segregation, which is observed in both natural and artificial populations created by plant breeding, is characterized by the occurrence of minority phenotypic outliers relative to parental range across segregating or recombinant population derived from genetically divergent parents. In addition to the classic explanations attributing

complementation and epistatic interactions as major mechanisms behind transgressive traits, the possible roles of coupling and uncoupling effects and genetic network rewiring have also been recently proposed (Vega and Frey, 1980; Rieseberg *et al.,* 1999; Dittrich-Reed and Fitzpatrick, 2013; de Los Reyes, 2019). Combined with the paradigms of genomic biology, the potential of transgressive individuals for enhanced yield of crops have been established, but its true potential for adaptive traits is yet to be determined (DeVicente and Tanksley, 1993).

The soil sodicity is a major factor that adversely affects the growth and yield of crop plant. Approximately one third of the land area on which rice grown is affected by salinity. Approximately 10% of the world's total land area (950 million ha), 20% of the world's arable land (300 million ha) and 50% of the total irrigated land (230 million ha) are affected by soil salinization. Further, it is expected to influence 50% of total cultivated land in 2050 at a dis-quieting rate. Every year almost 12 billion US$ are globally lost due to salt stress that significantly affects the agricultural production (Shrivastav *et al.,* 2022a).

Materials and Methods

This experiment was carried out at the Main Experimental Station of A.N.D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) India. The experimental material was based on a line x tester set of 63 hybrids (F_1s) and 63 F_2s developed by crossing 21 lines (females) *viz.,* NDRK 5004, NDRK 5093, NDRK 5040, NDRK 5062, NDRK 5037, NDRK5025, NDRK 50059, NDRK 5081, NDRK 50047, NDRK 5039, IR 66946-3R-178-1-1 (FL 478), Sushk Samrat, IR 85897, Pant 10, CSR 10, Sarjoo 52, Narendra 2064, Narendra Usar Dhan 2, Deepak, Sundri and Pusa Basamati 1 with 3 testers (males) *viz.,* Narendra Usar Dhan 3, CSR 23 and IR 28. An attempt was made to make a sixty three cross combinations during *kharif* season 2016 for F_1s production and grown in *kharif* season 2017 for F_2s production and *kharif* season 2017 again fress F_1s generated by crossing The 63 F_1s and 63 F_2s along with their parents including two checks, Jaya and CSR 43 (total set of 152 genotypes) were studied to work out the heterosis, transgressive segregation and inbreeding depression effects of their various attributes on grain yield under the sodic soil in randomized complete block design with three replications during *Kharif* 2018 (Arunachalam, 1974). Data on various attributes *viz*., days to 50% flowering, chlorophyll content, leaf nitrogen, leaf temperature, flag leaf area (cm^2), plant height (cm), panicle bearing tillers per plant, panicle length(cm), spikelets per panicle, grains per panicle, spikelet fertility (%), biological yield per plant (g), harvest-index (%), L:B ratio, 1000-grain weight (g), amylose content, protein content and grain yield per plant (g) were recorded and analysed as per Kempthorne (1957). Heterobeltiosis and standard heterosis estimated as per Fonseca and Patterson (1968) and inbreeding depression as per Hill (1966). For the transgressive segregation the observations were recorded on fifteen randomly selected plants taken from each genotype of each replication. The per centage of superior segregants in particular cross is recorded by calculating the number of plants exceeding mean value of best check to the total number of plants in a cross.

The selected genotypes of different breeding populations were used to work out the SDS PAGE protein profiling of rice seed following method described by Laemmli, (1970).

Results and Discussions

The heterosis breeding has been used extensively in improving yield potential through development of hybrid cultivars in most of the allogamous crops and some autogamous crops like rice as well. The exploitation of heterosis for developing high yielding commercial hybrids in rice has been found highly fruitful inspite of its autogamous nature because significant heterosis is encountered in F_1 hybrids and successful and economical technology for commercial hybrid seed

production is available. A wide range of variation in the estimates of heterobeltiosis and standard heterosis was observed for grain yield per plant and other related traits. Top five F_1s that showed good heterotic potential for grain yield and yield contributing traits over Jaya (SV1) as well as CSR 43 (SV2) were NDRK 5037 x Narendra Usar Dhan 3, NDRK 5062 x IR 28, NDRK 5062 x CSR 23, NDRK 5037 x CSR 23 and NDRK 5040 x Narendra Usar Dhan 3 (**Table 1**). The findings will help promote rice improvements in context to establishment of heterotic patterns as a requirement for a sustainable long-term success of hybrid rice breeding (Shrivastav *et al.,* 2022a).

The estimates of inbreeding depression of eighteen characters of sixty-three crosses are presented in **Table 2.** The range of inbreeding depression for grain yield per plant was ranged from 4.39 (NDRK 5004 x Narendra Usar Dhan 3) to 38.74% (NDRK 5037 x CSR 23). The depressed cross was 38.74% (NDRK 5037 x CSR 23) followed by 31.98 (NDRK 5047 x Narendra Usar Dhan 3), 30.95 (Sundri x IR 28), 30.90 (NDRK 5004 x IR 28) and 30.56% (NDRK 5025 x CSR 23). Among 63 crosses all were positively significant while none had negatively significant inbreeding depression.

Table 1: Most promising crosses based on mean performance, heterobeltiosis and standard heterosis (SV_1 and SV_2), SCA effect, GCA effect of parent for grain yield / plant

S. No.	Crosses	*per se* Performance	Heterosis over better-parent	Heterosis over SV_1	Heterosis over SV_2	SCA effect	GCA effect of parent	Traits for which these the cross also exhibited desirable heterosis
1	NDRK 5004* NarendraUsarDhan 3	19.73**	26.47**	45.32**	36.10**	3.08**	HxH	CC, FLA, PL, S/P, G/P, SF, BY/P, HI, 1000-GW, AC
2	Sarjoo 52 * NarendraUsarDhan 3	19.61**	25.41**	44.44**	35.27**	1.92**	HxH	LN, PBT/P, PL, S/P, G/P, SF, BY/P, HI, AC, PC
3	NDRK 5040* NarendraUsarDhan 3	19.48**	24.89**	43.51**	34.40**	3.68**	HxH	CC, S/P, G/P, SF, BY/P, HI,
4	NDRK 5062 * IR 28	18.92**	21.26**	39.33**	30.49**	2.10**	HxL	CC, PH, PL, S/P, G/P, BY/P, L/B
5	CSR 10* NarendraUsarDhan 3	18.65**	19.55**	37.37**	28.65**	0.63**	HxH	CC, PH, PBT/P, PL, S/P, G/P, SF, BY/P, HI
6	NDRK 5062* CSR 23	18.47**	18.38**	36.02**	27.39**	0.50*	HxA	CC, LN, PL, S/P, G/P, BY/P
7	Narendra 2064* Narendra UsarDhan 3	17.80**	7.81**	31.11**	22.79**	1.26**	HxH	CC, FLA, PH, PBT/P, S/P, G/P, BY/P, 1000-GW, AC
8	NDRK 5039* NarendraUsarDhan 3	17.61**	12.88**	29.71**	21.48**	1.73**	HxH	DF, CC, PL, S/P, BY/P, L/B, 1000-GW, AC
9	NDRK 5059* IR 28	17.12**	17.39**	26.10**	18.10**	3.35**	HxL	CC, LN, FLA, PH, PL, G/P, SF, BY/P, L/B, AC
10	NDRK 5037* NarendraUsarDhan 3	16.82**	7.84**	23.91**	16.05**	1.22**	HxH	CC, FLA, PH, PL, S/P, G/P, SF, BY/P, HI, L/B, PC

Traits: DF=Days to 50% flowering, **CC=**Chlorophyll content (spad value), **LN**= Leaf nitrogen (spad value), **LT**= Leaf temperature (spad value), **FLA**=Flag leaf area(cm^2), **PH**=Plant height (cm), **PBT/P**=Panicle bearing tillers / plant, **PL**=Panicle length (cm), **S/P**=Spikelets / panicle, **G/P=** Grains per panicle, **SF**=Spikelet fertility (%), **BY/P**= Biological yield / plant (g), **HI**=Harvest index (%), **L/B**=L/B ratio**, 1000-GW=**1000- grain weight (g), **AC**= Amylose content, **PC**= Protein content and **GY/P**=Grain yield / plant(g)

Table 2: Estimates of inbreeding depression (%) in different yield and yield contributing traits of rice under sodic soil

S. No.	Crosses	Days to 50% flowering	Chlorophyll content	Leaf nitrogen	Leaf temperature	Flag leaf area (cm^2)	Plant height (cm)	Panicle bearing tillers/ plant	Panicle length (cm)	Spikelets/ panicle	Grains/ panicle	Spikelet fertility (%)	Biological yield/ plant (g)	Harvest index (%)	L/B ratio	1000-grain weight (g)	Amylose content	Protein content (%)	Grain yield/ plant (g)
1	NDRK 5004*NarendraUsarDhan 3	-2.01	4.90**	-12.08**	9.23**	0.92**	-0.93	8.65**	1.06*	1.33	5.43**	4.17**	2.96**	1.42	0.72**	0.51	1.18**	0.63**	4.39**
2	NDRK 5004*CSR 23	-0.40	-6.85**	-8.80**	8.53**	2.40**	-0.30	10.03**	1.81**	1.76	3.86*	2.08	10.61**	7.87**	0.11	0.13	0.99**	0.58**	17.59**
3	NDRK 5004*IR 28	-1.54	1.68**	-0.62**	-0.29	0.86**	0.63	16.57**	1.60**	1.71	2.03	0.31	2.34*	29.14**	0.11	0.18	1.40**	0.45**	30.90**
4	FL478*NarendraUsarDhan 3	-2.81	26.96**	-17.72**	1.55**	-1.05**	5.36**	8.78**	2.75**	-12.18**	-12.18**	0.04	9.45**	13.39**	0.54**	0.09	1.08**	0.51**	21.54**
5	FL478*CSR 23	-0.78	-20.78**	-19.06**	6.70**	-1.05**	0.66	9.40**	2.02**	4.01*	-5.00**	-9.49**	14.41**	2.97**	0.42**	0.52	0.55**	0.57**	16.97**
6	FL478*IR 28	-0.80	4.06**	-23.28**	-6.61**	-1.03**	1.34	10.06**	1.90**	3.74*	0.00	-3.87**	8.62**	7.47**	0.22**	0.41	1.26**	0.53**	15.50**
7	NDRK 5093*Narendra U sarDhan 3	-0.79	13.68**	-8.44**	5.56**	-2.19**	-0.17	15.96**	4.11**	3.04	19.61**	17.03**	7.30**	20.29**	0.32**	0.15	1.19**	0.26**	26.17**
8	NDRK 5093*CSR 23	0.40	-7.09**	13.75**	3.71**	-5.48**	-1.14	15.78**	2.93**	4.34*	11.82**	7.87**	2.52*	24.56**	0.73**	0.56	2.20**	0.26**	26.49**
9	NDRK 5093*IR 28	0.39	2.66**	8.94**	7.96**	-2.22**	-0.29	16.26**	3.09**	3.74*	3.83*	0.06	3.45**	7.00**	0.54**	0.49	2.00**	0.28**	10.10**
10	SushkSamrat*NarendraUsarDhan 3	-0.39	-1.25**	-11.46**	0.32	3.90**	-1.31	17.16**	2.23**	4.63**	6.87**	2.33	4.12**	19.73**	0.33**	0.20	1.90**	0.54**	23.17**
11	SushkSamrat*CSR 23	-3.23*	-20.35**	-17.38**	4.73**	2.38**	-0.71	17.29**	3.00**	3.29	7.97**	4.85**	4.69**	16.01**	-0.11	0.22	2.34**	0.64**	20.14**
12	SushkSamrat*IR 28	-2.37	-7.00**	-1.76**	-8.18**	3.88**	-1.22	17.49**	2.17**	3.69*	8.28**	4.78**	4.30**	14.35**	3.73**	0.18	3.66**	0.66**	18.27**
13	IR 85897*NarendraUsarDhan 3	-1.59	7.96**	9.30**	10.07**	0.74**	-0.32	11.72**	2.70**	11.28**	18.81**	8.47**	11.93**	2.39	1.06**	0.18	3.48**	0.27**	13.99**
14	IR 85897*CSR 23	0.00	11.41**	-6.98**	6.41**	2.97**	-0.59	10.12**	2.23**	12.02**	18.72**	7.62**	7.08**	4.63**	1.53**	0.31	3.49**	0.30**	11.30**
15	IR 85897*IR 28	0.00	8.58**	-7.32**	1.81**	1.47**	-0.19	12.74**	1.23*	8.96**	17.03**	8.87**	16.07**	-0.82	1.13**	0.28	3.93**	0.53**	15.51**
16	Pant 10*NarendraUsarDhan 3	-2.79	14.12**	1.10**	-3.92**	-2.92**	0.32	10.59**	1.63**	10.93**	13.58**	2.97*	9.85**	3.28**	-2.91**	0.37	2.86**	0.56**	12.88**
17	Pant 10*CSR 23	-3.23*	17.06**	-18.56**	0.27**	-0.55	0.11	11.42**	1.50**	14.90**	15.78**	1.07	4.00**	11.75**	-1.34**	0.23	3.43**	0.56**	15.25**
18	Pant 10*IR 28	-1.61	9.21**	-10.40**	6.55**	-0.91**	0.20	12.31**	3.21**	6.87**	10.19**	3.58*	2.52**	21.85**	-0.34**	0.22	3.46**	0.55**	23.80**
19	CSR 10*NarendraUsarDhan 3	0.79	16.60**	-1.19**	0.12	-2.54**	3.26**	7.33**	3.19**	4.49**	10.12**	5.92**	8.39**	-3.96**	-6.53**	0.45	1.17**	1.17**	4.80**
20	CSR 10*CSR 23	-3.23*	6.48**	0.00	5.55**	-2.61**	3.48**	7.73**	2.39**	3.93*	10.11**	6.43**	3.13**	5.28**	-0.59**	0.22	0.84**	0.66**	8.28**
21	CSR 10*IR 28	-1.59	-1.00**	0.55**	1.49**	0.00	1.11	1.40**	1.37**	3.32*	6.58**	3.39	2.29*	3.58**	1.96**	0.37	1.67**	0.72**	5.82**
22	NDRK 5040*NarendraUsarDhan 3	-1.99	7.79**	9.96**	-4.16**	3.25**	0.92	10.14**	2.04**	8.98**	7.67**	-1.43	2.19*	2.33	-5.29**	0.16	1.43**	0.48**	4.42**
23	NDRK 5040*CSR 23	-4.15**	16.70**	20.44**	-5.21**	3.00**	1.36	9.03**	2.78**	9.75**	6.46**	-3.65*	6.40**	17.99**	-1.85**	0.24	29.26**	0.38**	23.26**
24	NDRK 5040*IR 28	-3.60**	10.76**	15.90**	-1.42**	4.09**	-0.60	11.50**	2.87**	9.48**	8.17**	-1.42	2.46*	19.50**	-1.70**	0.21	0.84**	0.15**	21.51**
25	Sarjoo 52*NarendraUsarDhan 3	-0.39	34.47**	-4.05**	-6.71**	5.78**	0.39	15.05**	1.93**	5.34**	7.86**	2.63	3.50**	5.55**	0.28**	0.38	0.54**	1.02**	8.89**
26	Sarjoo 52*CSR 23	-2.33	17.29**	-10.59**	-0.55**	3.47**	-0.18	15.92**	2.15**	8.96**	6.34**	-3.03*	4.48**	21.62**	1.26**	0.35	0.43**	2.33**	25.26**
27	Sarjoo 52*IR 28	-0.38	17.61**	-8.20**	-6.20**	2.06**	0.26	14.71**	2.11**	7.95**	8.25**	0.18	7.63**	11.52**	2.82**	0.23	0.50**	1.13**	18.33**
28	NDRK 5062*NarendraUsarDhan 3	-2.02	13.32**	-3.55**	-7.92**	2.88**	0.05	14.91**	2.13**	4.63**	7.46**	2.96*	7.09**	9.13**	-0.89**	0.41	1.30**	0.38**	15.65**
29	NDRK 5062*CSR 23	-1.93	12.62**	-14.27**	-4.00**	4.83**	0.15	8.73**	2.49**	5.09**	5.04**	-0.08	4.86**	6.45**	-1.08**	0.12	1.58**	0.32**	11.03**
30	NDRK 5062*IR 28	-1.59	12.61**	-9.78**	-5.04**	3.86**	0.10	13.61**	2.32**	3.68*	8.89**	5.39**	0.68	12.03**	-0.86**	0.29	1.35**	0.36**	12.64**
31	Narendra 2064*NarendraUsarDhan 3	-1.59	9.92**	-4.01**	1.84**	2.64**	-0.18	7.44**	2.67**	5.88**	5.10**	-0.89	-2.61**	16.67**	0.80**	0.21	0.60**	0.35**	14.49**
32	Narendra 2064*CSR 23	-2.42	16.53**	-3.78**	-6.05**	2.77**	-0.66	7.39**	1.96**	4.33*	6.40**	2.18	2.70**	24.99**	0.76**	1.35**	12.44**	0.39**	27.00**
33	Narendra 2064*IR 28	-6.02**	18.31**	-10.11**	0.02	0.51	0.00	5.45**	1.55**	8.96**	9.31**	0.40	5.26**	21.89**	2.01**	1.04*	0.90**	0.36**	26.07**

34	NDRK 5037*NarendraUsarDhan 3	-1.59	5.95**	13.64**	-2.32**	2.46**	-0.62	8.73**	2.85**	10.16**	8.56**	-1.78	2.47**	20.44**	0.53**	0.27	0.73**	2.55**	22.43**
35	NDRK 5037*CSR 23	-4.38**	14.86**	9.17**	2.35**	4.20**	0.21	0.00	1.93**	8.22**	11.06**	3.09*	6.21**	34.58**	1.31**	0.66	0.71**	0.51**	38.74**
36	NDRK 5037*IR 28	-4.44**	10.14**	8.80**	-2.47**	3.07**	-0.76	9.26**	1.77**	11.17**	11.66**	0.55	3.80**	27.67**	1.37**	0.31	0.28**	0.52**	30.40**
37	NDRK 5025*NarendraUsarDhan 3	-5.18**	21.27**	-2.86**	-6.12**	0.12	0.54	13.52**	2.11**	10.09**	8.13**	-2.16	9.86**	14.39**	1.42**	1.11*	1.25**	0.59**	22.77**
38	NDRK 5025*CSR 23	-1.21	21.94**	-2.38**	-5.81**	2.00**	0.08	14.35**	1.73**	12.36**	10.90**	-1.67	6.25**	26.00**	1.53**	0.53	1.43**	0.46**	30.56**
39	NDRK 5025*IR 28	-2.38	15.42**	7.15**	-6.34**	1.34**	0.16	9.42**	1.85**	11.98**	11.62**	-0.40	10.22**	11.29**	-4.60**	0.31	0.88**	0.40**	20.45**
40	NDRK 5059*NarendraUsarDhan 3	-1.57	14.95**	-5.37**	1.66**	1.15**	-0.06	13.45**	2.07**	16.39**	19.80**	4.08**	12.12**	19.79**	0.84**	0.62	0.66**	0.24**	29.53**
41	NDRK 5059*CSR 23	-1.22	16.29**	0.56**	-3.78**	2.32**	-0.74	16.22**	2.27**	11.24**	14.97**	4.20**	6.92**	0.84	0.44**	-0.63	0.55**	0.23**	7.74**
42	NDRK 5059*IR 28	-1.58	16.13**	-3.97**	-6.20**	2.18**	0.00	14.91**	2.01**	15.35**	20.35**	5.96**	8.57**	0.46	0.92**	0.16	0.48**	0.31**	9.02**
43	NDRK 5081*NarendraUsarDhan 3	-4.45**	18.79**	8.82**	-1.53**	-5.96**	-0.83	12.04**	2.99**	19.19**	23.93**	5.86**	12.95**	15.91**	-2.73**	0.19	0.82**	0.33**	26.81**
44	NDRK 5081*CSR 23	-4.03**	18.42**	15.74**	-3.92**	1.57**	-0.55	13.50**	2.04**	19.92**	29.20**	11.58**	11.11**	6.79**	1.33**	0.35	1.20**	0.31**	17.19**
45	NDRK 5081*IR 28	-9.36**	19.84**	15.65**	-0.32	3.02**	-0.30	13.26**	2.10**	20.49**	29.81**	11.72**	5.67**	17.09**	0.14*	0.44	0.59**	0.35**	21.75**
46	NDRK 5047*NarendraUsarDhan 3	-3.17*	25.76**	3.86**	-4.26**	3.06**	0.22	4.70**	2.74**	5.67**	8.52**	3.05*	1.60	30.82**	0.72**	0.07	0.81**	0.61**	31.98**
47	NDRK 5047*CSR 23	-4.44**	19.89**	33.77**	-0.69**	1.02**	0.03	9.21**	1.91**	4.68**	18.02**	14.00**	6.67**	10.46**	1.40**	0.14	0.52**	0.72**	16.45**
48	NDRK 5047*IR 28	-3.57**	12.80**	23.94**	-1.22**	2.62**	0.45	9.19**	3.02**	3.82*	9.07**	5.45**	7.94**	15.79**	1.10**	0.23	0.81**	0.70**	22.33**
49	NDRK 5039*NarendraUsarDhan 3	0.00	9.23**	23.45**	5.60**	0.21	-0.39	14.19**	2.90**	4.89**	22.93**	18.92**	-2.67*	20.14**	0.19**	0.36	0.71**	0.45**	18.03**
50	NDRK 5039*CSR 23	-1.20	23.99**	26.81**	-7.48**	2.76**	0.40	18.24**	1.91**	4.34**	7.00**	2.78	5.22**	12.02**	-1.15**	0.20	0.59**	0.47**	16.66**
51	NDRK 5039*IR 28	-1.19	24.43**	19.90**	0.96**	1.68**	0.05	17.20**	1.13*	3.85*	3.57	-0.36	10.24**	17.80**	1.50**	0.58	0.76**	0.49**	26.11**
52	NarendraUsarDhan 2*NarendraUsarDhan 3	-2.38	13.23**	-11.11**	0.26	2.56**	-0.43	7.47**	1.84**	6.71**	7.14**	0.44	2.31*	10.14**	-0.22**	0.30	0.43**	0.77**	12.39**
53	NarendraUsarDhan 2*CSR 23	-2.79*	17.13**	9.10**	1.88**	1.73**	-0.79	8.09**	2.86**	7.37**	-5.14**	-13.51**	4.10**	9.81**	0.78**	0.81	0.76**	0.31**	13.72**
54	NarendraUsarDhan 2*IR 28	-1.21	10.37**	-64.65**	4.16**	2.61**	-0.14	8.16**	2.64**	13.03**	10.65**	-2.75	5.88**	6.44**	0.76**	0.30	1.01**	0.23**	12.01**
55	Deepak*NarendraUsarDhan 3	-2.01	-2.76**	-34.29**	0.47	4.22**	0.24	6.82**	4.12**	10.64**	5.82**	-5.40**	4.46**	15.36**	1.51**	0.61	0.92**	0.27**	19.16**
56	Deepak*CSR 23	-2.40*	0.92**	-36.24**	1.23**	2.16**	-1.80	10.76**	1.65**	10.43**	14.07**	4.04**	9.57**	5.36**	-0.22**	0.60	0.65**	0.35**	14.53**
57	Deepak*IR 28	-2.83*	-1.78**	-19.27**	1.47**	-0.45	-1.31	8.83**	2.48**	11.28**	9.65**	-1.83	15.69**	11.86**	2.22**	0.22	0.86**	0.22**	25.96**
58	Sundri*NarendraUsarDhan 3	-4.78**	8.11**	-18.24**	-1.31**	0.43	0.00	11.07**	1.87**	13.13**	13.62**	0.57	19.05**	-0.16	0.37**	0.44	0.61**	1.09**	19.01**
59	Sundri*CSR 23	-2.72*	9.04**	-1.36**	-0.80**	2.60**	-0.45	10.87**	1.72**	11.65**	15.21**	4.06**	18.26**	5.94**	0.75**	0.47	0.95**	0.99**	23.09**
60	Sundri*IR 28	-3.57**	6.58**	7.94**	1.19**	4.17**	0.15	14.81**	1.56**	17.60**	15.68**	-2.35	6.38**	26.08**	0.26**	0.92*	1.16**	0.92**	30.95**
61	Pusa Basmati 1*NarendraUsarDhan 3	-1.74	10.18**	4.90**	1.14**	2.05**	0.42	10.28**	2.12**	4.03*	15.02**	11.43**	4.46**	18.70**	1.23**	0.26	0.78**	0.13**	22.34**
62	Pusa Basmati 1*CSR 23	-1.02	17.73**	1.82**	2.38**	3.23**	-0.63	10.59**	1.92**	14.06**	23.67**	11.20**	11.29**	9.29**	0.41**	0.18	0.70**	0.17**	19.61**
63	Pusa Basmati 1*IR 28	-4.00**	17.24**	1.81**	3.55**	3.81**	0.28	10.59**	2.76**	13.08**	19.93**	7.90**	4.40**	22.31**	0.53**	0.47	0.69**	0.46**	25.63**
Range of Inbreeding depression	**Min.**	-9.36	-20.78	-64.65	-8.18	-5.96	-1.80	0.00	1.06	-12.18	-12.18	-13.51	-2.67	-3.96	-6.53	-0.63	0.28	0.13	4.39
	Max.	0.79	34.47	33.77	10.07	5.78	5.36	18.24	4.12	20.49	29.81	18.92	19.05	34.58	3.73	1.35	29.26	2.55	38.74
No. of crosses with significant positive inbreeding depression		**0**	**54**	**27**	**29**	**45**	**3**	**62**	**63**	**57**	**58**	**30**	**59**	**56**	**44**	**4**	**63**	**63**	**63**
No. of crosses with significant negative inbreeding depression		**22**	**9**	**35**	**28**	**11**	**0**	**0**	**0**	**1**	**3**	**6**	**2**	**1**	**16**	**0**	**0**	**0**	**0**

Majority of the crosss combinations possessing high heterosis also had high estimates of inbreeding depression. Further, it indicated that both the heterosis as well as inbreeding depression is closely related phenomenon with preponderance of non additive gene action. The similar findings have also been reported by Alam *et al.,* (2004), Verma and Srivastava (2005), Sharma *et al.,* (2013) and Venkanna *et al.,* (2014). The presence of high heterosis for economically important characters is not only useful for developing hybrids, synthetic or composites through exploitation of heterosis, but also helps in obtaining transgressive segregants for development of superior homozygous lines.

In genetics, transgressive segregation is the formation of extreme phenotypes, or transgressive phenotypes, observed in segregated hybrid populations compared to phenotypes observed in the parental lines. The transgressive segregation was estimated as appearance of these trangressive (extreme) phenotypes either positive or negative in terms of fitness. The estimates of transgressive segregation for eighteen characters of sixty-three crosses are presented in **Table 3**.

For grain yield per plant twenty-one crosses over better parent, twenty-eight crosses over SV_1 and nineteen crosses over SV_2 exhibited positive and significant Transgressive segregation, due to increased *per se* performance in F_2 generation. As such selection of promising lines in segregating generation, especially to pick up the transgressive segregants by maintaining more number of progenies would be best perspective method to make progress for this trait. The top five transgressive segregants over better parent were NDRK 5004 x Narendra Usar Dhan 3 (26.47), Sarjoo 52 x Narendra Usar Dhan 3 (25.41), NDRK 5040 x Narendra Usar Dhan 3 (24.89), NDRK 5062 x IR 28 (21.26) and CSR 10 x Narendra Usar Dhan 3 (19.55) in grain yield per plant and these same crosses have best heterotic potential as well as high amount of inbreeding depression; it clearly indicated that preponderance of non additive gene action (additive x additive) in such type of cross combinations and showing transgressive segregation as well due to heritable and fixable nature of gene action. These results are similar to those of Verma and Srivastava (2005), Saleem *et al.,* (2008) and Seetharam *et al.,* (2013). For amylose content none of the crosse over better parent, twenty-four crosses over SV_1 and forty-two over SV_2 exhibited positive and significant residual heterosis, due to increased *per se* performance in F_2 generation. As such selection of promising lines in segregating generation, especially to pick up the transgressive segregants by maintaining number of progenies would be more persepective method to make progress for this trait. For protein content three crosses over better parent, forty-five over SV_1 and nine over SV_2 exhibited positive and significant residual heterosis. As such selection of promising lines in segregating generation, especially to pick up the transgressive segregants by maintaining number of progenies would be more persepective method to make progress for this trait. In F_2s segregating population, some of the crosses were found as transgressive segregants.

Table 3: Extent of transgressive segregation in F_2s for 18 characters in rice under sodic soil

S. No.	Crosses	Days to 50% flowering	Chlorophyll content	Leaf nitrogen	Leaf temperature	Flag leaf area (cm^2)	Plant height (cm)	Panicle bearing tillers/plant	Panicle length (cm)	Spikelets/ panicle	Grains/ panicle	Spikelet fertility (%)	Biological yield/ plant (g)	Harvest Index(%)	L/B ratio	1000-grain weight (g)	Amylose content	Protein content (%)	Grain yield/ plant (g)
1	NDRK 5004*NarendraUsarDhan 3	-1.93	8.08	3.73	-10.49**	-0.38	-7.39**	1.60	-0.53	-2.63	-6.36**	-2.99	-2.96	26.33**	-21.56**	2.34	-0.31	-5.34**	26.47**
2	NDRK 5004*CSR 23	-3.09	-9.64	0.00	-5.68*	1.12	-1.47	0.64	-2.26	7.21**	-0.57	-11.22 **	3.51	-17.45**	-0.43	3.22	-0.24	-1.66*	0.59
3	NDRK 5004*IR 28	1.54	-15.34*	-0.62	-7.53**	-0.54	-7.33**	-8.01 **	-2.26	10.58**	-0.59	-12.70 **	9.65**	-14.01**	-3.64	2.53	-0.59	-2.92**	-5.84*
4	FL478* NarendraUsarDhan 3	1.59	-20.53**	4.40	-6.37*	-8.23**	-9.66**	2.46	-3.35	-23.25**	-25.67**	-2.30	-14.81**	-1.91	-25.47**	1.04	-30.56 **	-0.02	-1.32
5	FL478*CSR 23	3.60	-8.65	13.84	-3.98	1.53	5.23**	1.76	-3.35	-18.49**	-16.24**	-0.40	-3.81	1.26	4.08	-0.68	-40.94 **	0.56	0.40
6	FL478*IR 28	0.40	-19.57**	13.21	-1.05	-9.11**	0.44	0.70	-3.98	-24.82**	-22.79**	1.94	0.95	-8.70*	1.43	0.51	-33.12 **	0.59	-7.85**
7	NDRK 5093*Narendra U sarDhan 3	0.39	-12.33*	-1.10	-2.61	-11.02**	2.21*	-7.60 **	-1.77	-23.03**	-38.88**	-19.83 **	-5.93*	-17.17**	-24.82**	-13.35**	-39.83 **	-2.40**	-6.60**
8	NDRK 5093*CSR 23	-1.57	31.09**	-13.74	-3.55	5.09**	0.51	-7.89 **	-5.57*	-11.53**	-21.37**	-11.34 **	19.59**	-29.49**	0.96	-5.96*	-49.40 **	0.61	-15.65**
9	NDRK 5093*IR 28	1.57	24.08**	-4.95	-5.56*	-15.14**	5.04**	-9.65 **	-6.39**	8.73**	-0.79	-22.70 **	24.44**	-8.85*	-2.56	-13.71**	-43.24 **	-0.72	13.55**
10	SushkSamrat*NarendraUsarDhan 3	-0.77	-19.49**	0.54	-6.93*	-4.69**	4.08**	-10.83 **	-0.99	-9.65**	-17.11**	-7.45 **	-31.11**	-14.76**	-26.36**	-0.42	-43.78 **	-11.68**	-33.06**
11	SushkSamrat*CSR 23	-1.54	1.55	2.72	-6.49*	-4.52**	-0.42	-8.60 **	-4.51	3.26	-4.56**	-7.80 **	25.77**	-13.59**	-6.90*	4.32*	-52.63 **	-9.03	8.49**
12	SushkSamrat*IR 28	-0.38	-14.84**	-5.98	-8.68**	-3.98**	5.20**	-9.87 **	1.41	0.00	-13.71**	-12.87 **	9.88*	-12.28**	9.95**	2.92	-47.53 **	-9.91	-3.92
13	IR 85897*NarendraUsarDhan 3	-1.92	-13.80*	-11.70	-6.92*	-0.78	2.16*	-18.35 **	-2.96	-12.06**	-19.80**	-8.00 **	-28.89**	9.14*	-24.33**	2.65	-69.71 **	0.17	-14.06**
14	IR 85897*CSR 23	-4.21 *	-2.91	-2.13	-6.07*	-3.52**	2.16*	-7.56 **	-5.66*	-2.76	-9.69**	-7.36 **	8.25*	-0.93	12.79**	3.56	-74.40 **	1.79*	7.36**
15	IR 85897*IR 28	-1.53	-0.12	-6.38	-4.77	-1.32	2.43*	0.00	-2.43	-0.79	-1.29	-2.99	5.62	-3.84	5.46	3.04	-71.34 **	1.47	1.14
16	Pant 10*NarendraUsarDhan 3	0.39	-20.90**	-0.55	-3.70	-12.53**	-0.32	-17.63 **	3.15	-14.25**	-19.07**	-4.80 **	-11.85**	18.25**	-36.78**	-5.48*	-71.91 **	0.25	4.17
17	Pant 10*CSR 23	-0.39	-8.72	8.79	-8.12**	4.28*	-1.40	-9.96 **	3.41	-5.51*	-5.70**	-0.46	6.19	-26.09**	1.97	-1.83	-75.97 **	0.24	-8.54**
18	Pant 10*IR 28	-1.95	-1.24	4.95	-5.70*	-15.79**	9.40**	4.73	-1.18	2.08	3.49*	-1.44	2.65	-21.17**	10.33**	-5.28*	-73.34 **	0.26	0.58
19	CSR 10*NarendraUsarDhan 3	-0.40	-12.58*	-7.57	-1.97	-15.27**	-9.66**	2.02	2.50	29.85**	28.12**	-1.13	-2.96	23.26**	-41.58**	0.43	-25.52 **	-5.04**	19.55**
20	CSR 10*CSR 23	2.40	19.47**	-6.49	-5.04	4.37*	5.72**	-0.29	2.06	22.44**	35.33**	0.48	-6.06*	-12.54**	-9.27*	2.82	-36.69 **	-1.47	5.20*
21	CSR 10*IR 28	2.00	20.09**	-2.70	-4.44	-18.94**	0.48	1.15	5.59*	27.02**	31.25**	-1.57	-3.03	11.97**	6.08	8.39**	-28.84 **	-2.79**	13.48**
22	NDRK 5040*NarendraUsarDhan 3	1.59	2.63	-13.81	-4.60	-9.05**	-1.64	-7.15 **	-2.95	-2.19	-2.93*	-1.82	-0.74	21.82**	-38.49**	-3.53	-62.33 **	-1.41	24.89**
23	NDRK 5040*CSR 23	-0.40	-16.40**	-14.76	-2.75	-2.01	-2.82**	3.56	-2.33	9.02**	11.40**	-0.86	20.62**	-22.63**	9.67**	0.21	-77.12 **	0.83	-6.63**
24	NDRK 5040*IR 28	2.78	-14.58**	-11.90	-4.40	-13.34**	-0.30	0.40	-5.28	14.44**	11.41**	-2.58	22.68**	-19.15**	10.85**	-0.23	-64.42 **	-0.20	-0.86

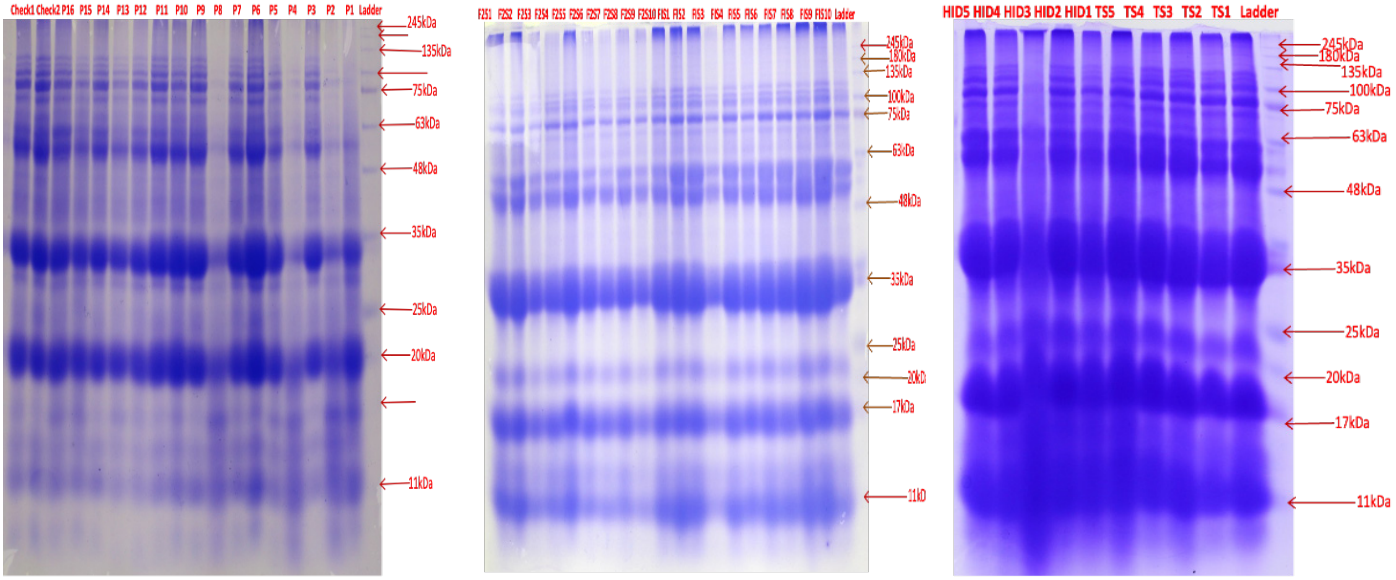
S. No.	Crosses	Days to 50% flowering	Chlorophyll content	Leaf nitrogen	Leaf temperature	Flag leaf area (cm^2)	Plant height (cm)	Panicle bearing tillers/plant	Panicle length (cm)	Spikelets/ panicle	Grains/ panicle	Spikelet fertility (%)	Biological yield/ plant (g)	Harvest Index(%)	L/B ratio	1000-grain weight (g)	Amylose content	Protein content (%)	Grain yield/ plant (g)
25	Sarjoo 52*NarendraUsarDhan 3	-1.15	-18.72**	7.29	-3.33	-6.61**	0.45	-7.06 **	0.99	18.18**	21.70**	-0.77	-2.82	22.97**	-41.99**	-2.30	0.92	0.60	25.41**
26	Sarjoo 52*CSR 23	0.38	-8.05	-2.08	-9.03**	-2.91	0.24	-6.76 **	-3.26	31.31**	29.01**	-4.44 **	-9.86**	-18.73**	-6.49	-0.88	1.27	3.77**	-6.61**
27	Sarjoo 52*IR 28	1.15	-17.34**	3.13	-2.30	-7.72**	1.11	-6.18 **	-1.28	30.91**	31.13**	-0.27	-14.79**	9.13*	-4.23	-0.60	1.11	0.64	-3.11
28	NDRK 5062*NarendraUsarDhan 3	-0.78	-16.45**	7.94	-0.68	-4.12*	0.83	1.46	0.91	-5.50**	-12.08**	-7.85 **	-2.96	0.25	-44.67**	-0.18	-3.82	1.45	6.67**
29	NDRK 5062*CSR 23	3.53	1.09	10.05	-4.08	-3.90*	0.33	0.58	1.42	-11.01**	-29.38**	-20.96 **	11.38**	-4.11	6.49	-0.54	-17.94 **	0.51	18.38**
30	NDRK 5062*IR 28	0.00	0.99	1.06	-1.70	-7.93**	-0.48	1.75	3.36	-8.81**	-23.13**	-16.07 **	18.70**	2.17	8.73*	1.46	-8.01 **	0.59	21.26**
31	Narendra 2064*NarendraUsarDhan 3	0.00	-19.01**	-1.62	-2.78	-1.93	3.48**	0.54	-1.45	21.36**	-0.22	-17.42 **	16.30**	-23.08**	-18.96**	5.50**	2.51	0.15	7.81**
32	Narendra 2064*CSR 23	-0.78	-24.54**	3.78	1.86	-1.87	2.93**	1.35	1.74	23.55**	1.12	-17.82**	28.57**	-32.19**	11.35**	2.12	-9.01 **	0.49	-12.82**
33	Narendra 2064*IR 28	3.13	-25.34**	5.95	-5.19	0.33	2.55*	2.96	1.74	21.76**	-6.47**	-22.87**	28.57**	-35.32**	18.77**	4.68**	2.58	0.48	-16.94**
34	NDRK 5037*NarendraUsarDhan 3	-2.30	-12.10*	-13.64	-2.64	-0.73	-2.78*	0.88	-2.74	30.71**	30.13**	-0.71	16.18**	-7.85	-23.03**	-22.05**	-4.15	-0.66	7.84**
35	NDRK 5037*CSR 23	0.38	-20.30**	-5.05	-8.81**	-2.70*	-1.35	0.58	-3.48	32.82**	28.85**	-3.25*	11.03**	-40.43**	8.76**	-10.41**	-18.44 **	1.51*	-18.46**
36	NDRK 5037*IR 28	-0.77	-9.59*	-16.16	-4.74	1.11	0.47	0.29	-6.43**	25.14**	23.08**	-1.92	11.76**	-21.83**	19.07**	-22.59**	-9.10 **	1.37	-11.98**
37	NDRK 5025*NarendraUsarDhan 3	4.76*	-19.86**	-6.25	-3.93	-20.18**	-0.38	0.00	-0.13	38.51**	34.20**	-2.40	-5.19	-31.63**	-43.69**	-14.57**	-13.54 **	-5.27**	-14.17**
38	NDRK 5025*CSR 23	0.00	-22.39**	-10.42	-2.82	-8.91**	0.14	0.00	0.38	38.07**	32.07**	-3.65*	17.65**	-40.97**	2.12	-3.94	-27.05 **	-1.96*	-30.53**
39	NDRK 5025*IR 28	3.20	-15.32**	-11.98	-4.67	-24.99**	-0.41	-0.27	0.76	35.01**	28.27**	-4.30**	20.59**	-21.49**	-6.75	-12.54**	-18.54 **	-3.21**	-5.43*
40	NDRK 5059*NarendraUsarDhan 3	0.39	-10.41*	7.69	-6.54*	-9.86**	-1.85	-4.07*	4.11	-0.44	-3.91**	-2.65	-14.07**	-26.88**	-42.39**	3.87	1.92	-1.51	-20.66**
41	NDRK 5059*CSR 23	-3.49	-11.51*	-2.75	-4.18	-1.54	-2.44*	-6.23**	1.03	9.91**	8.29**	-4.62**	21.00**	-12.68**	-10.33**	3.83	1.78	0.04	5.65*
42	NDRK 5059*IR 28	-0.39	-16.83**	0.55	-2.49	-12.99**	-1.72	-5.69**	0.15	-1.18	-0.55	1.42	28.00**	-8.37*	13.36**	3.19	1.95	0.11	17.39**
43	NDRK 5081*NarendraUsarDhan 3	-1.15	-17.86**	-10.14	-3.93	-32.01**	-14.01**	0.80	-2.73	-12.28 **	-17.60**	-5.22**	-10.37**	-22.05**	-48.01**	-1.23	-4.07	-0.68	-12.52**
44	NDRK 5081*CSR 23	-1.15	-14.19**	-12.08	-1.82	-19.81**	-3.25*	0.27	-1.77	-0.25	-12.25**	-12.25**	31.96**	-14.47**	-1.72	-1.98	-18.51 **	0.84	16.26**
45	NDRK 5081*IR 28	-1.53	-16.07**	-19.32*	-4.47	-37.76**	-0.40	-1.06	1.77	-0.26	0.00	-8.44**	43.01**	-23.57**	-3.57	-2.00	-9.18 **	0.77	9.28**
46	NDRK 5047*NarendraUsarDhan 3	3.17	-15.51**	-16.67*	-3.81	-9.33**	0.28	1.75	1.61	-12.50 **	-18.58**	-11.19**	-8.89**	-26.85**	-33.12**	-5.50**	-5.19	0.80	-27.86**
47	NDRK 5047*CSR 23	3.60	-7.48	-29.05**	-6.97*	0.98	-1.67	0.58	-0.81	-3.01	-9.78**	-11.18**	29.90**	-12.34**	-5.48	-6.42**	-19.48 **	-0.06	13.99**
48	NDRK 5047*IR 28	4.40*	-0.12	-22.86**	-4.03	-10.92**	0.73	0.87	4.51	0.00	-10.34**	-9.59**	28.89**	-22.16**	-1.58	-4.67	-9.65 **	0.93	0.24

S. No.	Crosses	Days to 50% flowering	Chlorophyll content	Leaf nitrogen	Leaf temperature	Flag leaf area (cm^2)	Plant height (cm)	Panicle bearing tillers/plant	Panicle length (cm)	Spikelets/ panicle	Grains/ panicle	Spikelet fertility (%)	Biological yield/ plant (g)	Harvest Index(%)	L/B ratio	1000-grain weight (g)	Amylose content	Protein content (%)	Grain yield/ plant (g)
49	NDRK 5039*NarendraUsarDhan 3	-1.59	-0.42	-27.60**	-7.44**	-9.87**	2.36*	-7.64**	2.47	6.58**	-11.25**	-16.39**	14.07**	-1.05	-15.70**	6.02**	3.65	-1.75*	12.88**
50	NDRK 5039*CSR 23	0.40	-21.85**	-27.15**	-5.47	1.62	0.64	-9.72**	2.94	21.55**	17.38**	-4.96**	13.39**	-13.13**	0.31	4.51*	3.45	-0.05	13.77**
51	NDRK 5039*IR 28	1.99	-22.35**	-28.96**	-3.23	-13.34**	-2.23*	-9.72**	2.94	23.12**	-6.63**	-23.50**	1.79	-17.27**	16.18**	2.39	3.31	0.02	-14.44**
52	NarendraUsarDhan 2*NarendraUsarDhan 3	1.98	6.84	-16.67*	-4.72	-8.90**	-2.12*	2.22	-6.22**	-14.69**	-20.54**	-6.03**	-5.93*	-8.93*	-26.77**	-0.25	3.72	-2.73**	-7.71**
53	NarendraUsarDhan 2*CSR 23	1.98	0.51	-12.04	-7.57**	0.41	-4.57**	0.95	-8.11**	0.75	-0.85	-1.81	6.36	-22.98**	-2.54	-0.03	3.64	0.84	-7.92**
54	NarendraUsarDhan 2*IR 28	-1.19	8.56	-11.57	-5.03	-10.44**	-3.70**	0.00	-5.41*	-7.32 **	-7.36**	-2.22	1.82	-0.51	0.11	0.86	3.97	-0.21	1.21
55	Deepak*NarendraUsarDhan 3	-1.17	-25.95**	21.85	0.71	-37.05**	-17.27**	1.06	2.52	-7.89 **	-12.96**	-4.96**	-20.74**	-7.41	-25.47**	2.12	-8.63 **	-0.70	-26.18**
56	Deepak*CSR 23	-0.39	-4.67	10.19	-3.06	-21.94**	6.64**	-0.70	2.36	3.26	-4.27**	-8.54**	7.22	-8.25*	-16.25**	2.07	-22.43 **	-0.01	-1.86
57	Deepak*IR 28	-1.17	-6.09	8.05	-0.94	-37.71**	0.34	1.41	-1.10	10.54**	-7.21**	-15.29**	-5.49	-14.78**	-26.69**	2.60	-13.12 **	0.06	-19.76**
58	Sundri*NarendraUsarDhan 3	4.37*	-29.60**	7.36	-3.93	-33.34**	-4.69**	-29.19**	2.60	-24.56 **	-31.78**	-8.78**	-24.44**	12.33**	-13.34**	-2.11	4.66	-5.10**	-13.61**
59	Sundri*CSR 23	6.02**	-8.33	-9.20	-6.60*	-17.26**	-2.57*	-17.97**	3.90	-18.30**	-25.36**	-8.87**	-3.09	-15.01**	-14.47**	-4.90*	-0.60	-2.15**	-17.58**
60	Sundri*IR 28	4.40*	-6.28	-7.36	-6.36*	-36.41**	-0.35	-12.26**	-1.30	-8.58 **	-4.35*	-6.92**	22.22**	-28.95**	5.07*	-5.82**	4.96	-3.16**	-13.68**
61	Pusa Basmati 1*NarendraUsarDhan 3	2.82	-12.30*	-17.11	-5.76*	-38.41**	-20.11**	-17.99**	-5.13*	-11.18**	-30.81**	-21.78**	-20.74**	-8.68*	-21.40**	-7.74**	1.79	-2.11**	-27.82**
62	Pusa Basmati 1*CSR 23	4.23*	4.77	-13.37	-7.32*	-28.18**	-5.80**	-8.76**	-10.12**	-6.52 **	-26.50**	-22.60**	13.40**	-29.14**	-2.52	4.81*	1.74	0.34	-19.78**
63	Pusa Basmati 1*IR 28	0.70	5.13	-12.83	-5.98*	-41.76**	-7.25**	4.73	-1.91	1.70	-22.71**	-23.64**	10.13*	-35.17**	-4.83	-7.72**	1.74	-0.63	-24.33**
Range of transgressive segregation	**Min.**	-4.21	-29.60	-29.05	-10.49	-41.76	-20.11	-29.19	-10.12	-24.82	-38.88	-23.64	-24.44	-40.97	-48.01	-22.59	-77.12	-11.68	-30.53
	Max.	6.02	31.09	21.85	1.86	5.09	9.40	4.73	5.59	38.51	35.33	1.94	43.01	26.33	19.07	8.39	4.96	3.77	26.47
No. of crosses with significant positive segregation		**6**	**4**	**0**	**0**	**3**	**15**	**0**	**1**	**25**	**17**	**0**	**29**	**9**	**12**	**6**	**0**	**3**	**21**
No. of crosses with significant negative segregation		**1**	**35**	**8**	**23**	**43**	**19**	**26**	**9**	**22**	**37**	**41**	**15**	**43**	**27**	**16**	**36**	**16**	**30**

*, ** significant at 5 and 1 per cent probability levels, respectively

The most promising crosses based on mean performance, heterobeltiosis and standard heterosis (SV1 and SV2), SCA effect, GCA effect of parent for grain yield per plant and the traits for which these crosses also exhibited desirable heterosis in F_1s and F_2s have been depicted in **Table 1**. The ten most promising crosses *viz*., NDRK 5037 x Narendra Usar Dhan 3, NDRK 5062 x IR 28, Sarjoo 52 x Narendra Usar Dhan 3, Narendra 2064 x Narendra Usar Dhan 3, NDRK 5062 x CSR 23, NDRK 5004 x Narendra Usar Dhan 3, NDRK 5037 x CSR 23, NDRK 5040 x Narendra Usar Dhan 3, NDRK 5093 x Narendra Usar Dhan 3 and Narendra 2064 x CSR 23 in F_1s while in F_2s are NDRK 5004 x Narendra Usar Dhan 3, Sarjoo 52 x Narendra Usar Dhan 3, NDRK 5040 x Narendra Usar Dhan 3, NDRK 5062 x IR 28, CSR 10 x Narendra Usar Dhan 3, NDRK 5062 x CSR 23, Narendra 2064 x Narendra Usar Dhan 3, NDRK 5039 x Narendra Usar Dhan 3, NDRK 5059 x IR 28 and DRK 5037 x Narendra Usar Dhan 3. It indicated that additive and non-additive genetic effects were responsible for increased grain yield in these F_1s over the SV_1 and SV_2. Such type of hybrid could be meaningful for heterosis breeding and desirable segregants could also be screened out in succeeding generations as a substantial part of variance which was considered as fixable one. Heterosis for grain yield in these crosses could be due to desirable heterotic response for component traits such as days to 50% flowering, chlorophyll content, leaf nitrogen, leaf temperature, flag leaf area, plant height, panicle bearing tillers / plant, panicle length, spikelets / panicle, grains per panicle, spikelet fertility, biological yield / plant, harvest index, L/B ratio, 1000- grain weight, amylose content, protein content, indicating genetic association of these character with grain yield. The hybrid combinations showing non additive gene action, may be exploited through the use of CMS system, since the stable CMS with perfect restoration in rice are available.

Therefore, the yielding ability in the present set of material might be enhanced due to higher level of manifestation from yield, physiological and few quality contributing traits. Further, rice workers have also observed that grain yield might be due to



A. Protein profiling of selected parents including checks by SDS-PAGE

B. Protein profiling of selected F1s and F2s crosses by SDS-PAGE

C. Protein profiling of selected transgressivesegregants and highly inbreeding depressed crosses by SDS-PAGE

Where, P-Parents, F1S- F_1S crosses, F2s- F_2s segregants, TS-Transgressive segregants, HID- Highly inbreeding depressed

Figure 1: Protein profiling of selected rice genotypes of different breeding populations by SDS-PAGE

heterotic response through all other yield contributing traits. Similar findings have also been reported by Janardanam *et al*., 2001; Punitha *et al*., 2004; Verma and Srivastava, 2005; Singh *et al*., 2007; Roy *et al*., 2009 Chougule *et al.,* 2012 and Sudeepthi *et al.,* 2018.

Seed protein profiling is the most promising tool in determining the molecular polymorphism and genetic homology. Seed storage proteins help in cultivar identification by avoiding the external environmental influences. Electrophoretically detectable proteins in rice grains possess the potential of characterizing the germplasm by their taxonomic and evolutionary aspects. This study was aimed at exploiting the genetic variations among 48 (parents+F_1s+ F_2s+transgressive segregants+checks) elite rice genotypes through electrophoretical separation of grain proteins by sodium dodecyl sulphate polyacryamide gel electrophoresis (SDS PAGE) at 12% (**Figure 1**).

At 35 kDa the medium to dark bands were present in parents, F_1s, F_2s, transgressive segregants and checks while in highly inbreeding depressed cross combinations, variable range of the bands were observed *viz.,* absence of band, light, medium and dark bands.

Majority of these populations have two distinct protein bands in parents; three in F_1s and F_2s; and only one in transgressivesegregants and highly inbreeding depressed cross combination, which indicated that these proteins are developed in the salt tolerant breeding populations and play an important role in salt tolerance. The SDS-PAGE in combination with 2-D electrophoresis is further suggested for documenting contrasting variations of isoforms of protein peptides.

The RM values and banding pattern of different breeding populations *viz.,* parents, F_1s, F_2s, transgressive segregants including checks have been depicted in **Tables 4, 5** and **6.** Seed protein showed variability in banding pattern of polypeptide at 12% acrylamide gel during SDS-PAGE.

Table 4: Relative mobility at 12% SDS-PAGE of selected parents in rice

kDa value	Length of gel (cm)	R.M. Value	Parents																	
			Check 1	Check 2	P16	P15	P14	P13	P12	P11	P10	P9	P8	P7	P6	P5	P4	P3	P2	P1
	0																			
100	1	0.10	+++	+++	+++	+	++	+	+	+++	+++	+++	-	++	+++	+	-	++	-	-
75	2	0.13	+++	+++	+++	++	+++	+	++	+++	+++	+++	-	++	++	+++	-	+++	-	-
71	3	0.15	+	++	+	-	++	+	+	++	++	++	-	++	+++	+	-	++	-	-
63	4	0.20	+	+	+	-	+	-	+	+	+	+	-	+	++	+	-	+	-	-
55	5	0.24	++	++	++	+	++	+	++	++	++	++	-	++	++	++	-	++	-	+
35	6	0.40	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	++	+++	+++	+++	++	+++	++	+++
25	7	0.45	+	+	+	+	+	+	+	+	++	++	-	+	++	+	-	+	+	++
20	8	0.60	+++	+++	+++	+++	+++	+++	+++	+++	+++	+++	++	+++	+++	+++	++	+++	+	+++
17	9	0.70	-	-	+	+	-	-	-	-	+	-	++	-	+	+	+	-	++	++
11	10	0.80	+	+	+	+	+	-	-	+	+	+	+	+	+++	-	+	-	+	+

+ Low intensity of the band, ++Medium intensity of the band, +++ High intensity of the band, -No band was found.

Where, P= Parents

P1-NDRK 5037, P2-NDRK 5062, P3-Sarjoo 52, P4-Narendra 2064, P5-NDRK 5004, P6-NDRK 5040, P7-NDRK 5093, P8-CSR 10, P9- NDRK 5039, P10-NDRK 5059, P11-NDRK 5047, P12-Sundri, P13-NDRK 5025, P14-Narendra UsarDhan 3, P15-CSR 23, P16- IR 28, Check1- Jaya, Check2- CSR 43

Result revealed that majority the parents including checks visualized high to medium intensity of bands on 0.40 and 0.60 RM values (**Table 5**). Similarly, elite hybrids and their segregants showed high to medium intensity of band on 0.50 and 0.75 RM value (**Table 6**). Further, elite transgressive segregants showed high to medium intensity of band on 0.11, 0.22, 0.40 and 0.65 RM value. However, highly inbreeding depressed crosses showed high to medium intensity of band only on 0.65 RM value.

Table 5: Relative mobility at 12% SDS-PAGE of promising F_1s and F_2s in rice

kDa value	Length of gel (cm)	R.M. Value	Crosses																		
			F2S1	F2S2	F2S3	F2S4	F2S5	F2S6	F2S7	F2S8	F2S9	F2S10	F1S1	F1S2	F1S3	F3S4	F1S5	F1S6	F1S7	F1S8	F1S9	F1S10
	0																					
135	1	0.14	-	+	-	++	++	+	-	+	+	+++	+++	+++	+	+	+	+	+	+	+++	+
100	2	0.17	+	++	-	++	++	+	+	+	+	+++	+++	+++	+	++	+	++	++	++	+++	+
75	3	0.20	+	++	+	+++	+++	++	++	++	++	+++	+++	+++	++	+++	+++	+++	+++	+++	+++	+++
63	4	0.28	++	++	+	+	++	+	+	+	+	++	+++	+++	+	++	++	++	++	++	++	++
48	5	0.34	+++	+++	+	+	++	+	+	+	+	++	+++	+++	+	++	++	++	++	++	+++	+
35	6	0.50	+++	+++	++	++	+++	+++	++	++	++	+++	+++	+++	++	+++	+++	+++	+++	+++	+++	+++
20	7	0.64	++	++	+	+	++	+	+	++	+	++	++	++	-	+	+	+	+	++	++	+
17	8	0.75	+++	+++	++	++	+++	++	++	++	++	+++	+++	+++	++	++	++	++	++	++	++	++
11	9	0.80	+	+	-	-	+	-	-	-	-	+	+	+	-	-	-	-	-	+	+	-
9	10	0.89	+++	+++	-	-	++	-	-	-	-	++	++	++	-	++	+	+	+	++	++	+

+ Low intensity of the band, ++Medium intensity of the band

+++ High intensity of the band, -No band was found.

Where,

F1S= F_1S crosses, F2s= F_2s segregants

F1S1- NDRK 5037 x NarendraUsarDhan 3, F1S2- NDRK 5062 x IR 28, F1S3- Sarjoo 52 x NarendraUsarDhan 3, F1S4- Narendra 2064 x NarendraUsarDhan 3, F1S5- NDRK 5062 x CSR 23, F1S6- NDRK 5004 x NarendraUsarDhan 3, F1S7- NDRK 5037 x CSR 23, F1S8- NDRK 5040 x NarendraUsarDhan 3, F1S9- NDRK 5093 x NarendraUsarDhan 3, F1S10-Narendra 2064 x CSR 23, F2S1- NDRK 5004 x NarendraUsarDhan 3 ,F2S2- Sarjoo 52 x NarendraUsarDhan 3, F2S3- NDRK 5040 x NarendraUsarDhan 3, F2S4- NDRK 5062 x IR 28, F2S5- CSR 10 x NarendraUsarDhan 3, F2S6- NDRK 5062 x CSR 23, F2S7-Narendra 2064 xNarendraUsarDhan 3, F2S8- NDRK 5039 x NarendraUsarDhan 3, F2S9- NDRK 5059 x IR 28, F2S10- NDRK 5037 x NarendraUsarDhan 3

Table 6: Relative mobility at 12% SDS-PAGE of highest depressed crosses and top transgressive segregants in rice

kDa value	Length of gel (cm)	R.M. Value	Crosses									
			HID5	HID4	HID3	HID2	HID1	TS5	TS4	TS3	TS2	TS1
	0											
135	1	0.08	++	+	-	++	+	+	++	++	+	++
100	2	0.09	+++	++	-	+++	+	++	++	++	++	++
75	3	0.11	+++	+++	-	+++	++	+++	+++	+++	+++	+++
74	4	0.12	++	++	-	++	+	++	++	++	+	++
63	5	0.19	++	++	-	++	++	++	++	++	++	++
57	6	0.22	++	++	-	++	++	++	++	++	++	++
35	7	0.40	+++	++	-	++	+	+++	+++	+++	++	+++
25	8	0.55	+	+	++	++	+	++	++	++	+	++
20	9	0.65	+++	+++	+	+++	++	+++	+++	+++	+++	+++
11	10	0.85	+++	+	+	+	+	+	+	++	+	+++

+ Low intensity of the band, ++Medium intensity of the band; +++ High intensity of the band, -No band was found.

Where,

TS= Transgressive segregants; HID= Highly inbreeding depressed

TS1- NDRK 5004 x NarendraUsarDhan 3, TS2- Sarjoo 52 x NarendraUsarDhan, TS3- NDRK 5040 x NarendraUsarDhan 3, TS4-), NDRK 5062 x IR 28, TS5- CSR 10 x NarendraUsarDhan 3, HID1-NDRK 5037 x CSR 23, HID2- NDRK 5047 x NarendraUsarDhan 3, HID3- Sundri x IR 28, HID4- NDRK 5004 x IR 28, HID5- NDRK 5025 x CSR 23

Tolerant and susceptible breeding populations showed similar banding pattern but possesses wide variations between tolerant and susceptible. At 35 kDa the medium to dark bands were present in parents, F_1s, F_2s, transgressive segregants and checks while in highly inbreeding depressed cross combinations, variable range of the bands were observed *viz.,* absence of bands, light, medium and dark bands. Such a banding patern reflects that similar banding pattern on 35 kDa may certainly have salt tolerant QTLs in elite parents, which have inherited successfully in F_1s and transgressive segregants. Hence, emphasis should be given to elute these desired QTLs inorder to incorporate these salt tolerant traits of interest in

local cultivar and / or widely adopted genotype for sustainability under salt affected soils. The similar reports have been reported by Tripathy *et al.,* (2015).

Authors' Contributions

The idea of this study was developed by Shiv Prakash Shrivastav and O.P. Verma who also assisted in its design and interpretation of the data. Dan Singh Jakhar helped to draft the manuscript. All authors read and approved the final manuscript.

Funding

This study has no funding assistance.

Availability of data and material

The experimental data used for analysis and further writing of this article are available with the corresponding author on reasonable request.

Declaration

Conflict of interest

We declare that there is no conflict of interest in connection with the work submitted by us.

References

Alam MF, Khan MR, Nuruzzaman M, Parvez S, Swaraz AM, Alam I and Ahsan N. 2004. Genetic basis of heterosis and inbreeding depression in rice (*Oryza sativa* L.). *Journal of Zhejiang University of Sciences*, 5(4): 406-411.

Allard RW. 1960. Inbreeding depression and heterosis, pp. 213- 223 in Principles of Plant Breeding. John Wiley & Sons, New York.

Arunachalam V. 1974. The fallacy behind the use of modified line x tester design. *Indian Journal of Genetics*, 34(2): 200-207.

Ayalneh TD. 2020. Heterosis and combining ability for yield and yield related traits in maize (*Zea mays* L.) inbred lines in central rift valley of Ethiopia, (Doctoral dissertation, Haramaya University).

Bruce AB. 1910. The Mendelian theory of heredity and the augmen- tation of vigor. *Science*, 32(827) : 627-628.

Chougule GR, Mehta HD. and Patil SA. 2012. Heterosis for qualitative and quantitative traits in rice (*Oryza sativa* L.). *Crop Research*, 44(3): 386-390.

DAC and FW. 2021-2022. Estimates of Production of Food Grains. Directorate of Economics and Statistics. (2021-2022), Ministry of Agriculture and Farmers Welfare, Government of India.

De Los Reyes BG. 2019. Genomic and epigenomic bases of transgressive segregation - new breeding paradigm for novel plant phenotypes. *Plant Science*, 288:110213. doi: 10.1016/j.plantsci.2019.110213.

DeVicente MC and Tanksley SD. 1993. QTL analysis of transgressive segregation in an interspecific tomato cross. *Genetics*, 134(2): 585-596.

Dylan RDR and Benjamin FM. (2013). Transgressive hybrids as hopeful monsters. *Evolutionary Biology*. 40, 310-315. doi: 10.1007/s11692-012-9209-0.

East EM. 1936. Heterosis. *Genetics*, 21: 375-397.

Falconer DS and Mackay TFC. 1981. Introduction to quantitative genetics, *Longman* 1981.

Fonseca S. and Patterson FL. 1968. Hybrid vigour in seven parent diallel cross in common wheat (*T. aestivum* L.). *Crop Science*, 8(1): 85-88.

Goodnight, CJ. 1999. Epistasis and heterosis, In The Genetics and Exploitation of Heterosis in Crops, edited by J. G. Coors and S. Pandey. American Society of Agronomy, Inc. Crop Science Society of America, Inc. ASA-CSSA-SSSA Societies, Madison, WI. 59-68.

Gu Z, Gong J, Zhu Z, Li Z, Feng Q, Wang C. and Han B. 2023. Structure and function of rice hybrid genomes reveal genetic basis and optimal performance of heterosis. *Nature Genetics*, 55(10): 1745-1756.

Hill J. 1966. Recurrent backcrossing in the study of quantitative inheritance. Heredity, 21: 85-120.

Janardanam V, Nandrajan N. and Jebaraj S. 2001. Study on heterosis in rice. *Madras Agriculture Journal*, 88(10-12): 721-723.

Jiang N, Yan J, Liang Y, Shi Y, He Z, Wu Y, Zeng Q, Liu X. and Peng J. (2020). Resistance genes and their interactions with bacterial blight/leaf streak pathogens (*Xanthomonas oryzae*) in rice (*Oryza sativa* L.) an updated review. *Rice*, 13(1):1-12.

Jones DF. 1917. Dominance of linked factors as a means of accounting for heterosis. *Genetics*, 2: 466-479.

Keeble F. and Pellew C. 1910. The mode of inheritance of stature and of time of flowering in peas (*Pisum sativum*). *Journal of Genetics*, 1: 47-56.

Kempthorne O. 1957. An Introduction to Genetic Statistics. John Willey and sons, Inc. New York, pp. 468-471.

Laemmli EK. 1970. Cleavage of structural proteins during the assembly of the head of bacteriophage T4. *Nature*, 227: 680-685.

Mather K and Jinks JL. 1982. Biometrical Genetics. Chapman and Hall, London.

Modunshim, MK, Madhu B. and Patel PB. (2022). Line x Tester analysis for deducing heterosis in rice (*Oryza sativa* L.). *Journal of Rice Research*, 15(1): 9-16.

Panse VG. and Sukhatme PV. 1967. Statistical Methods for Agricultural Workers. IInd Edn., pp.152-157.

Punitha D, Joel AJ, Manonmani S. and Thiyagarajan K. 2004. Combining ability for yield and its components in rice (*Oryza sativa* L.). *Advances in Plant Sciences*, 17(1): 345-348.

Rieseberg LH, Archer MA. and Wayne RK. 1999. Transgressive segregation, adaptation and speciation. *Heredity*, 83, 363-372. doi: 10.1038/sj.hdy.6886170.

Roy SS, Senapati BK, Sinhamahapatra SP. and Sarkar KK. 2009. Heterosis for yield and quality in rice. *Oryza*, 46(2): 87-93.

Saleem MY, Mirza JI. and Haq MA. 2008. Heritability, genetic advance and heterosis in line x tester crosses of Basmati rice. *Journal of Agriculture Research*, 46(1): 15-26.

Seetharaman K, Thirumeni, S, Paramsivam, K. and Nadaradjan S. 2013. Genetic diversity analysis of rice (*Oryza sativa* L.) genotype for seedling characters under saline-alkaline condition. *Electronic Journal of Plant Breeding*, 4(1): 1034-1042.

Sharma SK, Singh SK, Nandan R, Sharma A, Kumar R, Kumar V. and Singh MK. 2013. Estimation of heterosis and inbreeding depression for yield and yield related traits in rice (*Oryza sativa* L.). *Molecular Plant Breeding*, 4(29): 238-246.

Shrivastav SP, Verma OP, Jakhar DS, Singh V. and Lal K. 2022a. Studies on component of genetic variance and heterotic response in rice (*Oryza sativa* L.) for high yield with quality and sodicity tolerance. *Indian Journal of Genetics and Plant Breeding*, 82(04): 419-429.

Shrivastav SP, Verma OP, Lal K, Singh V. and Srivastava K. (2022b). Genetic divergence analysis in rice (*Oryza sativa* L.) germplasms under sodic soil. *Indian Journal of Agricultural Research*, DOI: 10.18805/IJARe.A-5976.

Shrivastav SP, Verma OP, Lal K. and Mishra S. (2022c). Assessment of sodicity tolerance in rice (*Oryza sativa* L.) Germplasm. *Journal of Rice Research*, 15(2): 104-117.

Shrivastav SP. and Verma OP. 2023. Correlation and path coefficients analysis for yield and its contributing traits in rice (*Oryza sativa* L.) under Sodic Soil. *Journal of Rice Research*, 16(1): 32-40.

Shull GH. 1908. The composition of a field of maize. *American Breeders Association*, 4: 296-301.

Simmonds, NW. 1979. Principles of Crop Improvement. *Longman Group*, London and New York.

Singh NK, Singh AK, Sharma CL, Singh PK. and Singh ON. 2007. Study of heterosis in rice using line x tester mating system. *Oryza*, 44(3): 260-263.

Stebbins, GL. 1958. The inviability weakness and sterility of interpecific hybrids. *Advances in Genetics*, 9:147-215.

Stuber, CW. 1994. Heterosis in plant breeding. *Plant Breeding Reviews*, 12:227-251.

Sudeepthi, K., Jyothula, D.P.B. and Suneetha, Y. (2018). Heterosis and combining ability studies for yield and yield component traits in rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences*, 7(10): 1205-1211.

Tripathy SK, Mohapatra BR, Nayak PK, Pal S, Senapati N, Dash GB, Lenka D, Swain D. and Ranjan R. 2015. Revea ing genetic variation in upland rice using seed storage protein profiling. *Research on Crops,* 16(2): 320-331.

Vega U and Frey KJ. 1980. Transgressive segregation in inter and intraspecific crosses of barley. *Euphytica*, 29, 585-594. doi: 10.1007/BF00023206.

Venkanna V, Raju Ch. S, Lingaiah N. and Rao VT. 2014. Studies on heterosis and inbreeding depression for grain yield and grain quality traits in rice (*Oryza Sativa* L.). *International of Journal of Science Environment and Technology*, 3(3): 910 - 916.

Verma OP. and Srivastava HK. 2005. Heterosis and segregation distortion for grain quality traits using diverse genotypes in rice (*O. sativa* L.). *Journal of Sustainable Agriculture*, 26(3): 15-30.

Wright S. 1977. Evaluation and the Genetics of Populations. University of Chicago Press, Chicago.

You H, Zafar S, Fan Z, Shuangbing Z, Kai C, Congcong S, Xiuqin Z, Wenzhong Z and Jianlong X. 2022. Genetic mechanism of heterosis for rice milling and appearance quality in an elite rice hybrid. *The Crop Journal,* 10(6): 1705-1716.

RESEARCH ARTICLE https://doi.org/10.58297/FBJS8734

Starch Kinetics, Cooking Quality and Phytochemical Composition of Geographical Indication (GI) Tagged Rice of Kerala

Chitra Pillai[1], Faseela KV[2] and Harikumaran Thampi[1*]

[1] Department of Life Sciences, University of Calicut-673635, Kerala, India.

[2]Department of Plant Breeding and Genetics, Regional Agricultural Research Station (Central zone), Kerala Agricultural University, Mele Pattambi-679306, Kerala

*Corresponding author Email: drhari@uoc.ac.in

Received: 30th September, 2024; Accepted: 5th November, 2024

Abstract

Geographical Indication (GI) tagged traditional rice of Kerala namely the red pigmented Palakkadan Matta and non-pigmented aromatic rice - Wayanadan Gandhakasala and Wayanadan Jeerakasala are well known for their cooking and eating quality, but are underutilized for their nutritional significance. The objective of this study was to classify these varieties based on their starch digestibility, biochemical composition and cooking characteristics. Results indicated significant ($p < 0.05$) variation among rice varieties for all the parameters evaluated. *In vitro* starch digestibility studies found significantly low glycemic index (< 68) but higher RS content for Wayanadan Gandhakasala and Chettadi. Aromatic varieties had lower cooking time (< 25 min) than Palakkadan Matta varieties. High water uptake ratio and elongation ratio was also noted for Wayanadan Gandhakasala. Total phenolic content correlated positively to total flavonoid content. Over all, Palakkadan Matta varieties had significantly higher free phenolic, free flavonoid and total flavonoid content than non-pigmented varieties. The study indicates that these GI tagged traditional rice varieties can thus be utilised in the functional food industry based on their intermediate glycemic index, desirable cooking qualities and the presence of beneficial bioactive components.

Key words: Geographical indication, Palakkadan Matta, Aromatic varieties, Glycemic Index, Cooking Properties, Total phenolic content

Introduction

Rice (*Oryza sativa* L.) is one of the most studied cereal crops of the world and forms the central part of the Indian diet. Rice gained popularity from the fact that it can be grown under diverse climatic conditions and can be cooked in many different ways. Therefore, quality of rice is a topic for which there can be different answers. Different countries or regions within a country prefer eating rice in different ways and therefore the definition of rice quality differs accordingly (Bhattacharya, 2009). The most commonly used quality traits include physical appearance, nutrition, milling and cooking characteristics. Numerous scientific studies suggest that both genetic and environmental factors can affect quality traits in rice grain (Chen et al., 2012; Custodio *et al.,* 2019; Krishnamrutha *et al.,* 2023). Some rice varieties are well known for their unique qualities because of the particular region in which they are grown. These special varieties found reference in historical scripts and were assigned with a unique status or tag known as geographical indication (GI) under the Geographical Indications of Goods

(Registration and Protection) Act, 1999 (Blakeney *et al.,* 2020). GI status gives them a unique status among other varieties and provides more market and export value.

Among the agriculture commodities, 12 GI tags are recorded for rice in India, six of which are cultivated in the state of Kerala. These include Palakkadan Matta, Kaipad rice, Navara rice, Pokkali rice, Wayanadan Gandhakasala and Wayanadan Jeerakasala. Among these varieties, Navara is the most popular and has the highest market income, which could be due to its medicinal properties (Radhika *et al.,* 2018). Majority of scientific literature available on traditional rice in Kerala has focused on Navara. Palakkadan Matta find reference in Tamil classic 'Thirukkural' and was consumed by the royal families of Chola and Chera dynasty. Under the GI registry, Palakkadan Matta include ten different varieties. However, only four varieties are most commonly cultivated in Palakkad, which include Thavalakannan, Chenkayama, Chettadi and Chitteni. They have bold grain with red pericarp and is known for their unique earthy flavour which is supposed to be due to the heavy soil they are grown in, which is rich in clay and silt. These varieties are mostly consumed in parboiled form and used in the preparation of a wide range of rice based dishes and snacks.

Wayanadan Gandhakasala and Wayanadan Jeerakasala are non-pigmented fine aromatic rice cultivated organically in high altitudes of Wayanad by the Kurichiya tribe, an agricultural based community in Kerala. Owing to their distinct aroma when cooked, they are known as 'Kerala Basmathi' and fetch higher price in the market than other varieties (Krishnankutty *et al.,* 2021; Soam, 2005). Agronomical features of the varieties taken for this study are listed in **Table 1.**

Table 1: Agronomical features of rice varieties

Sl. No.	Popular name	Crop maturation (days)	Agronomical features
Palakkadan Matta Varieties			
1	Chenkazhama	110- 120	Tall *indica* variety.
2	Chettadi	130 -160	Photosensitive and drought resistant.
3	Chitteni	130	Highly tolerant to Bacterial leaf blight and pests like Brown plant hopper, Gall fly and green leaf hopper.
4	Thavalakannan	130	Less prone to lodging, good straw yield and tolerant to Gall fly and Foot rot. Highly adaptive to adverse soil conditions and shows strong resistance to green leaf hopper.
Aromatic varieties			
5	Wayanadan Gandhakasala	160 - 180	Aromatic, highly tolerant to pest and disease, High priced, suitable as fodder (Blakeney 2020)
6	Wayanadan Jeerakasala	160 - 180	Aromatic, high priced

Even though these varieties are known for their unique properties, very few scientific studies are available on the nutritional and cooking properties of these GI rice varieties. The selected varieties are not explored for their phytochemical composition as most studies have focused on their agro morphological characteristics. The objective of this study is to evaluate and classify selected GI tagged rice varieties for their nutritional, phytochemical and cooking characteristics.

Materials and Methods

Rice samples

Six rice samples including four most commonly cultivated Palakkadan Matta rice varieties namely Chenkazhama, Chettadi, Chitteni and Thavalakannan and two aromatic varieties namely Wayanadan Gandhakasala and Wayanadan Jeerakasala were collected from Regional Agricultural Research Stations (Mele Pattambi and Ambalavayal), Kerala and Abhayam, Pattambi, Kerala. Varieties Wayanadan Jeerakasala and Wayanadan Gandhakasala were non-pigmented aromatic rice and all others were red pigmented varieties.

The dried paddy samples were kept at 4 °C in airtight plastic containers until used. The samples were dehulled manually and homogenised into fine rice flour (60 mesh sieve) freshly before analysis. For the determination of glycemic index and starch fractions, 50 mg rice flour was homogenised in 5 ml distilled water and cooked for 30 minutes.

Chemicals and Reagents

Glucose oxidase / peroxidase reagent, amyloglucosidase solution (from *Aspergillus niger)*, heat stable α-amylase (from *Bacillus licheniformis)*, standards of gallic acid and (+) - catechin were purchased from Sigma-Aldrich, USA. HPLC grade chemicals namely methanol, acetonitrile and pepsin from porcine stomach mucosa were purchased from HiMedia. All other chemicals used were of analytical grade.

Determination of Total Starch (TS) and its fractions

The TS content was determined following the method reported by Goñi *et al*., (1997)to calculate the glycemic index (GI). Briefly, 50 mg brown rice flour was added to 2M KOH (6 ml) and energetically shaken for 30 minutes at room temperature. To the mixture, added 0.4 M Sodium acetate buffer, pH-4.75 (3 ml) and amyloglucosidase (60 µl) and incubated for 45 minutes in a shaking water bath at 60 °C. Starch content was measured as glucose using glucose oxidase-peroxidase reagent and a factor of 0.9 was used for the conversion of glucose to starch.

Resistant starch (RS) content was measured following the enzymatic method described by Goñi *et al*., (1997)to calculate the glycemic index (GI. Briefly, to the brown rice flour (100 mg), added KCl-HCl buffer (10 ml), pH 1.5 and homogenized in 50 ml centrifuge tube. For the removal of proteins, the mixture was treated with freshly prepared pepsin solution containing 0.02 g pepsin in 0.2 ml KCl-HCl buffer at 40 °C for 60 minutes. Then added 9 ml Tris-Maleate buffer, pH 6.9 and the suspension was hydrolysed with solution containing α-amylase (40 mg) at 37 °C for 16 hours. The suspension was centrifuged and the residue was then incubated with 80 µl amyloglucosidase solution for 45 minutes at 60 °C with constant shaking. The hydrolysate was centrifuged and the supernatant was collected for the estimation of RS content, as described earlier. For the estimation of digestible starch (DS), the difference between TS and RS was calculated.

In vitro starch hydrolysis and determination of glycemic index

The rate of rice starch hydrolysis was studied following the *in vitro* method suggested by Goñi *et al*., (1997) to calculate the glycemic index (GI. Briefly, 50 mg brown rice flour was added to 10 ml of KCl- HCl buffer and pH adjusted to 1.5. To this suspension, 0.2 ml of freshly prepared Pepsin solution was added and kept for 1 hour at 40 °C in a shaking water bath. The volume was completed to 25 ml with Tris maleate buffer. The solution was then hydrolysed with α- amylase solution (2.6 units in Tris-Maleate buffer) and kept in a shaking water bath at 37 °C. One ml hydrolysate solution was drawn every 30 minutes for a total of 180 minutes.

The aliquots were then heated in boiling water bath followed by rigorous shaking in a vortex mixer to inactivate their enzyme activity. To these aliquots,

added 0.4 M sodium acetate buffer, pH 4.75 (3 ml) and amyloglucosidase (60 µl), mixed and incubated at 60 °C for 45 minutes in shaking water bath. The glucose content was determined by glucose oxidase/ peroxidase reagent and the amount of starch was calculated. The results were then expressed as the per centage of TS hydrolysed at a given time interval.

The data obtained was used for plotting starch hydrolysis curve and the area under curve (AUC) was calculated. A first order non-linear reaction equation followed for the starch hydrolysis as provide by Goñi *et al*., (1997)to calculate the glycemic index (GIto calculate the glycemic index (GI: $C=C_{\infty}(1-e^{-kt})$,

where C - Concentration at time t, C∞- Equilibrium concentration, k - kinetic constant and t - chosen time.

Parameters C∞, k and AUC were determined from the experimental data using software SYSTAT (Sigma plot 14), MS office version. The hydrolysis index (HI) was expressed as per centage and calculated using the formula:

Glycemic Index was determined by the following equation:

Glycemic Index = 39.71 + 0.549 HI

Determination of cooking characteristics

Cooking characteristics of rice varieties were determined following the method suggested by Singh *et al*., (2005).

Minimum cooking time

Brown rice kernels (1g) were added to 10 ml distilled water and heated in a boiling water bath. The rice grains were removed every 2 minutes during cooking and pressed between two glass slides. The time (min) at which no white residue was left in the glass slides was taken as the minimum cooking time.

Water uptake ratio

After cooking rice kernels for their minimum cooking time as described above, the water was drained and the cooked samples were weighed after pressing in filter paper. The difference in weight of cooked sample was calculated as the water uptake ratio.

Elongation ratio

Elongation ratio was obtained by dividing the average length of cooked rice kernels by the average length of uncooked rice kernels (n=10).

Cooked length-breadth ratio

The average length of cooked rice kernels was divided by the average breadth of cooked kernels and termed as l/b ratio (n=10).

Extraction of free form phenolic compounds

Free form phenolic compounds were extracted from brown rice flour using the method of Gong *et al.,* (2017). Briefly, 500 mg of whole grain flour was blended with 80% chilled Ethanol (5 ml) for 15 minutes. After centrifuging the mixture (5000 rpm) for 10 minutes, the supernatant was pooled and the residue was extracted twice. The pooled extract was then subjected to evaporation at 45 ºC until the extract was reduced to 3 ml. Reconstituted the extract with distilled water to 6 ml and kept at -40 ºC until use.

Extraction of bound form phenolic compounds

The residue obtained after extracting free form phenolics, was treated with 2M NaOH solution (10 ml) at room temperature for 1 hour under nitrogen gas. The mixture was then acidified with 2 M HCl solution (10 ml) until pH 2 was obtained. The acidic solution was then extracted with hexane (10 ml). The final solution was then extracted with Ethyl acetate (10 ml) thrice. The extracts were pooled, dried and reconstituted in 5 ml of distilled water. The extract was then stored at -40 ºC until use (Gong *et al.,* 2017).

Determination of phenolic content

The total phenolics content was estimated by the colorimetric method reported by Sompong et al., (2011). Briefly, extract solution (120 µl) was treated

with freshly prepared Folin-Ciocalteu reagent diluted 10-folds (600 µl) and incubated for 2 minutes. To the mixture, added 960 µl NA_2CO_3 solution (75 g/l) and kept at 50ºC for another 2 minutes. The blue colour developed was then read at 760 nm. Gallic acid was taken as the standard and the results were expressed as mg gallic acid equivalent (GAE) per 100 g brown rice.

Determination of flavonoid content

The total flavonoid content was determined following the modified colorimetric method of Dewanto *et al*., (2002). The extract solution (300 µl) was initially diluted with 1.5 ml of distilled water in a test tube. Then added 5% $NaNO_2$ solution (90 µl) and kept at room temperature for 6 minutes followed by the addition of 10% $AlCl_3.6H_2O$ solution (180 µl) and incubated for 5 minutes. To the mixture, finally added 1 M NaOH (600 µl) and the volume was made up to 3 ml with distilled water. The colour developed was measured at a wavelength of 510 nm and compared with the standard + (-) Catechin solution. Total flavonoid contents were expressed in terms of mg + (-) catechin equivalents (CE) per 100 g of brown rice.

Statistical analysis

All the analytical assays were performed thrice (n-3) and reported as mean ± standard deviation on fresh weight basis. The results were analysed by Analysis of Variance (ANOVA) SPSS version 20 using Duncan's Multiple Range Test (DMRT) to compare means at $p < 0.05$ significance level. Pearson's correlation analysis was performed for calculating the relationship between different variables.

Results and Discussions

TS and its fractions

TS, RS and DS contents of rice samples are shown in **Table 2.** The amount of TS in rice samples ranged from 72.99% in Wayanadan Jeerakasala to 83.68% in Chenkazhama. All the varieties were subjected to same cooking method for TS determination. Higher TS content in rice could result from leaching of starchy fragments during cooking because of different degree of damage to the grain structure (Ahmed and Urooj, 2003). RS and DS content were in the range of 0.56 - 0.69% and 72.35- 76.01% respectively. Wayanadan Jeerakasala had significantly lower TS and DS content among all varieties, which is a desired parameter for managing blood glucose response. The values obtained were comparable to other studies by Deepa *et al*., (2010) and Hu *et al*., (2004).

Table 2: Total starch, resistant starch and digestible starch content of rice varieties (%)

Sample	Total Starch	Resistant Starch	Digestible Starch
Chenkazhama	83.68 ±2.06^{a}	0.64 ±0.01^{b}	83.03 ±2.07^{a}
Chettadi	77.75 ±2.33^{b}	0.69 ±0.02^{a}	77.10 ±2.33^{b}
Chitteni	76.58 ±1.83^{bc}	0.56 ±0.03^{d}	76.01 ±1.82^{c}
Thavalakannan	73.86 ±1.96^{c}	0.63 ± 0.02^{c}	73.22 ±1.96^{d}
Wayanadan Gandhakasala	74.60 ±0.36^{bc}	0.64 ±0.0^{bc}	73.96 ±0.36^{d}
Wayanadan Jeerakasala	72.99 ±2.5^{c}	0.63 ±0.03^{c}	72.35 ±2.53^{e}
Mean	76.57	0.63	75.94
CV	2.76	0.38	2.77
CD (0.05)	3.85	0.00	3.08

Values with the same letters in a column are not significantly different ($p < 0.05$). TS, total starch; RS, resistant starch; DS, digestible starch

Rice mainly comprises Type 1 RS, which is the physically inaccessible starch normally found in whole grains or Type 5, which is formed by amylose-lipid complexes (Sajilata *et al.,* 2006). Amylose content is predicted as a major factor affecting the RS content. Retrogradation of amylose was found to be the

primary mechanism for the formation of RS (Deepa *et al.,* 2010; Berry, 1986) . Lehmann and Robin, (2007) and Sajilata *et al.,* (2006) reported a positive correlation between RS and amylose content in rice. In contrast, some of the intermediate amylose varieties found in the study had higher RS than high amylose varieties (reported elsewhere) (Pillai *et al.,* 2020). In a similar study by Hu *et al.,* (2004) rice cultivars with similar amylose content had different RS content due to difference in planting seasons and varietal factors. His study also characterized highamylose varieties with high RS content to be associated with low RVA (Rapid visco analyser) parameters like peak viscosity, hot plate viscosity and cool paste viscosity.

Cooking characteristics

Significant differences were observed for cooking characteristics of rice varieties as shown in **Table 3**. Minimum cooking time ranged between 23.83 to 35.50 min. Wayanadan Gandhakasala and Wayanadan Jeerakasala had significantly lower cooking time than Matta varieties. Highest cooking time was observed in Thavalakannan, which also had significantly higher protein content (11.4 g/100 g) among the varieties analysed (Pillai *et al.,* 2020). This was similar to the observation made by Juliano *et al.,* (1965) that high protein rice varieties require longer cooking time. However, no positive correlation was found between protein content and cooking time of the rice varieties. Protein content of Chenkazhama, Chettadi, Chitteni, Gandhakasala and Jeerakasala were 6.75, 8.01, 7.77, 10.67 and 8.16 g/100g respectively (reported elsewhere) (Pillai *et al.*, 2020). Longer cooking times can lead to low acceptability of brown rice among consumers (Adebamowo *et al.,* 2017).

Table 3: Cooking properties of rice varieties

Rice varieties	Minimum cooking time (min)	Water uptake ratio	Elongation ratio	Cooked l/b ratio
Chenkazhama	26.46±0.41^{d}	1.76±0.01^{d}	1.15±0.00^{c}	1.82±0.02^{f}
Chettadi	33.5±0.50^{b}	2.03±0.00^{b}	1.10±0.01^{d}	2.44±0.04^{e}
Chitteni	32.4±0.36^{c}	2.01±0.02^{c}	1.18±0.02^{b}	3.04±0.03^{c}
Thavalakannan	35.5±0.50^{a}	2.15±0.01^{a}	1.16±0.03^{c}	3.35±0.04^{a}
Wayanadan Gandhakasala	24.4±0.36^{e}	2.16±0.01^{a}	1.29 ±0.01^{a}	2.84±0.04^{d}
Wayanadan Jeerakasala	23.83±0.28^{e}	2.01±0.01^{c}	1.11±0.02^{d}	3.18±0.02^{b}
Mean	29.35	2.02	1.17	2.78
CV	1.21	0.51	1.07	1.10
CD (0.05)	0.65	0.02	0.02	0.05

Values with the same letters in a column are not significantly different ($p < 0.05$)

Water uptake ratio is a measure of volume expansion of rice during cooking and was significantly higher in Gandhakasala (2.16) and Thavalakannan (2.15). ER refers to the length wise elongation of rice after cooking and is the most desirable cooking traits especially in varieties like Basmathi. Significantly higher ER was observed in Wayanadan Gandhakasala (1.29) followed by Chitteni and Thavalakannan whereas Wayanadan Jeerakasala had significantly lower ER value. Wayanadan Gandhakasala had better price and demand than Wayanadan Jeerakasala in the market (Radhika *et al.*, 2018), which could

also be attributed to its better cooking qualities. Results obtained for ER and water uptake ratio were comparable to the observations made by Rajesh *et al*, (2018) and Nirmala Devi *et al.,* (2015). Cooked l/b ratio ranged from 1.82 to 3.35 and was higher for Thavalakannan which could be due to its higher water uptake ratio.

In vitro starch digestion

More than 50% of the TS was digested within the first 30 minutes of hydrolysis except for Wayanadan Gandhakasala and Chettadi. When the rate of starch hydrolysis was plotted against time, the curve obtained reached a plateau after 60 minutes of digestion as shown in **Figure 1.** According to Goñi *et al.,* (1997), rate of starch hydrolysis after 90 minutes (H 90 Experimental) was found to be the best hydrolysis value for determining the in vivo glycemic response. H 90 values were also calculated theoretically (H 90 Theory) as shown in **Table 4**. There was good agreement between H 90 Exp and H 90 Theory values. Rate of starch hydrolysis after 90 min was highest for Wayanadan Jeerakasala (62.56%) followed by Chitteni (59.74%) which suggests that they get digested more rapidly than other varieties and could elicit a high glycemic response. Significantly lower H 90 value was observed in Chettadi (51.41%) and Wayanadan Gandhakasala (52.16%). From 120 to 150 min, rate of starch hydrolysis was slow.

Table 4: Rate of starch hydrolysis (%) at 90 min

Sl. No.	Rice variety	H_{90} Exp*	H_{90} Theory**
1.	Chenkazhama	56.35±0.23^{c}	56.78 ±0.13^{d}
2.	Chettadi	51.41 ±0.22^{d}	53.02 ±0.34^{e}
3.	Chitteni	59.74 ±0.71^{b}	60.20 ±0.61^{b}
4.	Thavalakannan	56.46 ±3.56^{c}	59.09 ±1.68^{c}
5.	Gandhakasala	52.16 ±1.07^{d}	53.14 ±0.85^{e}
6.	Jeerakasala	62.56 ±0.43^{a}	64.91 ±0.32^{a}

*based on experimental results; **based on the equation, C = C∞ (1-e-kt)

Glycemic index

There were significant variations in C ∞ values of rice varieties which refers to the amount of starch hydrolysed after a prolonged time (180 minutes) as depicted in **Table 5**. C ∞ values of all varieties suggests that starch hydrolysis terminated before 180 min and significantly lower values were observed for Chettadi and Wayanadan Gandhakasala. The k value ranged between 0.05-0.10. Itdetermines the rate of starch digestion and absorption in the body. The C ∞ and k values are good predictors of glycemic index (Edwards *et al.,* 2019).

Table 5: Starch kinetics parameter of rice varieties

Rice variety	k	C_{∞}	AUC*	HI	GI
Chenkazhama	0.10	56.79±0.13^{c}	9293 ±17^{c}	55.93 ±0.10^{c}	70.41±0.06^{c}
Chettadi	0.06	53.16±0.44^{d}	8505 ±٣٦^{d}	51.19 ±0.21^{d}	67.81±0.12^{d}
Chitteni	0.07	60.32±0.49^{b}	9717±173^{b}	58.48±1.04^{b}	71.81±0.57^{b}
Thavalakannan	0.05	59.80±1.68^{b}	9365±230^{c}	56.36±1.39^{c}	70.65±0.76^{c}
Wayanadan Gandhakasala	0.07	53.30±0.93^{d}	8525±116^{d}	51.30±0.70^{d}	67.87±0.38^{d}
Wayanadan Jeerakasala	0.06	65.22±0.32^{a}	10373±44^{a}	62.43±0.27^{a}	73.98±0.15^{a}

Values with the same letters in a column are not significantly different ($p < 0.05$)

AUC of glucose (reference food) was calculated as 16,616

The HI values ranged between 51.19- 62.43%. HI refers to the proportion of starch that is theoretically digestible and is a predictor of glycemic index. Glycemic Index values ranged from 67.81 to 73.98. Brand-Miller *et al.,* (2009) classified food based on their glycemic index values as low (55 or less), intermediate (56 to 69) or high (70 or more). Accordingly, Wayanadan Jeerakasala, Chitteni, Thavalakannan and Chenkazhama had high glycemic index whereas Chettadi and Wayanadan Gandhakasala were varieties with intermediate glycemic index.

Some of the physico-chemical factors that can affect the starch digestibility in rice include amylose and amylopectin ratio, size of starch granules, presence of fiber, natural amylase inhibitors, starch- protein interactions and formation of lipid-amylose complexes (Panlasigui *et al.,* 1991 and Sagum and Arcot, 2000).

Total phenolic content

Table 6 provides the total phenolic content of brown rice flour along with its fractions namely free form and bound form phenolics. The free form phenolic content ranged from 34.45 mg GAE/100 g in Wayanadan Gandhakasala to 132.82 mg GAE/100 g in Chettadi. A range of 49.76 to 103.77 mg GAE/100g was found for bound form phenolics. Palakkadan Matta varieties had significantly higher free phenolic content than non-pigmented varieties. However, the highest amount of bound phenolics was recorded in Wayanadan Jeerakasala followed by Chitteni, Wayanadan Gandhakasala, Chenkazhama, Chettadi and Thavalakannan.

Table 6: Phenolics and flavonoid content of brown rice flour

Variety	Phenolics content (mg GAE / 100 g)			Flavonoid content (mg CE/ 100 g)		
	Free form	Bound form	Total	Free form	Bound form	Total
Chenkazhama	109.98±0.71^{c}	74.30±0.87^{c}	184.29±0.66^{c}	272.50±4.44^{b}	9.74±0.64^{d}	282.24±4.90^{b}
Chettadi	132.82±4.07^{a}	66.36±2.47^{d}	199.19±5.38^{b}	388.50±9.5^{a}	3.37±0.21^{f}	391.87±9.73^{a}
Chitteni	116.77±4.30^{b}	94.43±0.58^{b}	211.20±4.88^{a}	264.66±8.5^{b}	14.37±0.37^{a}	279.04±8.81^{b}
Thavalakannan	57.14±2.64^{d}	49.76±1.26^{e}	106.90±2.95^{e}	101.00±1.5^{c}	6.49±0.12^{e}	107.49±1.43^{c}
Wayanadan Gandhakasala	34.45±1.28^{e}	72.89±0.47^{c}	107.34±1.23^{e}	81.33±3.01^{d}	11.49±0.12^{c}	92.83±2.94^{d}
Wayanadan Jeerakasala	36.94±1.03^{e}	103.77±0.95^{a}	140.71±0.30^{d}	85.66±2.51^{d}	13.33±0.06^{b}	98.99±2.58^{cd}
Mean	81.35	76.91	158.27	198.94	9.80	208.74
CD (0.05)	5.41	2.18	6.31	11.20	0.61	11.68
CV	3.66	1.56	2.19	3.09	3.45	3.07

Values with the same letters in a column are not significantly different ($p < 0.05$).

The free phenolic content of the Palakkadan Matta varieties was greater than their respective bound form phenolics. This was consistent with the observation made by Sumczynski *et al.,* (2016) for red and black rice varieties. Non-pigmented rice varieties on the other hand, had higher content of bound form phenolics than their free form phenolic content, as also observed by Goufo and Trindade (2014). Therefore, pigmented and non-pigmented rice varieties can be good sources of free and bound form phenolics respectively and their distribution in rice kernel might be related to their bran colour.

Free and bound form phenolics perform different physiological functions in the body. Free form phenolics are readily absorbed in the small intestine and exhibit inhibitory action against LDL cholesterol oxidation whereas bound form phenolics are released by enzymatic or microbial fermentation in the colon, have anti-inflammatory properties and provide protection against colon cancer (Chandrasekara and Shahidi, 2011; Shao and Bao, 2015).

Total phenolic content ranged between 106.90 mg GAE/100g in Thavalakannan to 211.20 mg GAE/100g in Chitteni. The values obtained falls within the range of 79.18 to 691.37 mg GAE/100g reported for red and black rice varieties by Sompong *et al.,* (2011). Three out of four Palakkadan Matta varieties namely Chettadi, Chitteni and Chenkazhzma had higher total phenolic content than non-pigmented varieties. However, another red rice variety Thavalakannan had significantly less total phenolic content than non-pigmented variety Wayanadan Jeerakasala. This could be explained by the observation made by Sumczynski *et al.,* (2016) that total phenol content is more of a cultivar specific property rather than a colour dependent trait. Their study further suggested that phenolic compounds are secondary metabolites, significantly affected by stress conditions like wounding, extreme temperatures as well as environmental factors like cultivation techniques, altitude and use of fertilizers.

Total flavonoid content

Flavanoids are phenolic compounds with wide range of biological activities. They are potent antioxidants, antimicrobial and anti-inflammatory compounds. They are primarily known for their antioxidant or radical scavenging activities (Pietta, 2000). Free form flavonoid content of rice varieties exhibited significant variations with high CD value of 11.20 (p <0.05) as shown in **Table 6**. The range obtained was 81.33 in Wayanadan Gandhakasala to 388.50 mg CE/100g in Chettadi with a mean value of 198.94 mg CE/100g. Free form flavonoids content was significantly higher in Palakkadan Matta varieties than non-pigmented aromatic varieties, as also observed for free form phenolic content.

Bound form flavonoids ranged from 3.37mg CE/100g (Chettadi) to 14.37 mg CE/100g (Chitteni) and constituted a maximum of 5.15% towards total flavonoid content. This suggests that the flavonoids found in free form are the major contributor towards total flavonoid content (> 95%). This was in line with the observation made by Sumczynski *et al.,* (2016) for red and black rice varieties.

Total flavonoid content was significantly higher in Palakkadan Matta varieties (Chettadi> Chenkazhama > Chitteni > Thavalakannan) than Wayanadan Jeerakasala and Wayanadan Gandhakasala. The width of variation between the lowest (92.83) and highest value (391.87) of total flavonoid content was high (299.04 mg CE/100g). High CD value was observed for total flavonoid content, suggesting high varietal variation among rice varieties. The results obtained for total flavonoid content and total phenolic content in the present study was comparable to the data reported by Goufo and Trindade (2014). Total flavonoid content and total phenolic content of rice (r- 0.76, p-0.001) were found to be positively correlated, as also reported in a study done by Zhang *et al.,* (2010) (**Table 7**). Their study also found significant correlation between total phenolic content and total flavonoid content of black rice bran with its total antioxidant activity. Therefore, rice varieties with elevated levels of total phenolic content and total flavonoid content can be used for their antioxidant properties in developing rice based functional foods.

Table 7: Correlation among different characteristics studied in rice varieties

	Total phenolic content	Total flavonoid content	Total starch	Resistant starch	Glycemic index
Total phenolic content	1				
Total flavonoid content	0.760**	1			
Total starch	0.301	0.484	1		
Resistant starch	0.126	0.348	-0.042	1	
Glycemic index	0.210	-0.363	-0.311	-0.329	1

** Correlation is significant at 0.01 probability level

Conclusion

GI tagged rice varieties of Kerala were evaluated for various grain quality parameters and significant differences (p & lt; 0.05) were observed for every parameter studied. All varieties had high TS content (& gt; 70%) however, their rate of starch digestibility was different. For all varieties except Wayanadan Gandhakasala and Chetttadi, more than 50% of the TS was digested within 30 min and the hydrolysis reaction terminated before 180 min. Wayanadan Gandhakasala was also noted for significantly lower cooking time but higher water uptake and elongation ratio. Palakkadan Matta varieties had comparatively higher free phenolic, free flavonoid and total flavonoid content than the non-pigmented varieties. Pearson's correlation analysis revealed significant positive correlation between total phenolic and total flavonoid content. The width of variation for lowest and highest flavonoid content was high amongst varieties suggesting the necessity of screening rice varieties for their phytochemical composition. The study suggests that GI tagged varieties, which are known for their eating and cooking qualities, can also prove to be a potent ingredient for the development of functional food.

Acknowledgements

Authors acknowledge the Associate Director of Research, Kerala Agricultural University for providing rice samples and the Director, Central Sophisticated Instrumentation Facility, University of Calicut for laboratory support.

References

Adebamowo SN, Eseyin O, Yilme S, Adeyemi D, Willett WC, Hu FB, Spiegelman D and Adebamowo CA. 2017. A Mixed-Methods Study on Acceptability, Tolerability and Substitution of Brown Rice for White Rice to Lower Blood Glucose Levels among Nigerian Adults. *Frontiers in Nutrition*, 4(33): 1-9.

Ahmed F and Urooj A. 2003. *In vitro* starch digestibility and nutritionally important starch fractions in processed roots and tubers. *Starch/ Stärke*, 55(2): 94-99.

Bhattacharya KR. 2009. Physicochemical basis of eating quality of rice. *Cereal Foods World*, 54(1): 18-28.

Berry CS. 1986. Resistant starch: Formation and measurement of starch that survives exhaustive digestion with amylolytic enzymes during the determination of dietary fibre. *Journal of Cereal Science*, 4(4): 301-314.

Blakeney M, Krishnankutty J, Raju RK and Siddique KHM. 2020. Agricultural Innovation and the Protection of Traditional Rice Varieties: Kerala a Case Study. *Frontiers in Sustainable Food Systems*, 3(1): 1-11.

Brand-Miller JC, Stockmann K, Atkinson F, Petocz P and Denyer G. 2009. Glycemic index, postprandial glycemia and the shape of the curve in healthy subjects: Analysis of a database of more than 1000 foods. *American Journal of Clinical Nutrition*, 89(1): 97-105.

Chandrasekara A. and Shahidi F. 2011. Bioactivities and antiradical properties of millet grains and hulls. *Journal of Agricultural and Food Chemistry*, 59(1): 9563-9571.

Chen Y, Wang M and Ouwerkerk PBF. 2012. Molecular and environmental factors determining grain quality in rice. *Food and Energy Security*, 1(2): 111-132.

Custodio MC, Cuevas RP, Ynion J, Laborte AG, Velasco ML and Demont M. 2019. Rice quality: How is it defined by consumers, industry, food scientists and geneticists? *Trends in Food Science and Technology*, 92: 122-137.

Deepa G, Singh V and Naidu KA. 2010. A comparative study on starch digestibility, glycemic index and resistant starch of pigmented ("Njavara" and 'Jyothi') and a non-pigmented ('IR 64') rice varieties. *Journal of Food Science and Technology*, 47(6): 644-649.

Dewanto V, Xianzhong W, Adom KK and Liu RH. 2002. Thermal Processing Enhances the Nutritional Value of Tomatoes by Increasing Total Antioxidant Activity. *Journal of Agricultural and Food Chemistry*, 50(10): 3010-3014.

Edwards CH, Cochetel N, Setterfield L, Perez-Moral N and Warren FJ. 2019. A single-enzyme system for starch digestibility screening and its relevance to understanding and predicting the glycaemic index of food products. *Food and Function*, 10(8): 4751-4760.

Gong ES, Luo SJ, Li T, Liu CM, Zhang GW, Chen J, Zeng Z C and Liu RH. 2017. Phytochemical profiles and antioxidant activity of brown rice varieties. *Food Chemistry*, 227: 432-443.

Goñi I, Garcia-Alonso A and Saura-Calixto F. 1997. A starch hydrolysis procedure to estimate glycemic index. *Nutrition Research*, 17(3): 427-437.

Goufo P and Trindade H. 2014. Rice antioxidants: phenolic acids, flavonoids, anthocyanins, proanthocyanidins, tocopherols, tocotrienols, γ -oryzanol and phytic acid. *Food Science and Nutrition*, 2(2): 75-104.

Hu P, Zhao H, Duan Z, Linlin Z and Wu D. 2004. Starch digestibility and the estimated glycemic score of different types of rice differing in amylose contents. *Journal of Cereal Science*, 40(3): 231-237.

Juliano BO, Oñate LU and del Mundo AM. 1965. Relation of starch composition, protein content and gelatinization temperature to cooking and eating qualities of milled rice. *Food Technology*, 19(6): 116-121.

Krishnamrutha TS, Sai Prasad SV, Sameer Kumar CV and Ramesh T. 2023. Study on Genetic Variability and Correlation Coefficient for Grain Quality Parameters in South Indian Rice (*Oryza sativa* L.) Varieties. *Journal of Rice Research*, 16(2): 66-72.

Krishnankutty J, Blakeney M, Raju RK and Siddique KHM. 2021. Sustainability of traditional rice cultivation in Kerala, India-a socio-economic analysis. *Sustainability (Switzerland)*, 13(2): 1-16.

Lehmann U and Robin F. 2007. Slowly digestible starch - its structure and health implications: a review. *Trends in Food Science and Technology*, 18(7): 346-355.

Nirmala Devi G, Ravindra Babu V, Padmavathi G and Sunitha T. 2015. Genetic Diversity in Grain Quality Traits of Rice Genotypes. *Journal of Rice Research*, 8(1): 6-14.

Panlasigui LN, Thompson LU, Juliano BO, Perez CM, Yiu SH and Greenberg GR. 1991. Rice varieties with similar amylose content differ in starch digestibility and glycemic response in humans. *American Journal of Clinical Nutrition*, 54(5): 871-877.

Pietta PG. 2000. Flavonoids as Antioxidants. *Journal of Natural Products,* 63(7), 1035-1042.

Pillai C, Faseela K V and Thampi H. 2020. Nutritional composition of selected traditional rice varieties of Kerala. *Journal of Tropical Agriculture*, 58(1), 33-43.

Radhika AM, Jesy Thomas K and Anil Kuruvila R. 2018. Assessing the impact of Geographical Indications on well-being of rice farmers in Kerala. *International Journal of Intellectual Property Rights*, 9(2): 1-11.

Rajesh T, Radhakrishnan V, Pressana Kumari K, Francies R, Sreenivasan E, Ibrahim K and Latha A. 2018. Grain quality characteristics of two-line rice hybrids in Kerala. *Journal of Rice Research*, 11(1): 19-25.

Sagum R and Arcot J. 2000. Effect of domestic processing methods on the starch, non-starch polysaccharides and *in vitro* starch and protein digestibility of three varieties of rice with varying levels of amylose. *Food Chemistry*, 70(1): 107-111.

Sajilata MG, Singhal RS and Kulkarni PR. 2006. Resistant Starch - A Review. *Comprehensive Reviews in Food Science and Food Safety*, 5(1): 1-17.

Shao Y and Bao J. 2015. Polyphenols in whole rice grain: Genetic diversity and health benefits. *Food Chemistry*, 180, 86-97.

Singh N, Kaur L, Singh Sodhi N and Singh SK. 2005. Physicochemical, cooking and textural properties of milled rice from different Indian rice cultivars. *Food Chemistry*, 89(2): 253-259.

Soam SK. 2005. Analysis of Prospective Geographical Indications of India. *The Journal of World Intellectual Property*, 8(5): 679-704.

Sompong R, Siebenhandl-Ehn S, Linsberger-Martin G and Berghofer E. 2011. Physicochemical and antioxidative properties of red and black rice varieties from Thailand, China and Sri Lanka. *Food Chemistry*, 124(1): 132-140.

Sumczynski D, Kotásková E, Družbíková H and Mlček J. 2016. Determination of contents and antioxidant activity of free and bound phenolics compounds and *in vitro* digestibility of commercial black and red rice (*Oryza sativa* L.) varieties. *Food Chemistry*, 211: 339-346.

Zhang MW, Zhang RF, Zhang FX and Liu RH. 2010. Phenolic profiles and antioxidant activity of black rice bran of different commercially available varieties. *Journal of Agricultural and Food Chemistry*, 58(13): 7580-7587.

RESEARCH ARTICLE https://doi.org/10.58297/NRPW8939

Impact of High Temperature Stress on Morpho-Physiological Components and Yield Traits in Rice

Veronica N*, Venkata Ramana Rao P, Suneetha Y and Vasantha Ch

Regional Agricultural Research Station, Maruteru, ANGRAU - 534 122, India

*Corresponding author Email: n.veronica@angrau.ac.in

Received: 11th September, 2024; Accepted: 10th November, 2024

Abstract

Rice production is being threatened by increase in temperature around the globe. This is affecting the production and productivity of the crop. Changing climate scenario demands the need to identify thermotolerant genotypes to be used as donor in future breeding programmes. The effect of high temperature from panicle initiation to maturity was imposed in twenty-six rice genotypes. The difference in mean monthly maximum and minimum temperature was 3.5 ºC and 1.4 ºC, respectively between the polyhouse and ambient control. Results revealed a reduction in important physiological traits *viz*., membrane thermostability as well as chlorophyll content. Of the genotypes tested, MTU 1290, MTU 1153, MTU 1156, JB 683-1, N22 and IL 19211 maintained a higher stability of membranes and lesser reduction in chlorophyll content when exposed to high temperature stress. High temperature resulted in reduction of grain yield as well as yield attributes in rice genotypes. The above genotypes also had a higher spikelet fertility and lesser yield penalty when exposed to high temperature. The results indicated that these genotypes could be selected as thermotolerant and could serve as potential donors for future breeding programmes.

Key words: Chlorophyll content, Grain yield, Membrane thermostability, Rice, Spikelet fertility

Introduction

Rice production is the backbone of Indian agriculture. Majority of the population depends on this cereal crop to meet either their economic needs or for their caloric intake. Rice production is hindered by abiotic as well as biotic stresses. Keeping the climate change scenario in view, abiotic stresses play a major role in decreasing the crop production and productivity resulting in need of a sustainable crop development and resistance to abiotic stress (Randive *et al*., 2019). Of this, high temperature is one of the major constraints in rice production.

The fifth assessment report of the Inter-governmental Panel on Climate Change (IPCC, 2014) stated that the increase in global average temperature from 1880 to 2012 was 0.85 °C and by 2100 the projected increase of global mean surface temperature is 3-5 °C. This rise in temperature affects the growth and development resulting in morphological, physiological and biochemical changes in plants (Ashraf and Hafeez, 2004).

High temperature affects rice at every growth stage beginning from the inhibition of germination, seedling stage, tillering, reproductive and also at grain filling stage (Dubey *et al.,* 2018). Of all the stages, booting and flowering are the most sensitive stages to high temperature stress which leads to disruption of cell membranes as well as breaking of cell compartmentalization (Larkindale and Huang,

2004). High temperature at flowering stage results in inhibition of anther dehiscence and loss of stigma receptivity resulting in increase of spikelet sterility and lesser number of grains in the panicle. It also reduces the photosynthetic efficiency and ultimately resulting in yield reduction (Narayanan *et al*., 2016). High temperature results in damage to the thylakoid membrane as well as inhibition of key enzymes in photosynthetic pathway (Bita and Gerats, 2013). In chlorophyll, the thylakoid granum and membranes are degraded to increase in temperature resulting in reduced photosynthesis (Xu *et al*., 2021).

Imposition of high temperature at reproductive stage leads to reduction in panicle weight, number of spikelets and decreased grain weight (Wang *et al*., 2019). Lyman *et al*., (2013) reported that for every 1°C increase in average temperature during rice growing season the paddy yields reduced by 6.2%. It was also reported that in rice spikelet sterility was increased by 80% when high temperatures coincided the reproductive stage of the crop (Xu *et al*., 2020).

Rice production plays a prominent role in ensuring food security in the country and at this juncture there is a need to identify and breed for thermo tolerant rice varieties that can withstand the future temperature elevations. With this aim, twenty-six genotypes of rice were screened and impact of high temperature was studied in these genotypes to identify thermo tolerant genotypes.

Materials and Methods

Plant material*:* Twenty-six rice genotypes were screened and tested for high temperature tolerance by conducting a field experiment in *kharif* 2023 at Regional Agricultural Research Station, Maruteru. The experiment was laid out in split plot design with three replications. A spacing of 20 cm between rows and 15cm between hills was maintained. Recommended dose of Nitrogen (N), Phosphorus (P) and Potassium (K) was applied. Water management as well as crop protection measures were taken up time to time. All the other package of practices recommended for irrigated transplanted rice were followed.

Imposition of treatments*:* One set of genotype was grown in ambient conditions and another set was subjected to high temperature stress by enclosing a polythene sheet supported by bamboo poles and iron frame at panicle initiation (PI) stage. Temperature inside the polyhouse was monitored continuously using data logger up to physiological maturity.

Morpho-phenological traits: Observations were recorded for various morpho-phenological from the sampled plants tagged in each treatment and genotype. Plant height on tagged plants was recorded at reproductive stage by measuring the height from base of the plant to the tip of the terminal leaf or panicle on main stem and was expressed in centimetres (cm). The number of days taken for 50 per cent of plants to flower in each genotype and each treatment was noted as days to 50% flowering and was expressed in days. The number of days taken from sowing to physiological maturity was recorded and was expressed as days to maturity.

Membrane thermostability*:* Membrane thermostability (MTS) was measured following the procedure described by Haque *et al*., (2009). Mature leaves at reproductive stage were collected and first 2 to 4 cm was clipped off. The next 5 cm of leaf was washed three times with deionised water, cut into small pieces and placed in tubes with 10 ml de-ionized water. Two sets of each sample were prepared, one set designated as control was maintained at 28 °C while, other set was treated in water bath at 52 °C for one hour. Three replications were maintained for both the sets. After the treatment, control and treated tubes were kept at room temperature for 24 h. The initial conductance was measured using conductivity

meter. Thereafter, all the tubes were autoclaved at 121 °C at 15 lb for 20 mins and the next day final conductance was measured. This ensured complete electrolyte leakage from the plant tissue. The MTS was calculated using the following equation (Blum and Ebercon, 1981).

$$MTS\ (\%) = (1-(T1/T2)) / (1-(C1/C2) \times 100$$

Where, C1= initial conductance of control sample; C2=final conductance after autoclaving of control sample; T1= initial conductance of high temperature sample (after water bath treatment); T2= final conductance after autoclaving of high temperature sample.

Chlorophyll content*:* It was estimated in flag leaf at reproductive stage (1 week after anthesis). For this flag leaf was cut into small pieces and 25 mg of leaf sample was weighed. Chlorophyll was extracted by placing the sample in 80% acetone solution as per the methodology described by Porra *et al*., (1989). The absorbance was measured using a UV-VIS spectrophotometer. Chlorophyll a and chlorophyll b were measured at 663.2 nm and 646.8 nm, respectively and the chlorophyll content was expressed in mg g^{-1} fresh weight (mg g^{-1} FW). Chlorophyll a content, chlorophyll b content and the total chlorophyll content was calculated according to Lichtenthaler and Wellburn, (1983).

Yield and yield attributes*:* Yield and yield attributes such as grain number per panicle, 1000 grain weight, grain yield and total dry matter were recorded. At physiological maturity, panicles were threshed from a demarcated area of one square meter in all the genotypes under control and stress conditions. The number of panicles in one meter square area were threshed, cleaned and the weight of grains was recorded and expressed as grain yield in gm^{-2}. Five panicles were selected at random in every genotype and all the spikelets were separated from the panicle and filled grains were further separated and expressed as grain number per panicle. A sample of 1000 seeds at random were taken from every genotype under both the conditions and weighed in gm and expressed as test weight. After harvest the shoot was dried and shoot biomass was recorded. Spikelet fertility was calculated as the number of filled spikelets/ total number of spikelets x 100 and expressed in per cent. Harvest index was calculated as ratio of economic yield to biological yield and expressed in per cent.

Statistical analysis: Two-way analysis of variance (ANOVA) was performed using Statistix 8.1 package. Statistical significance of the parameter means was determined by performing Fisher's LSD test to test the statistical significance.

Results and Discussions

High temperature was imposed at panicle initiation and with the help of data loggers the temperature inside the polyhouse was monitored on daily basis. The mean maximum temperature in the ambient condition was 34.9 °C and the average mean minimum temperature was 25.6 °C. Whereas, under polyhouse the mean monthly maximum temperature was 31.5 °C and the average of monthly minimum temperature was 24.2 °C. The difference in mean monthly maximum and minimum temperature was 3.5 °C and 1.4 °C, respectively (**Figure 1**).

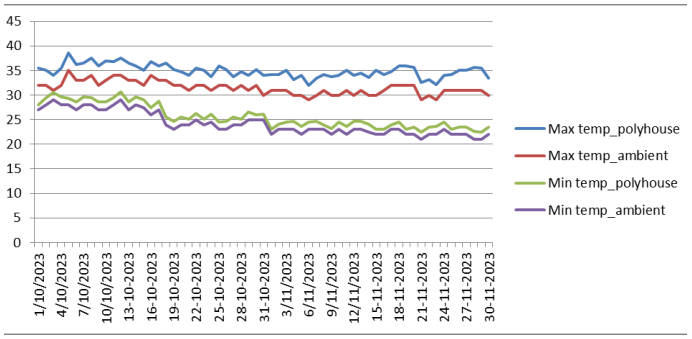


Figure 1: Temperature readings under polyhouse (heat stress) and ambient conditions (control)

Morpho-phenological traits:

The impact of high temperature was not significant on days to 50% flowering but the mean days to maturity

reduced by 3 days. At flowering, plant height reduced under high temperature among the genotypes. When compared to control maximum reduction was of 6 cm was noted in IL 19024 (**Table 1**). High temperature causes slower growth of the plants resulting in reduction of plant height and 50% flowering (Pooja and Ajit, 2022). It has been stated that high temperature influenced negatively the growth parameters of rice plants by Korres *et al*., (2017). In this study reduction of plant height as well as phonological traits was apparent.

Table 1: Impact of high temperature on morpho-phenological characters in rice genotypes

Entry	Days to 50% flowering			Days to maturity			Plant height (cm) at flowering			Chlorophyll content (mg /g FW)		
	C	Ht	M	C	Ht	M	C	Ht	M	C	Ht	M
IET 29859	90	88	89	122	115	119	105	104	104	2.26	1.92	2.09
IL 19019	93	91	92	124	119	122	100	99	99	2.43	2.13	2.28
IL 19020	94	93	93	122	119	121	106	102	104	2.38	1.80	2.09
IL 19021	96	94	95	126	123	124	107	105	106	3.24	2.52	2.88
IL 19022	91	90	91	121	118	120	103	102	103	2.52	2.07	2.30
IL 19024	93	91	92	123	119	121	112	106	109	3.08	2.72	2.90
IL 19185	93	92	93	123	120	122	106	105	106	2.45	2.04	2.25
IL 19198	88	86	87	117	114	116	88	84	86	3.26	2.83	3.05
IL 19202	91	90	91	120	118	119	88	87	87	2.31	1.97	2.14
IL 19211	97	96	97	127	123	125	109	109	109	3.34	3.13	3.24
IL 19247	92	91	92	121	119	120	107	102	105	2.45	2.08	2.26
IL 19396	91	90	91	122	118	120	117	114	116	3.04	2.60	2.82
JB 680-2	90	89	90	121	119	120	112	107	109	2.41	2.00	2.21
JB 683-1	91	90	91	121	118	120	107	105	106	2.65	2.42	2.53
JB 687-3	91	90	90	121	119	120	115	113	114	3.07	2.63	2.85
JB 689-1	96	94	95	124	121	123	112	111	111	2.39	2.00	2.20
JBC 159-11	91	90	90	121	119	120	110	108	109	2.35	1.97	2.16
Krishnahamsa	91	90	90	121	118	120	104	101	102	3.26	2.85	3.06
MTU 1153	94	93	94	124	122	123	110	106	108	3.00	2.70	2.85
MTU 1156	92	91	91	121	119	120	104	102	103	3.20	2.73	2.97
MTU 1273	94	91	93	123	121	122	113	109	111	3.26	2.50	2.88
MTU 1290	92	91	92	122	119	121	112	110	111	2.79	2.61	2.70
MTU 1293	92	91	92	122	119	121	106	103	105	3.01	2.46	2.74
N-22	97	96	96	126	123	125	115	111	113	2.81	2.37	2.59
NLR 3776	97	95	96	127	123	125	110	105	108	2.62	2.13	2.38
NLR 3778	95	94	94	126	123	124	122	118	120	2.59	2.16	2.37
Mean	**93**	**92**		**123**	**120**		**108**	**105**		**2.78**	**2.36**	
LSD (T)		NS			0.53			1.04			0.026	
LSD (V)		1.62			1.93			3.76			0.095	
LSD (TxV)		2.29			2.73			5.32			0.135	
CV (%)		1.54			1.39			3.1			3.26	

Physiological traits:

Membrane thermostability: Imposition of high temperature led to reduction in the cell membrane thermostability in all the genotypes. Among the genotypes, MTU 1290 (77.9%), JB 683-1 (75.4%), MTU 1156 (73.9%), Krishnahamsa (73.3%), MTU 1153 (72.9%) and N22 (72.4%) had higher thermostability under heat stress treatment. JBC 159-11 (25.3%), IL 19247 (27.8%) and JB 680-2 (29.4%) had lowest thermostability. Maximum reduction in thermostability when compared to control (more than 50%) was in JB 687-3, JB 680-2, IL 19247 and JBC 159-11. The reduction in thermostability was minimum (less than 12%) in MTU 1290, MTU 1153, MTU 1156, JB 683-1 and N22 (**Figure 2**). The cell membrane is one of the most sensitive structures which is affected by variations in temperature (Hu *et al*., 2018). In this study it was noted that when subjected to high temperature stress the cell membranes were disrupted leading to a higher electrolyte leakage. Prasertthai *et al*., (2022) treated 28 days old seedlings of rice at 42 °C for 7 days and noted an increase in electrolytic leakage however N22 showed the highest heat tolerance displaying the lowest increase in electrolyte leakage. In this study also MTU 1153, MTU 1156, JB 683-1, N22 and MTU 1290 recorded lesser reduction in electrolytic leakage that could confer tolerance to increase in temperature.

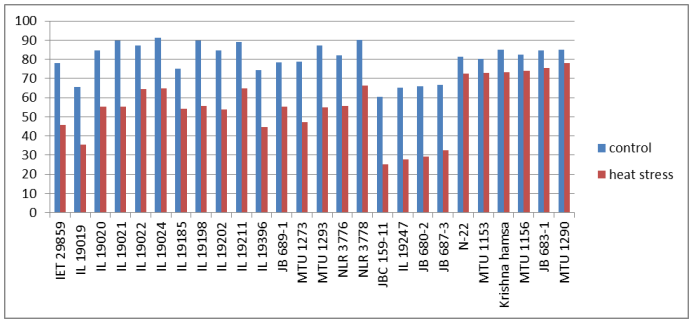


Figure 2: Impact of high temperature on Membrane thermo stability (%) in rice genotypes

***Chlorophyll content*:** The mean chlorophyll content reduced from 2.78 in control to 2.36 under heat stress. Highest chlorophyll content under high temperature stress was noted in IL 19211 (3.13 mg g^{-1} FW) followed by Krishnahamsa (2.85 mg g^{-1} FW), IL 19198 (2.83 mg g^{-1} FW) and MTU 1156 (2.73 mg g^{-1} FW). Lowest was in IL 19020 (1.8 mg g^{-1} FW) followed by IET 29859 (1.92 mg g^{-1} FW) and JBC 159-11 and IL 19202 (1.97 mg g^{-1} FW). The per cent reduction of chlorophyll content compared to control was less than 10% in MTU 1153, JB 683-1, MTU 1290 and IL 19211. Whereas more than 20% reduction was observed in IL 19021, MTU 1273 and IL 19020 (**Table 1**). Chloroplast is a vital organelle for photosynthesis and contains photosynthetic pigments. The integrity of the organelle as well as biosynthetic pathways for chlorophyll formation is impacted by temperature. In a study conducted by Sánchez-Reinoso *et al*., (2014), high temperature at 35 and 40 °C resulted in reduction of chlorophyll a, chlorophyll b as well as total chlorophyll content in rice seedlings. Similar chlorophyll degradation was noted in KDML 105 rice seedlings when imposed to heat stress (Taratima *et al*., 2022). In the present study also there was a reduction in chlorophyll content in the tested entries. However, the reduction of chlorophyll content compared to control was less in MTU 1153, JB 683-1, MTU 1290 and IL 19211 indicating their tolerant nature when compared to other genotypes.

Grain yield and yield attributes:

Spikelet fertility (%): The mean spikelet fertility dropped from 92.0% in control to 75.7% under high temperature stress. Among the genotypes tested, higher spikelet fertility under stress conditions was observed in IL 19211 (87.2%) followed by MTU 1290 (85.4%), JB 683-1 (82.0%). Less than 65% spikelet fertility was noted in JB 680-2 (63.4%) and IL 19247 (64.8%) (**Table 2**).

Table 2: Impact of high temperature on yield attributes characters in rice genotypes

Entry	Spikelet fertility (%)			Grain number per panicle			1000 grain weight (g)		
	C	Ht	M	C	Ht	M	C	Ht	M
IET 29859	93.0	76.0	84.5	146	114	130	20.5	18.2	19.3
IL 19019	92.2	73.3	82.8	118	88	103	22.2	20.7	21.5
IL 19020	88.5	68.1	78.3	85	62	73	22.4	21.2	21.8
IL 19021	88.7	71.4	80.0	86	65	75	21.5	20.2	20.9
IL 19022	86.2	65.9	76.1	81	60	71	20.3	18.7	19.5
IL 19024	90.2	75.9	83.1	111	88	100	23.3	22.1	22.7
IL 19185	91.4	73.2	82.3	106	82	94	24.1	23.2	23.6
IL 19198	89.8	72.5	81.2	97	74	86	21.0	19.9	20.5
IL 19202	91.9	81.7	86.8	124	107	115	20.9	19.5	20.2
IL 19211	94.6	87.2	90.9	210	177	193	18.4	17.5	18.0
IL 19247	91.1	64.8	78.0	92	59	76	23.1	21.2	22.2
IL 19396	92.1	74.8	83.4	116	89	103	24.0	22.5	23.3
JB 680-2	92.7	63.4	78.1	139	92	115	22.2	20.6	21.4
JB 683-1	92.6	82.0	87.3	125	109	117	22.1	21.3	21.7
JB 687-3	93.8	78.9	86.4	166	131	149	24.2	22.7	23.5
JB 689-1	91.7	77.3	84.5	132	109	120	21.2	19.3	20.2
JBC 159-11	91.8	78.7	85.3	123	100	112	17.2	15.7	16.5
Krishnahamsa	92.0	78.6	85.3	104	88	96	19.2	17.9	18.6
MTU 1153	94.5	75.6	85.1	155	118	136	22.1	20.6	21.4
MTU 1156	93.3	77.2	85.3	140	112	126	22.2	20.6	21.4
MTU 1273	92.6	75.7	84.1	150	115	132	24.4	22.8	23.6
MTU 1290	94.6	85.4	90.0	140	123	131	24.7	23.3	24.0
MTU 1293	92.5	73.4	82.9	135	102	119	21.2	20.0	20.6
N-22	95.6	78.7	87.2	241	177	209	17.2	15.1	16.1
NLR 3776	93.3	79.0	86.2	166	132	149	22.0	20.1	21.0
NLR 3778	92.6	79.3	86.0	138	111	125	21.3	19.4	20.4
Mean	**92.0**	**75.7**		**132**	**103**		**21.6**	**20.2**	
LSD (T)		5.6			2.86			0.10	
LSD (V)		1.5			10.3			0.37	
LSD (TxV)		2.8			14.5			0.52	
CV (%)		5.1			7.68			1.56	

Grain number per panicle: The average number of grains per panicle dropped from 132 to 103. N22 (177), IL 19211 (177), NLR 3776 (132) and JB 687-3 (131) had a higher grain number per panicle under high temperature stress and IL 19247 (59), IL 19022 (60) and IL 19020 (62) recorded lower number of grains per panicle (**Table 2**).

1000 grain weight (g): The average test weight reduced from 21.6g in control to 20.2g under high temperature conditions. The test weight was highest in MTU 1290 (23.3g) followed by IL 19185 (23.2g). Lowest test weight was noted in N22 (15.1 g) and JBC 159-11 (15.7) (**Table 2**).

Total Dry matter (gm^{-2}): The total dry matter reduced from 661 gm^{-2} in control to 587 gm^{-2} under high temperature conditions. Higher TDM under high temperature conditions were noted in JB 689-1 (680 gm^{-2}) followed by Krishnahamsa (667 gm^{-2}), IL 19185 (644 gm^{-2}). Lowest TDM was in MTU 1293 (490 gm^{-2}) (**Table 3**).

Table 3: Impact of high temperature on grain yield and yield attributes in rice genotypes

Entry	TDM (gm^{-2}) at maturity			Grain yield (gm^{-2})			Harvest index (%)		
	C	Ht	Mean	C	Ht	Mean	C	Ht	Mean
IET 29859	743	583	663	535	345	440	41.9	37.1	39.5
IL 19019	590	522	556	501	351	426	46.0	40.1	43.0
IL 19020	691	597	644	523	387	455	43.1	39.1	41.1
IL 19021	633	596	615	493	408	451	43.7	40.5	42.1
IL 19022	626	588	607	511	396	454	44.8	40.3	42.6
IL 19024	592	537	565	429	348	389	41.9	39.2	40.6
IL 19185	688	644	666	529	388	458	43.4	37.5	40.5
IL 19198	622	577	600	469	386	427	43.0	40.1	41.5
IL 19202	681	614	648	514	403	459	42.9	39.6	41.3
IL 19211	621	582	602	468	416	442	42.9	41.5	42.2
IL 19247	640	566	603	462	364	413	41.9	38.7	40.3
IL 19396	689	585	637	516	407	462	42.8	41.1	41.9
JB 680-2	577	566	572	422	228	325	42.2	28.6	35.4
JB 683-1	679	596	637	515	443	479	43.2	42.8	43.0
JB 687-3	670	544	607	511	366	439	42.9	40.1	41.5
JB 689-1	677	680	679	507	388	448	42.8	36.0	39.4
JBC 159-11	640	574	607	483	364	424	42.9	38.7	40.8
Krishnahamsa	737	667	702	552	434	493	42.9	39.4	41.2
MTU 1153	664	629	647	501	420	460	42.8	40.0	41.4
MTU 1156	622	596	609	486	378	432	43.8	38.7	41.2
MTU 1273	607	630	619	472	345	408	43.3	35.4	39.4
MTU 1290	697	563	630	501	418	460	42.8	40.2	41.5
MTU 1293	711	490	600	551	345	448	43.6	41.4	42.5
N-22	767	598	683	577	392	484	42.9	39.7	41.3
NLR 3776	583	498	540	416	290	353	41.6	36.5	39.1
NLR 3778	751	627	689	571	434	503	43.2	40.9	42.0
Mean	**661**	**587**		**501**	**379**		**43.1**	**39.0**	
LSD (T)		19.6			**19.7**			0.94	
LSD (V)		70.7			**71.3**			3.41	
LSD (TxV)		100.0			**100.9**			4.82	
CV (%)		9.9			**14.1**			7.27	

Grain yield (gm^{-2}): Grain yield reduced from 501 gm^{-2} in control to 379 gm^{-2} under high temperature stress. Higher grain yield under high temperature was noted in JB 683-1 (443 gm^{-2}) followed by NLR 3778 (434 gm^{-2}), Krishnahamsa (434 gm^{-2}), MTU 1153 (420 gm^{-2}) and MTU 1290 (418 gm^{-2}). Lower were in JB 680-2 (228 gm^{-2}), NLR 3776 (290 gm^{-2}) and IET 29859 (345 gm^{-2}). More than 35% reduction was in IET 29859, MTU 1293 and JB 680-2 and less than 16% reduction was in MTU 1290, MTU 1153, JB 683-1 and IL 19211 (**Table 3**).

Harvest index (%): Harvest index reduced from 43.1% in control to 39.0% under high temperature conditions. Highest harvest index was noted in JB 683-1 (42.8%) followed by IL 19211 (41.5%). Lowest was in JB 680-2 (28.6%) (**Table 3**).

High temperature during the flowering period reduces the spikelet fertility (Zhang *et al.,* 2018). High temperature leads to poor anther dehiscence and less pollen grains on the stigma resulting in reduction of spikelet fertility (Zhao *et al*., 2016). The number of spikelets reduced under high temperature majorly due to reduction in pollen production by preventing anther filling during the panicle initiation phase (Wang *et al*., 2016). Hazra *et al*., (2016), imposed high temperature at tillering, booting, panicle initiation as well as flowering stage in rice and reported that high temperature stress (36 ^{o}C) at PI stage resulted

in higher reduction of grain yield. Similarly high temperature exposure significantly decreased filled grains per panicle, 1000-grain weight and harvest index and increased the unfilled grains per panicle. Mahantashivayogayya *et al*., (2016), screened forty rice accessions for heat tolerance and results revealed that EC792239, EC792285 and EC792185 which had heat tolerance, recorded more number of panicles and minimum per cent of chaffyness. In this study, reduction in grain yield and yield attributes were evident under high temperature stress and high yielding genotypes had higher spikelet fertility.

Acknowledgments: This experiment is a part of AICRIP programme. ICAR-AICRIP is highly acknowledged for providing the material for the experiment.

Conclusion

High temperature has a negative impact on rice growth and development. It hampers the cell membranes leading to a higher electrolyte leakage as well as reduction in photosynthetic pigment. Impact of exposure at panicle initiation stage is evident from the reduction of yield and yield attributes of the genotypes tested, MTU 1290, MTU 1153, MTU 1156, JB 683-1, N22 and IL 19211 maintained higher membrane stability, lesser reduction in loss of chlorophyll content, high spikelet fertility and grain yield. These genotypes could thus be identified to be thermotolerant.

References

Ashraf M and Hafeez M. 2004. Thermotolerance of pearl millet and maize at early growth stages. *Biologia Plantarum*, 48(1): 81-86.

Bita CE and Gerats T. 2013. Plant tolerance to high temperature in a changing environment: Scientific fundamentals and production of heat stress-tolerant crops. *Frontiers in Plant Science*, 4(273): 1-18.

Blum A and Ebercon A. 1981. Cell membrane stability as a measure of drought and heat tolerance in wheat. *Crop Science*, 21(1): 43-47.

Dubey AN, Verma S, Goswami SP and Devedee AK. 2018. Effect of temperature on different growth stages and physiological process of rice crop. *Bulletin of Environment, Pharmacology and Life Sciences,* 7(11): 162-169.

Haque M, Hasan M, Rajib M and Hasan M. 2009. Identification of cultivable heat tolerant wheat genotypes suitable for Patuakhali district in Bangladesh. *Journal of the Bangladesh Agricultural University,* 7(2): 241-246.

Hazra P, Islam MT and Das GC. 2016. Effect of high temperature on some physiological parameters of grain growth and yield of boro rice varieties. *Journal of Bioscience and Agriculture Research*, 7(1): 600-607.

Hu L, Bi A, Hu Z, Amombo E, Li H and Fu J. 2018. Antioxidant metabolism, photosystem ii and fatty acid composition of two tall fescue genotypes with different heat tolerance under high temperature stress. *Frontiers in Plant Science*, 9(1242): 1-13.

IPCC. 2014. Contribution of working groups I, II and III to the fifth assessment report of the intergovernmental panel on climate change, Synthesis report, Geneva, Switzerland.

Korres N, Norsworthy J, Burgos N and Oosterhuis D. 2017. Temperature and drought impacts on rice production: an agronomic perspective regarding short-and long-term adaptation measures. *Water Resources and Rural Development*, 9: 12-27.

Larkindale J and Huang B. 2004. Changes of lipid composition and saturation level in leaves and roots for heat-stressed and heat-acclimated creeping bentgrass (*Agrotis stolonifera*). *Environmental and Experimental Botany,* 51(1): 57-67.

Lichtenthaler HK and Wellburn AR. 1983. Determination of carotenoids and chlorophyll a and b of leaf extracts in different solvents. *Biochemical Society Transactions*, 11(5): 591-592.

Lyman NB, Jagadish KSV, Nalley LL, Dixon BL, Siebenmorgen T and Nelson JC. 2013. Neglecting rice milling yield and quality underestimates economic losses from high-temperature stress. *PLoS ONE*, 8(8): e72157.

Mahantashivayogayya K, Basavaraj SL, Ramesha MS, Amaregouda, Mohammed I, Masthana Reddy BG, Guruprasad GS and Pramesh D. 2016. Response of rice genotypes for heat stress during summer season in the northern parts of Karnataka. *Journal of Rice Research,* 9(1): 1-6.

Narayanan S, Tamura PJ, Roth MR, Prasad PVV and Welti R. 2016. Wheat leaf lipids during heat stress: I. High day and night temperatures result in major lipid alterations. *Plant Cell Environmen*t, 39: 787-803.

Pooja K and Ajit KM. 2022. Impact of heat stress on growth of rice genotypes under greenhouse condition. *The Pharma Innovation Journal*, 11(11): 1537-1541.

Porra RJ, Thompson WA and Kriedemann PE. 1989. Determination of accurate extinction coefficients and simultaneous equations for assaying chlorophylls a and b extracted with four different solvents: verification of the concentration of chlorophyll standards by atomic absorption spectroscopy. *Biochimica et Biophysica Acta*, 975(3): 384-394.

Prasertthai P, Paethaisong W, Theerakulpisut P and Dongsansuk A. 2022. High Temperature Alters Leaf Lipid Membrane Composition Associated with Photochemistry of *PSII* and Membrane Thermostability in Rice Seedlings. *Plants*, 11(11): 1454.

Randive P, Gokhale NB, Sawardekar SV, Kunkerkar RL, Bhagwat SS and Kelkar VG. 2019. Molecular screening and diversity analysis of rice (*Oryza sativa* L.) genotypes for biotic and abiotic stresses using SSR markers. *Journal of Rice Research,* 12(1): 1-12.

Sanchez-Reinoso AD, Garces-Varon G and Restrepo-Diaz, H. 2014. Biochemical and physiological characterization of three rice cultivars under different day time temperature conditions. *Chilean Journal of Agricultural Research*, 74(4): 373-379.

Taratima W, Chuanchumkan C, Maneerattanarungroj P, Trunjaruen A, Theerakulpisut P and Dongsansuk A. (2022). Effect of heat stress on some physiological and anatomical characteristics of rice (*Oryza sativa* L.) cv. KDML105 callus and seedling. *Biology*, 11(11): 1587.

Wang DR, Bunce JA, Tomecek MB, Gealy D, McClung A, McCouch SR and Ziska LH. (2016). Evidence for divergence of response in Indica, Japonica and wild rice to high CO 2× temperature interaction. *Global Change Biology*, 22(7), 2620-2632.

Wang Y, Zhang Y, Zhang Q, Cui Y, Xiang J, Chen H, Hu G, Chen Y, Wang X, Zhu, D and Zhang Y. 2019. Comparative transcriptome analysis of panicle development under heat stress in two rice (*Oryza sativa* L.) cultivars differing in heat tolerance. *PeerJ*, 7: e7595.

Xu J and Henry A. 2020. Sreenivasulu N. Rice yield formation under high day and night temperatures-a prerequisite to ensure future food security. *Plant Cell Environment,* 43(7): 1595-1608.

Xu Y, Chu C and Yao S. 2021. The impact of high-temperature stress on rice: Challenges and solutions. *Crop Journal,* 9(5): 963-976.

Zhang C, Li G, Chen T, Feng B, Fu W, Yan J, Islam MR, Jin Q, Tao L and Fu G. 2018. Heat stress induces spikelet sterility in rice at anthesis through inhibition of pollen tube elongation interfering with auxin homeostasis in pollinated pistils. *Rice*, 11(1): 14

Zhao L, Zhu Z, Tian X, Kobayasi K, Hasegawa T, Zhang Y, Chen Z, Wang C and Matsui T. 2016. Inheritance analysis of anther dehiscence as a trait for the heat tolerance at flowering in japonica hybrid rice (*Oryza sativa* L.), *Euphytica*, 211(3): 311-320.

RESEARCH ARTICLE https://doi.org/10.58297/HNZH8897

Potential of Rice Straw as a Carbon Source in Organic Rice Farming and its Effect on Global Warming Potential

Surekha Kuchi*, Pragnya M, Kumar RM, Brajendra and Sundaram RM

ICAR-Indian Institute of Rice Research, Hyderabad, India.

*Corresponding author Email: surekhakuchi@gmail.com

Received: 2nd November, 2024; Accepted : 13th December, 2024

Abstract

The potential benefits of rice straw in organic farming in terms of rice productivity, soil organic carbon (SOC) stocks, carbon sequestration rate (CSR) and global warming potential (GWP) were studied for five years covering 10 wet (*kharif*) and dry (*rabi*) seasons with a wide seasonal temperature range (28-31 °C and 30-40 °C during wet and dry seasons, respectively). Field experiments were conducted at the ICAR-IIRR, Hyderabad, in a black clayey vertisol. The organic sources used were rice straw + green manure in *kharif* and rice straw + poultry manure in *rabi*. Organic system resulted in initial yield reduction by 15-20% than inorganic system and yields stabilized after two and five years in wet and dry seasons, respectively, with improved soil health parameters. The SOC stocks were higher with organics by 34-43% compared to inorganics after five years of study. The CSR was also positive with organics (0.97 and 0.57 t/ha/year during wet and dry seasons, respectively) compared to inorganics (-021 and -0.33 t/ha/year during wet and dry seasons, respectively) which recorded negative C sequestration rate. Organics recorded favourable C sequestration even under dry situations which is more desirable to mitigate the adverse effects of global warming to certain extent by reducing CO_2 emissions. The global warming potential under organic system was 20% higher than in conventional system with increased CO_2 and CH_4 and reduced N_2O emissions. Since GWP was higher with rice straw, mixing of straw with other potential organics in proper proportions reduce the GWP in addition to carbon sequestration in organic rice cultivation.

Key words: Organic farming, rice straw, greenhouse gases, carbon sequestration, global warming potential

Introduction

One of the major challenges faced by humankind is to cope up with the changing climate and managing it for the sustenance of healthy life. IPCC, (2014) report reaffirms that human influence on the climate system is clear and recent anthropogenic emissions of greenhouse gases (GHGs) are the highest in history. According to Intergovernmental Panel on Climate Change (IPCC) (2014) data, it shows that 0.15 ℃ increase in temperature per decade, which is causing a drastic change in different farming systems and their productivity, is expected to increase by 1.7-4.8 ℃ by the end of the century.

Climate change and agriculture, being interrelated, do influence each other and the relationship between them is of high importance as the imbalance between world population and world food production is increasing. Agriculture is considered both as a contributor to climate change and a victim as well. Soil health degradation has emerged as a major factor responsible for the stagnation in agricultural production. Continuous use of inorganic fertilizers has not only brought about loss of vital soil fauna and flora but also resulted in loss of secondary and

micronutrients. Agriculture, responsible for 20-30% of global GHG emissions, contributes to climate change through practices such as excessive use of synthetic fertilizers, fossil fuel combustion during fertilizer production and intensive tillage operations. These practices release significant amounts of greenhouse gases such as carbon dioxide (CO_2), methane (CH_4) and nitrous oxide (N_2O), which contribute to global warming. Global warming potential (GWP) is a metric that measures how much heat a greenhouse gas (GHG) traps in the atmosphere compared to carbon dioxide (CO_2) over a specific period of time.

Rice (*Oryza sativa* L.) is the major staple food crop in India, occupying around 45 million hectares (mha) of land and contributing about 135 million tons (mt) to the total food grain production (Agricultural Statistics at a Glance, 2023). Although rice production will be affected by climate change, rice farming also has the capacity to amplify the problem of GHG emission mediated global warming, which is a common phenomenon in rice growing countries especially in South Asia. Rapid mineralization of SOC compounds may lead to higher CO_2 flux to the atmosphere (Reicosky *et al.,* 1995) thus leading to global warming. Soil C sequestration restores degraded soils, enhances biomass production and reduces the rate of enrichment of atmospheric CO_2 (Lal, 2004). Organic agriculture enables ecosystems to better adjust to the effects of climate change and improves carbon sequestration potential of the soil (Bhooshan and Prasad, 2011) and carbon sequestration is considered as a mitigation option to adverse effects of climate change. Keeping this in view, field experiments were conducted to study the influence of rice straw in organic farming on soil organic carbon, greenhouse gas emissions and global warming potential.

Materials and Methods

Field experiments were conducted over a spread of five years covering ten rice cropping seasons [five wet (WS) and five dry (DS)] on a deep black clayey vertisol (Typic pellustert) at the Indian Institute of Rice Research (IIRR) farm, Rajendranagar, Hyderabad. Organic and conventional farming systems were compared in terms of rice productivity, soil organic carbon (SOC) stocks, carbon sequestration rate (CSR) and global warming potential (GWP). The experimental soil characteristics were slightly alkaline (pH 8.2); non-saline (EC 0.7l dS/m); calcareous (free $CaCO_3$ 5.01%); with CEC 44.1 C mol (p+)/ kg soil and medium soil organic carbon (0.69%) content. Soil available N was low (228 kg/ha); available phosphorus was high (105 kg P_2O_5 /ha$_{);}$ available potassium was high (530 kg K_2O/ha) and available zinc was also high (12.5 ppm). The temperature variation among the two seasons (wet and dry) was shown in **Table 1**.

Table 1: Mean Temperature (°C) range during crop growth period

Year	Wet season (August-December)		Dry season (February-May)	
	Range	Mean	Range	Mean
1st year	28.5-30	29.3	32.9-38.1	35.5
2nd year	28.6-30.9	29.7	31.4-31.2	36.0
3rd year	29.5-30.6	30.0	30.5-39	34.8
4th year	29.3-31.4	30.0	33.9-40.3	37.3
5th year	28.5-31.4	30.3	33.0-40.3	37.5
Overall range	**28.5-31.4**	**-**	**30.5-40.3**	**-**

The four treatments consisted of: control (T1); 100% inorganic fertilisers (T2); 100% organics (T3) and 50% inorganics + 50% organics (T4, INM) with five replications. The organic sources used were green manure, dhaincha (*Sesbania aculeata*) + paddy straw during wet seasons (WS) and poultry manure + paddy straw during dry seasons (DS). Super fine rice varieties, BPT 5204 and Vasumati were tested in wet and dry seasons, respectively. The local recommended dose of inorganic fertilizers were given to conventional system @ 100-60-40 kg N, P_2O_5, K_2O/ha during both seasons through urea, single super phosphate, muriate of potash and 25 kg of Zinc sulphate, respectively. Nitrogen was applied in three equal splits at basal,

maximum tillering and panicle initiation stages while P, K and Zn were applied as basal doses only. Through organics, N dose was adjusted to recommended level based on their moisture content and 'N' concentration on dry weight basis. Organic fertilizers were incorporated one day before transplanting rice. Grain yield was recorded at the end of each season. At the end of 5 years, soil samples were collected from 15 cm depth and analysed for various parameters. Carbon stocks and C sequestration rate were computed using the following formulae (Lal *et al*., 1998).

1) SOC storage (C stock t/ha) = [%C x bulk density x soil depth (m) x 10000] / 100

2) SOC sequestered (t C/ha) = SOC (current) - SOC (initial)

Integrated evaluation of GHG emissions expressed as GWP was computed for the current experiment by using the IPCC factors for calculating the combined GWPs for 100 years [GWP = 24.5 *CH_4+ CO_2+ 320 *N_2O kg CO_2-e ha^{-1}] from CH_4, N_2O and CO_2 efflux values under different treatment conditions (IPCC, 2007). The GHG emissions and GWP for inorganic fertilizers and organics sources used were calculated based on the studies of Snyder *et al.,* (2009); Bhattacharyya *et al.,* (2012); Wang *et al.,* (2019) and Fauzan *et al.,* (2021).

Results and Discussions

Grain yield trends

Grain yield trends showed that, during the wet season, yields in plots with fertilizer application and integrated nutrient management (INM) remained stable, ranging from 5.2-5.5 t/ha and 4.7-5.2 t/ha, respectively. These yields were 15-20% higher than those in organic plots in the first two years, but organic yields improved over time, reaching comparable levels with inorganic treatments (4.8-5.2 t/ha) in later years. In the dry season, however, inorganics and INM consistently outperformed organics for four consecutive years, with organic yields matching those of inorganics and INM only in the fifth year **(Table 2)**. Unfertilized control treatment recorded the lowest grain yields throughout the experiment. It was evident that all treatments with fertilization resulted in high yield increases, but yields were generally less in the DS.

Initially, organic farming led to a yield reduction of around 24% for rice, as reported by Mader *et al*., (2002), but a gradual yield increase with organic methods over time was noted by Surekha *et al*., (2010) and Urkurkar *et al*., (2010). This may be due to a mismatch between the nutrient release from organic sources and crop demand, influenced by seasonal conditions in the initial years. Once soil fertility reached an adequate level, the organic system produced yields comparable to the conventional system. The slow, gradual release of nutrients from organic sources during the early years of conversion to organic farming did not immediately lead to higher yields. However, repeated applications of organic inputs over time built up sufficient soil fertility by enhancing soil biological activity (Surekha and Satishkumar, 2014).

Soil Organic Carbon (SOC) stocks and C sequestration rate (CSR)

The carbon stock and sequestration rate for each treatment were shown in **Table 3**. After five years, SOC stocks were significantly higher in organic

Table 2: Grain yield (t/ha) as influenced by nutrient sources

Sl. No	Year	Wet season				Dry season			
		Control	Inorganics	Organics	INM	Control	Inorganics	Organics	INM
1	1st year	3.59^{c}	5.52^{a}	4.92^{b}	5.17^{ab}	1.92^{c}	3.82^{a}	3.62^{b}	4.36^{a}
2	2nd year	3.55^{c}	5.63^{a}	4.92^{b}	5.56^{a}	2.33^{c}	3.81^{a}	3.11^{b}	3.81^{a}
3	3rd year	3.32^{b}	5.50^{a}	5.22^{a}	5.31^{a}	2.77^{c}	4.22^{a}	3.37^{b}	4.04^{a}
4	4th year	3.43^{b}	5.52^{a}	5.60^{a}	5.48^{a}	1.98^{c}	3.74^{a}	3.14^{b}	3.82^{a}
5	5th year	3.34^{b}	5.29^{a}	5.27^{a}	5.02^{a}	2.13^{b}	4.21^{a}	3.98^{a}	4.22^{a}

Numbers followed by the same letter in each row are not statistically significantly

treatments, with values of 19.54 t/ha in the wet season and 17.55 t/ha in the dry season, compared to inorganic treatments, which recorded 13.63 t/ha and 13.05 t/ha, respectively. CSR were also positive for organic treatments, at 0.97 t/ha/year in the wet season and 0.57 t/ha/year in the dry season. In contrast, inorganic treatments showed negative CSRs of -0.21 t/ha/year and -0.33 t/ha/year for the wet and the dry seasons, respectively. The INM treatment showed intermediate values, while the lowest SOC stock levels were recorded in the control treatment.

Carbon sequestration rate was nearly half during dry season which recorded higher temperatures than that of CSR during wet season that favoured the loss of SOC stocks due to faster decomposition and mineralization. The treatment, 100% organics recorded 43% and 34% higher SOC stocks followed by INM treatment that recorded 34% and 20% higher SOC stocks over 100% chemical fertilisers during wet and dry seasons, respectively. Thus, it was evident that organic rice farming can lead to better carbon accumulation under varied climatic conditions and increasing organic carbon in agricultural systems has been reported as an important mitigation option by IPCC (Muller, 2009). Bhattacharyya *et al.,* (2012) also noticed that carbon storage rate was also found to be significantly higher (0.35 Mg C ha^{-1} y^{-1}) in the application of rice straw. An increase in soil carbon by 15-28% in organic systems was also reported by Paul (2003). Similarly, higher values of SOC by 0.18 ± 0.06%, for C stocks by 3.50 ± 1.08 Mg C ha^{-1} and for sequestration rates by 0.45 ± 0.21 Mg C ha^{-1} y^{-1} in organically farmed soils over non-organic management was reported by Gattinger *et al*., (2012).

Table 3: Soil Organic carbon (SOC) stocks and C sequestration rate after five years

Treatments	Soil organic Carbon (%)	Bulk density (g/cc)	Carbon stock (t/ha)	SOC sequestered (t/ha)	C seq. rate (t/ha/yr)
Wet season					
Control	0.59	1.36	12.04	-2.66	-0.53
Inorganics	0.64	1.42	13.63	-1.07	-0.21
Organics	1.01	1.29	19.54	4.84	0.97
INM	0.91	1.34	18.29	3.59	0.71
Dry season					
Control	0.54	1.38	11.18	-3.52	-0.70
Inorganics	0.60	1.45	13.05	-1.65	-0.33
Organics	0.90	1.30	17.55	2.85	0.57
INM	0.79	1.32	15.64	0.94	0.19
Initial value	**0.69**	**1.42**	**14.7**	**-**	**-**

Global warming potential (GWP)

The global warming potential along with the emission of greenhouse gasses such as CO_2, CH_4 and N_2O with usage of inorganic fertilizers and organic fertilizers were presented in **Table 4.** For inorganic fertilizers, urea contributed the most to emissions, particularly during application, where N_2O emissions were high compared to organics. Combined across both seasons, inorganic sources emitted a total GWP of 13,157 kg CO_2-e/ha. Organic applications resulted in higher CO_2 and CH_4 emissions but lower N_2O emissions compared to inorganics. The total emissions from organic sources across both seasons were with a GWP of 15,909.6 kg CO_2-e/ha. Greenhouse gas emissions and GWP from organics were higher in *rabi* season than in *kharif* season. The application of organic fertilizers increased the CO_2 and CH_4 emissions by 15.5% and 33.2% and reduced N_2O emissions by 27.4% over inorganics though there was an increase of 20.9% in GWP with the application of organics. The data suggests that using organic fertilizers, such as rice straw and poultry manure, increased total greenhouse gas emissions compared to inorganic fertilizers. However, it also reduced N_2O emissions, a particularly potent greenhouse gas, by 27.4%

over inorganics. This trade-off highlights that while organic fertilizers may contribute more to CO_2 and CH_4 emissions in rice, they offer environmental benefits by lowering N_2O emissions, which could be advantageous for climate mitigation strategies focused on this gas. Wang *et al.,* (2018) also reported that rice straw increased CO_2 and CH_4 emissions but reduced N_2O emissions. According to He *et al.,* (2024) the straw return might facilitate soil respiration and oxygen depletion, leading to oxygen limitation and eventually spurring the reduction of N_2O to N_2 during denitrification, especially in oxygen-depleted paddy fields. Thus, it leads to a reduction in N_2O emissions.

GHG emissions when rice straw along with green manure (7764 kg CO_2-e/ha) applied were less compared to the rice straw and poultry manure (8145 kg CO_2-e/ha). The high C/N ratio in rice straw also contributes to increased GHG emissions from organic sources. Poultry manure and green manure have lower C/N ratios than rice straw, which contains abundant cellulose and hemicellulose (Li *et al.,* 2023). Gao *et al*., (2023) reported that green manure increases soil fertility and rice yields without increasing CH_4 emissions in green manure-rice system than fallow-rice practice. Bayer *et al.,* 2014 reported that the high C/N ratio of rice straw increased the metabolic C substrate available to methanogenic bacteria, thus promoting the production of CH_4 and lead to carbon loss by accelerating soil organic matter mineralization through the priming effect. Khosa *et al*., (2010) reported that rice straw compost reduced the GHG emissions compared to sole application of straw/ green manure, as direct straw use leads to increased GHGs. He *et al.,* (2024) reported that GHG and GWP were influenced by a combination of straw size, straw return method and straw amount and recommended straw incorporation > 7.5t/ha with size ≥ 5 cm for reducing GHG emissions and GWP from straw return in paddy fields. Though rice straw has high potential as carbon source in organic farming, due to its contribution to global warming, its positive effects may not be visible. Hence, it is essential to find out suitable organic sources and their proportions to mix with straw so that GWP from straw can be reduced.

Table 4 : GHG emissions and GWP from inorganic and organic sources (kg CO_2-e ha^{-1} yr^{-1})

	GHG Emissions			GWP
Inorganics	**CO_2**	**CH_4**	**N_2O**	
Kharif	**(kg CO_2-e ha^{-1})**	**(kg CO_2-e ha^{-1})**	**(kg CO_2-e ha^{-1})**	**(kg CO_2-e ha^{-1})**
During Manufacture				
Urea 100 kg	310	7.77	0.93	320
Phosphate (SSP) 60 kg	60	2.268	0.372	60
Potash (KCl) 40 kg	28	0.084	0.124	28
During Application				
Urea-N 100 kg N/ ha	2412.83	3241.00	516.67	6170.50
Rabi				
During Manufacture				
Urea 100 kg	310	7.77	0.93	320
Phosphate (SSP) 60 kg	60	2.268	0.372	60
Potash (KCl) 40 kg	28	0.084	0.124	28
During Application				
Urea-N 100 kg N/ ha	2412.83	3241.00	516.67	6170.50
TOTAL (*Kharif* + *Rabi*)	**5621.67**	**6502.24**	**1036.19**	**13157.00**
ORGANICS				
Kharif				
During Application				
Rice straw + Green Manure @100 kg N	3097.50	4294.50	372.00	7764.00
Rabi				
During Application				
Rice Straw + Poultry Manure @100 kg N	3397.50	4368.00	380.14	8145.64
TOTAL (*Kharif* + *Rabi*)	**6495.00**	**8662.50**	**752.14**	**15909.64**
% Increase/decrease with organics	**15.5%**	**33.2%**	**-27.4%**	**20.9%**

Conclusion

Organic farming in rice production, though initially yields less, can match conventional yields over time by enhancing soil fertility through sustained nutrient release. Organic practices significantly improved soil organic carbon stocks and sequestration rates, supporting soil resilience and adaptation for climate change. However, organic treatments increased CO_2 and CH_4 emissions but reduced N_2O emissions by 27.4%, indicating potential climate change mitigation benefits. Overall, organic farming enhances soil health and carbon storage supporting long-term sustainable productivity amidst climate change. Alternative ways of effective straw utilization like composting must be explored to reduce the GHG emissions and also to obtain fullest benefits from rice straw utilization in organic farming.

References

Agricultural Statistics at a Glance. 2023. Government of India, Ministry of Agriculture and Farmers Welfare, Department of Agriculture and Farmers Welfare Economics and Statistics Division. http://desagri.gov.in.

Bayer C, de Souza Costa F, Pedroso GM, Zschornack T, Camargo ES, de Lima MA, Frigheto RT, Gomes J, Marcolin E. and Macedo VRM, 2014. Yield-scaled greenhouse gas emissions from flood irrigated rice under long-term conventional tillage and no-till systems in a humid subtropical climate. *Field Crops Research*, 162: 60-69.

Bhattacharyya P, Roy KS, Neogi S, Adhya TK, Rao KS. and Manna MC, 2012. Effects of rice straw and nitrogen fertilization on greenhouse gas emissions and carbon storage in tropical flooded soil planted with rice. *Soil and Tillage research*, 124:119-130.

Bhooshan N and Prasad C. 2011. Organic Farming: Hope of posterity. *In:* Organic Agriculture: Hope of Posterity (Eds.) Neeru Bhooshan and Chandrika Prasad. UP Council of Agricultural Research (UPCAR), Lucknow. pp. 1-10.

Fauzan MI, Anwar S, Nugroho B, Ueno H. and Toma Y. 2021. The study of chicken manure and steel slag amelioration to mitigate greenhouse gas emission in rice cultivation. *Agriculture*, 11(7): 661.

Gao SJ, Shun LI, Zhou GP. and Cao WD. 2023. The potential of green manure to increase soil carbon sequestration and reduce the yield-scaled carbon footprint of rice production in southern China. *Journal of Integrative Agriculture*, 22(7): 2233-2247.

Gattinger A, Muller A, Haeni M, Skinner C, Fliessbach A, Buchmann N, Mader P, Stolze M, Smith P, Scialabba NE and Niggli U. 2012. Enhanced topsoil carbon stocks under organic farming. *Proceedings of National Academy of Sciences*, 109(44): 18226-18231.

He Z, Cao H, Qi C, Hu Q, Liang J. and Li Z, 2024. Straw management in paddy fields can reduce greenhouse gas emissions: A global meta-analysis. *Field Crops Research*, 306: 109218.

IPCC (Intergovernmental Panel on Climate Change). 2014. Stocker, T., Field, C., Dahe, Q., Barros, V. and Plattner, G.K., 2009. In IPCC Expert Meeting on Detection and Attribution Related to Anthropogenic Climate Change. Geneva, Switzerland: Meeting Report https://archive.ipcc.ch/pdf/supporting-material/expert-meeting-detectionanthropogenic-2009-09. pdf.

IPCC [Intergovernmental Panel on Climate Change], 2007. Agriculture. In: Metz, B., Davidson, O.R., Bosch, P.R. (Eds.), Climate Change 2007: Mitigation. Contribution of Working Group III to the Fourth Assessment Report of the Intergovernmental Panel on Climate Change. Cambridge University Press, Cambridge, United Kingdom/New York, NY, USA.

Khosa MK, Sidhu BS. and Benbi DK, 2010. Effect of organic materials and rice cultivars on methane emission from rice field. *Journal of Environmental Biology*, 31(3): 281-285.

Lal R, Kimble JM, Follett RF, Cole CV,1998. The Potential of U.S. Cropland to Sequester Carbon and Mitigate the Greenhouse Effect. *Ann Arbor Science Publications*, Chelsea, MI. 128 pp.

Lal R. 2004. Soil carbon sequestration impacts on global climate change and food security. *Science*, 304(5677): 1623-1627.

Li P, Zhang A, Huang S, Han J, Jin X, Shen X, Hussain Q, Wang X, Zhou J. and Chen Z, 2023. Optimizing management practices under straw regimes for global sustainable agricultural production. *Agronomy*, 13(3): 710.

Mader P, Fliessbach A, Dubois D, Gunst L, Fried P. and Niggli U. 2002. Soil fertility and biodiversity in organic farming. *Science,* 296(5573): 1694-1697.

Muller ML. 2009. Organic Agriculture and carbon sequestration-Possibilities and constrains for the consideration of Organic agriculture within carbon accounting systems. FAO Publication, Rome.

Paul H, 2003. Organic farming sequesters atmospheric carbon and nutrients in soils. Rodale Institute Farming Systems Trial Findings.

Reicosky DC, Kemper WD, Langdale GW, Douglas CL Jr and Rasmusspen PE. 1995. Soil organic matter changes resulting from tillage and biomass production. *Journal of Soil and Water Conservation* 50(3): 253-261.

Snyder CS, Bruulsema TW, Jensen TL. and Fixen PE. 2009. Review of greenhouse gas emissions from crop production systems and fertilizer management effects. *Agriculture, Ecosystems and Environment*, 133(3-4): 247-266.

Surekha K, Jhansilakshmi V, Somasekhar N, Latha PC, Kumar RM, Rani NS, Rao KV. and Viraktamath BC, 2010. Status of organic farming and research experiences in rice. *Journal of Rice Research*, 3(1): 23-35.

Surekha K. and Satishkumar YS, 2014. Productivity, nutrient balance, soil quality and sustainability of rice (*Oryza sativa* L.) under organic and conventional production systems. *Communications in Soil Science and Plant Analysis*, 45(4): 415-428.

Urkurkar JS, Chitale S and Tiwari A. 2010. Effect of organic vs. chemical nutrient packages on productivity, economics and physical status of soil in rice (*Oryza sativa*)-potato (*Solanum tuberosum*) cropping system in Chhattisgarh. *Indian Journal of Agronomy*. 55(1): 6-10.

Wang H, Shen M, Hui D, Chen J, Sun G, Wang X, Lu C, Sheng J, Chen L, Luo Y. and Zheng J, 2019. Straw incorporation influences soil organic carbon sequestration, greenhouse gas emission and crop yields in a Chinese rice (*Oryza sativa* L.)-wheat (*Triticum aestivum* L.) cropping system. *Soil and Tillage Research*, 195: 104377.

Wang N, Yu JG, Zhao YH, Chang ZZ, Shi XX, Ma LQ. and Li HB, 2018. Straw enhanced CO_2 and CH_4 but decreased N_2O emissions from flooded paddy soils: Changes in microbial community compositions. *Atmospheric Environment*, 174: 171-179.

RESEARCH ARTICLE https://doi.org/10.58297/KLCF6831

Study of Skewness and Kurtosis for Spikelet Sterility and Yield Related Traits in Segregating Generations of a Rice (*Oryza sativa* L.) Cross to Identify Gene Action

Priyanka Kumari[1,2], Jenny Priya Ekka[1], Swapnil[3], Krishna Prasad[1], Ekhlaque Ahmad[1*] and Manigopa Chakraborty[1]

[1]Department of Genetics and Plant Breeding, Birsa Agricultural University, Ranchi, Jharkhand;
[2]Department of Plant Breeding and Genetics, Veer Kunwar Singh College of Agriculture, Bihar Agricultural University, Sabour, Bhagalpur,
[3]Department of Genetics and Plant Breeding, Centurion University of Technology and Management, Paralakhemundi, Odisha.

*Corresponding author Email: ekhlaque.bau@gmail.com

Received : 5th November, 2024; Accepted : 15th December, 2024

Abstract

An investigation was performed in the F_6 and F_7 generation of the cross Pusa-1176 x BPT-5204. The phenotypic screening was done intensely for spikelet sterility in F_6 generation (*Kharif,* 2021) based on which some families were selected and grown as F_7 generation *(Kharif,* 2022) that were sown as panicle to progeny rows at two different dates as set I and set II with the interval of 15 days in order to study the influence of environment on the traits under study. The segregates were studied for skewness and kurtosis to identify the presence of gene interactions in 13 quantitative traits including grain yield per plant (Fisher *et al.,* 1932). The results displayed that various traits exhibited positive skewness along with platykurtic and leptokurtic frequency distribution in set I and set II. Similarly, a combination of negative skewness with platykurtic and leptokurtic frequency distribution was observed for diverse traits in set I and set II. Normal curve without skewness indicating symmetry of the trait and platykurtic frequency distribution was observed for L/B ratio in set I and for 100 seed weight in set II.

Keywords: Kurtosis, Gene Action, Skewness, Spikelet, Sterility

Introduction

Rice (*Oryza sativa* L.) belongs to Poaceae family and is one of the major staple foods for more than half of the world's population. It is also an essential commodity for food and nutritional security since it provides 20% of the regular calorie intake (Ricepedia, 2020). It is cultivated nearly on 162 million hectares of land in a wide range of environments with an annual production of about 756 million tonnes globally (FAO, 2022) that mostly does not reach its potentiality in terms of production and productivity due to various factors affecting the yield of the crop such as biotic and abiotic stresses that are unpredictable in nature. Thus, a breeder should be capable of selecting the better-performing genotypes from a large population which requires intensive studies on various yield and yield-attributing traits. The extent of selection pressure given to the population depends on the study of a frequency distribution that is analyzed via skewness and kurtosis estimation (Choo and Reinbergs, 1932). The nature of gene action is

revealed by the estimates of skewness whereas the number of genes controlling the trait is determined by kurtosis (Savitha *et al.,* (2015) and accordingly choice is made whether selection should be mild or intensive. Thus, to enhance the selection efficiency and breeding strategy, appropriate information on the gene interactions is essential which may lead to progressive research work thereby improving the performance of the population. The present investigation was thereby undertaken in the F_7 generation of the cross Pusa-1176 x BPT-5204. The main objective of the experiment was to assess the existence of variability among the characters under study, nature of gene action, number of genes controlling the trait and statistical analysis through frequency distribution patterns based on skewness and kurtosis (Roy, 2000, Robson, 1956).

Materials and Methods

The present investigation was carried out at the experimental plot of Birsa Agricultural University, Kanke under the rainfed conditions of Jharkhand, India during *Kharif* 2021. The phenotypic screening was done intensely for spikelet sterility in 23,083 F_6 plants (from 482 families) of the cross Pusa-1176 x BPT-5204 as large number of plants in a family showed sterile panicles as well as segregation among the traits under study. The parents of Pusa-1176 and BPT-5204 are [Bindli mutant 34 (BM34) x ARC line] and [GEB-24 x T(N)1 x Mahsuri], respectively. The parent, Pusa-1176 is an aromatic rice and the other parent BPT-5204 is resistant to blast. Also, both the parents were well suited to rainfed and shallow land. As the families of F_6 generation showed segregation among the traits under study, 15 families comprising of 158 sterile F_6 plants were selected based on the maximum number of sterile progeny plant with sterility % above 55% within the family. In the next generation (F_7 generation), it was sown as panicle to progeny rows on the seed bed nursery and thereafter transplanted into the field. Sowing was done at different dates designated as set I and set II with the interval of 15 days in order to study the influence of the environment on the traits under study. The method of sowing adopted was panicle to progeny row. The transplanting was done by maintaining row-to-row distance as well as plant-to-plant distance of 20 cm. Other recommended agronomic practices were followed throughout the crop growth period. The data was recorded on individual plants representing each of the segregants due to segregation pattern observed among the traits under study. The traits for which observations were taken are days to flowering, number of tillers, plant height, panicle length, panicle number, number of filled spikelets, number of unfilled spikelets, spikelet fertility, grain length, grain width, L/B ratio, 100 seed weight and grain yield per plant. After that statistical analysis was done based on the estimation of skewness and kurtosis which was calculated using the frequency distribution of the characters under study (Kapur, 1981; Savitha *et al.*, 2015).

Results and Discussions

The study of frequency distribution via skewness and kurtosis provides information about the nature of gene action and the number of genes controlling the traits respectively. The genes controlling the character with skewed frequency distribution tend to be predominantly dominant regardless of whether the effect on the trait has been enhanced or reduced. The results obtained have been presented in **Table 1.** The frequency distribution was found to be positively skewed and platykurtic for the number of panicles, number of unfilled spikelets, 100 seed weight and seed yield per plant in set I and for days to flowering, number of tillers, number of panicles and spikelet fertility in set II. Positive skewness in the segregants indicates its association

with complementary gene actions and platykurtic distribution shows that it is controlled by a large number of genes **(Figure 1)**. Similar results were reported by Kiran *et al.,* (2012) for number of tillers panicle length and grain yield per plant, Harshiya and Jagadeesh (2014) for plant height and test weight, Raghavendra and Hittalmani (2015) for number of filled grains and grain length, Savitha *et al.,* (2015) for 1000-grain weight and single plant yield and Rani *et al.,* (2016) for number of tillers per plant, panicle length and also for grain yield per plant. It is also supported by Sheshaiah *et al.,* (2018) for panicle length and grain yield per plant. Sushma Lilly *et al.,* (2018) reported for the number of filled grains and grain length whereas Prisca Seeli *et al*., (2021) reported for number of unfilled grains.

The positively skewed and leptokurtic frequency distribution was observed for days to flowering, number of tillers, plant height and number of filled spikelets in set I and for plant height, number of filled spikelets, number of unfilled spikelets and seed yield per plant in set II that exhibited the presence of complementary gene action by the estimation of skewness and the leptokurtic nature indicated that it is controlled by a few genes. The results were appropriately supported by Kiran *et al.,* (2013) for panicle length, Harshiya and Jagadeesh (2014) for spikelet fertility, Manjappa *et al.,* (2014) found positively skewed distribution for grain yield plant per plant and tiller number, Lestari *et al.,* (2015) for panicle weight, Savitha *et al.,* (2015) and Nikhitha *et al*., (2020) for the number of productive tillers per plant, panicle length and Govintharaj *et al.,* (2017) for number of grains.

The presence of gene interactions is represented by a positive value of kurtosis while it is negative or close to zero in the absence of gene interaction (Kotch *et al.,* 1992). Negatively skewed and platykurtic frequency distribution was observed for spikelet fertility and grain width in the set I and for panicle length, grain width and L/B ratio in set II. It is also supported by Kiran *et al.,* (2013) who noticed duplicate interaction for panicle length, Harshiya and Jagadeesh (2014) for panicle length, grain yield per plant, grain length, grain breadth, length to breadth ratio, Manjappa *et al.,* (2014) found negatively skewed distribution for plant height, days to flowering, days to maturity, panicle length, panicle exertion, test weight and spikelet fertility, Lestari *et al.,* (2015) reported that the panicle length and weight. Savitha *et al.,* (2015) found platykurtic with left-skewed distribution for days to 50 per cent flowering, plant height, number of productive tillers per plant, panicle length, hundred-grain weight and single plant yield. Vijaya and Shailaja (2016) reported platykurtic and negatively skewed distribution for plant height, Rani *et al.,* (2016) recorded for test weight, grain length and grain breadth.

Negative skewness and leptokurtic frequency distribution were found for panicle length and grain length in set I and for grain length in set II. Similar results were supported by Kiran *et al.,* (2013) for plant height, Savitha *et al.,* (2015) for the number of productive tillers per plant, panicle length and Sushma Lilly *et al.,* (2018) for L/B ratio. The frequency curve depicting negative skewness is associated with duplicate (additive x additive) gene interactions and it is controlled by many genes or by few genes indicating platykurtic or leptokurtic nature respectively. Normal curve without skewness indicating symmetry of the trait and platykurtic frequency distribution was observed for L/B ratio in set I and for 100 seed weight in set II. A similar result was reported by Kiran *et al.,* (2013) for test weight indicating complete ambi-directional epistasis.

Table 1: Estimates of skewness and kurtosis for different characters under study in F_7 generation of the cross Pusa-1176 and BPT-5204 for both sets

Sl. No.	Characters	Mean		Skewness		Kurtosis	
		Set I	Set II	Set I	Set II	Set I	Set II
1	Days to Flowering	89.40	87.77	0.69	0.75	1.40	0.18
2	Number of Tillers	11.02	21.59	0.87	0.67	1.02	0.49
3	Plant Height	93.78	77.76	1.09	0.68	4.86	1.36
4	Panicle Length	23.66	22.01	-0.13	-0.20	1.18	0.54
5	Panicle Number	9.76	18.4	0.82	0.90	0.92	0.95
6	Number of Filled Spikelets	69.72	36.27	0.84	1.19	1.12	1.28
7	Number of Unfilled Spikelets	58.63	80.86	0.77	0.76	0.23	1.31
8	Spikelet Fertility	54.77	30.89	-0.13	0.56	-1.12	-0.92
9	Grain Length	0.90	0.89	-0.25	-0.92	1.19	3.11
10	Grain Width	0.28	0.28	-0.01	-0.12	-0.49	-0.14
11	L/B Ratio	3.23	3.14	0.00	-0.11	0.06	0.47
12	100 Seed Weight	1.74	1.82	0.24	0.02	0.66	-0.27
13	Grain Yield per plant	12.83	10.37	0.24	3.40	0.66	16.88

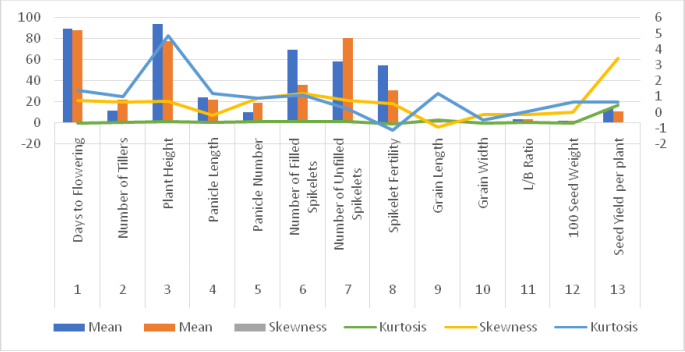


Figure 1: Graphical representation of the estimates of skewness and kurtosis

Conclusion

To increase the efficiency of selection in breeding programs among large populations, breeders should have adequate knowledge of the prevailing amount of gene interaction and the number of genes governing the trait. The results indicated that mild selection would be sufficient for improvement in the characters number of panicles, number of unfilled spikelets, 100 seed weight and seed yield per plant in the set I and for days to flowering, number of tillers, number of panicles and spikelet fertility in set II whereas stringent selection might be deployed for trait improvement in panicle length and grain length in set I and only for grain length in set II. Therefore, it is concluded from the study that progress in improving the performance of genotypes would be higher under complementary gene interaction as compared to duplicate gene interaction.

References

Choo TM and Reinbergs E.1982. Analysis of skewness and kurtosis for detecting gene interaction in a double haploid population. *Crop Science*, 22(2): 231-235.

FAO (Food and Agricultural Organisation of the United Nations) (2022). World: Rice, Paddy Production Quantity [2021-12-24]. https://knoema.com/atlas/world/topics/Agriculture/Crops-Production-Quantity-tonnes / Rice-paddy-production.

Fisher RA, Immer FR and Tedin O.1932. The genetical interpretation of statistics of the third-degree in the study of quantitative inheritance. *Genetics*, 17(2): 107-124.

Govintharaj P, Tannidi S, Swaminathan M, Sabariappan Nachimuthu VV, Gunasekaran K and Aravindhan B. 2017. Genetic Variability for Yield and Yield Components Characters in Bacterial Blight and Blast Resistance Genes Introgressed Backcross Populations in Rice. *International Journal of Current Microbiology and Applied Sciences*, 6(2): 100-103.

Harshiya B and Jagadeesh BN. 2014. Genetic analysis of skewness and Kurtosis for yield and its parameters,

total grain protein, macro and micronutrients in F_7 generation of rice (*Oryza sativa* L.). *Environment and Ecology*, 32(1A): 381-385.

Kapur SK. 1981. Elements of Practical Statistics. *Oxford and IBH Publishing Co, New Delhi*, pp. 148-154.

Kiran KK, Rao GMR and Suresh K. 2013. Variability and frequency distribution studies in F_2 population of two crosses of rice (*Oryza Sativa* L.). *Asian Journal of Bio Science*, 8(2): 153-159.

Kiran KK. 2012. Genetic variability for grain yield, its components and inheritance of resistance to BPH in two F_2 populations of rice (*Oryza sativa* L.). *M. Sc. (Agri.) Thesis,* University of Agricultural Sciences, Bangalore.

Kotch GP, Ortiz R and Ross WM. 1992. Genetic analysis by use of potato haploid populations. *Genome*, 35(1): 103-108.

Lestari P, Angelita, Suwano, Trikoesoemaningtyas, Sopandie, Aswidinnoor D and Hajria l. 2015. Panicle Length and Weight Performance of F_3 Population from Local and Introduction Hybridization of Rice Varieties. *Hayati Journal of Biosciences*, 22(2): 87-92.

Manjappa G, Uday and Hittalmani S. 2014. Identification of drought tolerant and high yielding F_2 genotypes of rice under aerobic condition. *Oryza*, 51(4): 273-278.

Nikhitha TC, Pushpam R, Raveendran M and Manonmani S. 2020. Genetic variability and frequency distribution studies in F_2 population involving traditional variety mappillai samba. *Electronic Journal of Plant Breeding*, 11(3): 933-938.

Prisca Seeli FD, Manonmani S, Pushpam R and Raveendran M. 2021. Parent progeny regression analysis in segregating generations of drought QTLs pyramided rice lines (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 12(4): 1178-1188.

Raghavendra P and HittalmaniS. 2015. Genetic Parameters of Two BC_2 F_1 Populations for Development of Superior Male Sterile Lines Pertaining to Morpho-Floral Traits for Aerobic Rice (*Oryza sativa* L.) *SAARC Journal of Agriculture*, 13(2): 198-213.

Rani CS, Ananda kumar CR, Raveendran M, Subramanian KS and Robin S. 2016. Genetic variability studies and multivariate analysis in F_2 segregating populations involving medicinal rice (*Oryza sativa* L.) cultivar Kavuni. *International Journal of Agricultural Sciences*, 8(15): 1733-1735.

Ricepedia, *http://ricepedia. org/rice-as-food/*, accessed on 15 June 2020.

Robson DS. 1956. Application of K4 statistics to genetic variance component analysis. *Biometrics*, 12(4): 433- 444.

Roy D. 2000. Plant Breeding - The Analysis and Exploitation of Variability. Narosa Publishing House, New Delhi, India.

Savitha P and Kumari RU. 2015. Studies on skewness, kurtosis and parent progeny regression for yield and its related traits in segregating generations of rice. *Oryza*, 52(2): 80-86.

Sheshaiah BM, Kumar D, Gangaprasad S, Gowda TH, Hosagoudar GN and Shashidhar HE. 2018. Studies on Variability and Frequency Distribution of Yield and Yield Related Traits in F_2 Population of Rice (*Oryza sativa* L.). *International Journal of Current Microbiology and Applied Sciences,* 7(09): 2048-2052.

Sushma Lilly M, Sassikumar Dand Suresh R. 2018. Variability and Heritability Analysis for Yield and Grain Quality Attributes in F_2 Intervarietal Populations of Rice. *International Journal of Current Microbiology and Applied Sciences*, 7(07): 4329-4338.

Vijaya I and Shailaja H. 2016. Assessment of genetic parameters for yield and its related traits in F_2 population of KRH-4 hybrid rice (*Oryza sativa* L.). *International Journal of Agricultural Sciences and Research*, 6(3): 87-96.

RESEARCH ARTICLE https://doi.org/10.58297/ZDXH1349

Economic Worth Assessment of Implementing Baler Technology for the Management of Paddy Straw

Sharma A[1], Mavi HK[2*] and Brar AS[3]

[1]Department of Farm Machinery and Power Engineering, Punjab Agricultural University, Ludhiana;
[2]Department of Economics and Sociology, Punjab Agricultural University, Ludhiana; and
[3]Krishi Vigyan Kendra, Moga, Punjab

*Corresponding author Email: mavihk05@pau.edu

Received: 2nd August, 2024; Accepted: 15th October, 2024

Abstract

Mechanical collection of paddy straw with the help of the baler technology from the combine harvested paddy fields is a prevalent paddy straw management technique in the country. Baler technology manages the paddy straw by collecting it with the rectangular baler, rake and stubble shaver machines and preventing the on-farm paddy straw from burning. Finding the financial constraints for creating a tailored recruiting system for technology implementation at the field level in paddy straw management was one of the main goals of this study. The economic worth assessment showed that the total operating cost for systems I and II was estimated as ₹ 4285.74 and 2374.34 per hour and the net benefit was ₹ 998.09 and 991.16 per hour. The benefit-cost ratio of the system I and II of baler technology was found to be 1.23 and 1.42 and the break-even usage of the baler technology was assessed at 154.66 and 109.65 hours per year of machine operation, which is less than the machine's useful life used under baler technology implementation. Hence, machine owners, local service providers (LSPs) and forward-thinking farmers can seize this opportunity as a highly lucrative endeavour. Steering clear of on-farm burning of paddy straw is a crucial step toward reducing environmental pollution, making it a worthwhile contribution to environmental conservation.

Keywords: Baler, Break-Even Point, Burning, Cost, Paddy, Payback Period.

Introduction

Globally, India has the largest area (44.6M ha) under paddy and is second only to China in paddy production. Paddy constitutes 52 per cent of food grain production and 55 per cent of total cereal production (Hira *et al.,* 2015). Paddy-wheat cultivation is a common farming exercise in northern Indian region. India produces 117 Mt paddy per year and such a vast amount generates 185-200 Mt paddy straw. Twenty-five per cent of Asia's total paddy straw production comes from India (Bhuvaneshwari *et al.,* 2019). The states of Haryana and Punjab are recognized as India›s "food bowl" because they contain a highly fertile paddy-wheat area on the Indo-Gangetic plain. Only in Punjab are paddy and wheat cultivated in more than three and 3.5 million hectares of land, with about 22 million tonnes of paddy residue per year (Mander, 2018).

Residues from paddy crops consist of biomass remaining in the field following grain harvesting and other valuable elements. As a byproduct of harvesting rice, paddy straw is created. Irrespective of whether it was harvested manually or by machinery, it is taken out during harvest with the rice grains and then stacked up or scattered across the field. As labour

costs rise and rice production intensifies in Asia, combine harvesters are becoming more common in rice fields during harvest season. However, the loose rice straw left behind by these machines complicates the collection and transportation process, resulting in increased expenses and time requirements. Asia annually generates between 600 to 800 million tons of rice straw, with global production nearing 1 billion tons each year (Sarkar and Aikat, 2013; McLaughlin *et al*., 2016). Farmers chose to burn rice straw as a fast fix to swiftly eliminate the biomass and get the field ready for the forthcoming crop since they are unaware of the straw's other uses. Burning rice straw in the field poses risks to both human health and the environment, leading to increased greenhouse gas emissions. For every kilogram of dry rice straw burned, emissions of 0.7 to 4.1 grams of CH_4 and 0.019 to 0.057 grams of N_2O occur, along with additional gaseous pollutants such as SO2 and NOx. Additionally, though to a lesser extent, the burning process also releases dioxins and furans (Oanh *et al*., 2011; Jenkins *et al*., 2003). Burning rice straw serves as a crucial origin of aerosol particles, impacting both local air quality and the Earth's radiation balance (Engling *et al.*, 2009). These particles include small dust particles ($PM_{2.5}$) and coarse dusty particles (PM_{10}) (Chang *et al.,* 2013). Furthermore, biomass loses its potential energy content (Tabil *et al*., 2011). Ozone levels in the lower atmosphere are also raised by burning agricultural crop residue (Kumar *et al*., 2015). Burning agricultural leftovers raised soil temperatures to 33.8-42.2 °C to a depth of 1 cm, as Gupta *et al*., (2004) reported. This has an impact on soil ecology. Thus, due to the increased soil temperature, the favourable microbial population in the soil decreases to a depth of 2.5 cm and around 23-73% of the nitrogen in different kinds is taken from the soil. The burning of residue raises the soil's temperature considerably, which causes the upper three inches of the soil's carbon-nitrogen (C-N) balance to shift quickly. Nitrogen transforms into nitrate, while carbon is emitted into the environment as CO_2. Approximately 824 thousand metric tons of nutrients-nitrogen, potassium and phosphorus-are lost from the soil due to this process (Gupta *et al.*, 2004). Two more approaches to controlling paddy straw are baling the straw and integrating it into the field, in addition to infield burning (Singh *et al.,* 2005).

Rice straw management and collecting continue to be challenging tasks. In the past, several methods have been experimented with for collecting and managing rice straw. These include field cubers, stack wagons, buck rakes, standard three-wire balers, traditional large roll balers and high-flotation big roll balers, were documented by Dobie *et al*., (1977). Dobie concluded that, for a 16 km haul distance, the most economical system to be provided would be a 1.2 m comprehensive extended roll baler system. Though he had yet to test a big rectangular baler, Dobie (1980) also suggested that a substantial rectangular bale system would be more promising than the massive roll bale system. Rice straws should be gathered and used to provide electricity or be subject to alternative management alternatives for financial and environmental reasons. For individuals looking to develop a cost-effective structure using sustainable materials, straw bale construction may be one of the greatest options (Bhattarai *et al*., 2012).

A big rectangular baler for gathering rice straw was tested by Jenkins *et al.,* (1985). The performance of balers was contrasted with that of alternative handling methods and large roll balers. Economically speaking, large bale systems are preferable to tiny, rectangular bale systems. Big rectangular bales worked well for transportation, but they needed to be stored under cover to prevent spoiling. Large roll bales may be stored outside without losing much dry matter, although they were less popular for long-distance transportation. Straw delivery costs vary depending on the kind of packaging, distance

travelled, necessary processing steps and method of use. Timely use of the field for following planting, collecting and baling paddy straw in the combined harvested field is a suitable and financially feasible solution (Tathod *et al*., 2015). The economic and environmental performance of straw baler (Model 338 make: John Deere), for the collection of paddy straw generated after mechanical harvesting by combine harvester was determined by Pal *et al.,* (2019). Straw baler facilitated the collection of paddy straw of 4.36 tons/ha at a cost of just ₹1650. Nghi *et al*., (2015) conducted experiments which revealed an internal rate of return of 38%, a payback period of 2.1 years and a baling cost of US$ 19.0 per ton of rice straw. Along with the baling fee, the transportation cost ranges from US$24 for a 100-kilometer journey to US$32 for a 150-kilometer distance. In 2013, Shafie *et al.,* undertook a logistic cost analysis focusing on rice-straw-based power generation in Malaysia. They developed mathematical logistic models to assess the collection, storage and transportation costs associated with this form of power generation. The ideal quantity of storage facilities and the location of the power plant were determined using the optimization approach. According to the results, the transportation expenses for conveying rice straws to collection centres primarily stemmed from the influence of truck capacity, constituting 89.9% of the total expenditure in transportation. Transportation costs were also the highest, accounting for 54% to 63% of the overall logistic costs. The number of storage facilities might be decreased to lower the cost of transportation.

The baler has been introduced in India to recover straw from the combined harvested paddy field. Baler machine owners have the option to utilize their equipment on their own land and also generate revenue by offering custom hiring services to fellow farmers. Sharma and Chandel (2016) assess a baler's performance on loose paddy straw (system A) after the use of a stubble shaver (system B) and following the use of a rake in addition to the stubble shaver (system C). When the feed rate of paddy straw rose from 1.12 to 4.22 tonne per hour, the number of bales per hectare and density of bales also increased. The maximum feed rate was seen when the stubble shaver and rake were used before the baler (system C). Systems A, B and C had field capacities of 0.35, 0.40 and 0.53 ha per hour and ranged in the number of bales per ha from 266-292, 298-332 and 126-149, respectively. For systems A, B and C, the corresponding mean fuel consumption was 5.0, 10.0 and 12.0 litre per hour. System C had a more significant mean per centage increase in bale density, quantity of bales and baler productivity than did systems A and B. System C had the highest benefit-cost ratio at 1.16:1, while systems B and A had the highest ratios at 1.06:1 and 0.85:1, respectively. With systems B and C, the net savings per hectare were Rs. 471.05 and 1537.59, respectively. The economic and practical effectiveness of a straw baler in a combine-harvested rice field is assessed by Singh *et al.*, (2005). In the paddy field harvested by a combine, the baler's field capacity was 0.26 ha per hour; however, in the field where the stubble shaver was used before baling, it was 0.36 ha per hour. Bales ranged in size from 800×450×450 to 900×450×450 mm and correspondingly, their weight varied between 18 and 28 kg. In combine-harvested paddy fields, 205 bales were made; in stubble-shaved paddy fields, 425 bales were formed. The straw baler's economic analysis showed that baling in fields with stubble shaved fields costs Rs. 2276 per hectare, while transporting the bales costs Rs. 4400 per hectare. Baling in stubble-shaved fields costs Rs. 6676 per hectare, including bale transportation. The machine's extremely high shipping cost is the single factor keeping it from becoming more widely used. Straw sales brought in a total of Rs. 5865

per hectare. According to Mangaraj & Kulkarni's (2011) research, the cost of making a single twine-tied bale for wheat and paddy was ₹ 5.00 and ₹ 2.75, respectively. The net income from collecting and baling straw using the machine was ₹ 607.00 per hectare for rice straw and, ₹ 235.00 per hectare for wheat straw, assuming nominal prices of ₹ 0.25 kg^{-1} for paddy straw and ₹ 0.75 kg^{-1} for wheat straw. Not all of the villages in the area have had access to baler technology yet. Baler technology service providers, or new entrepreneurs, may get started and have a great potential to offer this service to end users nearly all year round. For this purpose, from the owner or custom operator's point of view, the economic worth assessment of baler technology is a dire need. Therefore, determining critical indicators related to the economic worth assessment of baler technology used by the service providers/progressive farmers to manage (collect) paddy straw is the need of the hour. So, the present study assessed the economic worth of baler technology implemented for managing paddy straw by its mechanical collection.

Materials and Methods

Data collection

The study was conducted in the district Moga of Punjab in India. Moga district is located in the central zone of the state, having a plain geographical area of 2230 sq. km., which comes to 4.42 per cent of Punjab state. It stretches between 75 degrees 15'E and 75 degrees 25' E longitude and 30 degrees 35' N and 31 degrees 15' N latitude. Farmers in the Moga district primarily rotate their crops using paddy wheat. The district of Moga is expected to have 195,237 hectares of total agricultural land, of which 176,000 hectares (91.27%) are under rice cultivation and 175,000 hectares (89.63%) are under wheat crop cultivation. In this study, secondary data were gathered from a variety of sources. Studies journals, published studies, progressive farmers and machine owners/ operators served as the primary sources of data. Using an information panel, several crucial operational data were gathered from primary sources and research on baler technology.

Baler technology

The baling process, a common automated technique for gathering hay, straw and other fibrous materials through densification, uses baler technology. This process effectively facilitates the removal of materials from the field, simplifies the transportation and manipulation of bales, addresses shortages and provides flexibility in storage options. (Van-Hung *et al*., 2016; Guerrieri *et al*., 2019; Lemos *et al*., 2014). This mechanical process of collecting straw is performed with the help of tractor-operated machinery. It requires three tractor-driven machines: a stubble shaver for cutting, a rake for lining and gathering and a baler for making bales.

Stubble shaver

Paddy stubble was trimmed with a stubble shaver when it was standing. The machine operates in 2nd low gear, maintaining engine rpm between 1500 and 1700, which can vary depending on the load of paddy straw. It features two blades mounted on a vertical shaft, enclosed within a frame on the top and all four sides. Through a gearbox, a tractor's PTO (power take-off) shaft rotates the shaft.

Rake

Following the stubble shaver's operation, leftover straw can be gathered in a small breadth with a tractor-driven rake equipment that needs between 40 and 50 horsepower (hp) of power. The rotating rake has a working width of 3.5 meters and a transport width of 1.5 meters. It weighs between 350 and 450 kg. The rake's job is to gather loose and chopped paddy straw from the field and create a windrow in the smaller area so that the baler machine has thick straw to work with.

Adjusting to the load of paddy straw, this machine is frequently operated in third low gear, maintaining engine RPMs between 1500 and 1700.

Straw Baler

In the present study, a rectangular baler was considered which picks up a pre-cut crop from a windrow and feeds it into the bale chamber, where it is cut again, compacted, tied and discharged out the back of the machine. It has the ability to regulate the bale density and level of compaction. The machine also has a measuring system for changing the bale length. The hypoid gear, which had spiral interactions between the crown wheel and pinions, served as the baler's main drive (**Figure 1**). This had the benefit of having a larger gear tooth contact area than with conventional gear meshing, which increased longevity and consistent power flow (Sharma and Chandel, 2016). In order to ensure smooth operation of the baler, a broad flywheel was installed in front of the transmission system to absorb the stresses of the ram. Depending on the amount of paddy straw, the baler was run in 2nd low gear in the current investigation, with engine rpm ranging from 1500 to 1800.

Mechanical operation of bale formation

Initially, the stubble shaver machine is employed to harvest the stubbles, left in the field subsequent to combine harvesting of the paddy, from the base level. Subsequently, the lining operation is executed by the rake machine, followed by the gathering and formation of rectangular bales by the baler. It automatically picks up the straw from the field with the help of a reel and transfers it into the bale chamber with the help of a feeder and then the straw is compressed with the reciprocating ram. Straw baler made highly compressed, firm and perfectly shaped bales (**Figure 1**), reducing the storage space (Sharma *et al*., 2014). All these machines are commercially available and can be operated by the 40-50 hp tractor.

Figure 1: Operational view of rake and baler machine

Economic assessment of baler technology for managing paddy straw

The economic assessment of agricultural systems is necessary to understand peasant practices and create and disseminate innovative systems. Agricultural machinery costs assessment is critical when considering structural or technological changes. Because the advantages and costs of machinery investments in agriculture accumulate over a number of years, it is more complicated than dealing with yearly monetary inputs like seed or fertilizer. A stream of cash inflows and outflows is connected to every machine action. In this study, the economic evaluation of baler technology for managing paddy straw was conducted from the perspective of the machine owner. At the field level, two systems of using baler technology were generally used: System I and System II. In system I, the machine owner is taking rent in Indian Rupees (₹) from farmers for operating stubble shaver, rake and baler machine on farmer's field for making bales and cleaning the field

by collecting them. After collection machine owner sold the bales to the biomass power generation plant (situated under a radius of 35 kilometers) @ ₹ 1300 per ton. On the other hand, in system II, the machine owner operates only the rake and baler machine at the farmer's field, as the farmers operate the stubble shaver (**Figure 2**). The farmer retains the bales made by the baler machine and gives the rental charges @ ₹ 6350 per ha to the machine owner. System I involve the twine and transportation cost (**Figure 3**) @ ₹ 185 per kg and ₹ 450 per tonne, but system II does not involve the transportation cost as the farmers retain the bales. The actual field capacity of the machines was calculated by recording the actual area covered by the machine in the total actual time taken. Fuel consumption was determined by measuring the amount of fuel that was added to the tank both before and after use (Malik *et al.,* 2017).

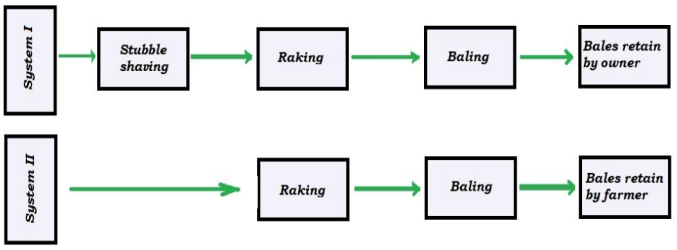


Figure 2: Flow diagram of use of baler technology in system I and II

Figure 3: View of transportation of bales formed by baler

There are many different definitions, each with its pros and cons, of the various economic criteria that must be considered. Therefore, it becomes essential to adopt precise definitions for the various economic terms used and clearly lay down the conventions of calculating them. The three assumptions used for the present study are:

1. The tractor is already available with the owner.
2. Throughout the project's duration, all of the equipment are paid for with cash and the operating technology is unchanging.
3. All inputs, outputs prices and conversion rates remain the same throughout the study period.

The complete cost of baler technology at the field level is comprised (Rahman *et al*., 2013) of fixed and variable costs. Fixed costs include depreciation, interest on investment, shelter expenses, taxes, insurance and housing costs, among others. Variable costs encompass fuel expenses, lubricants, operator salaries, labour costs, repairs and maintenance.

Fixed Cost (FC)

A *fixed cost* pertains to a resource with a definite quantity that does not vary when the output level does. Since the average yearly cost of the equipment is frequently the only factor to be considered, the straight-line technique, which is the easiest to calculate depreciation, is commonly employed in budgeting (Barnard and Nix, 1980). Consequently, straight-line depreciation is presumed in the computation of fixed cost and the yearly depreciation was determined using the following formula:

$$D = \frac{P\text{-}S}{L}$$

where,

D : depreciation, ₹ per yr

P : machine purchase price, ₹

S : machine salvage value, ₹

L : machine life in years, yr.

The fixed cost estimate considers the interest in purchasing a baler technology. Since the investment funds cannot be utilized for other interest-paying businesses, a charge is applied even if they are not

borrowed. There is a 12% interest rate. The investment interest was computed using the following formula:

where, i : interest rate, decimal.

Variable cost (VC)

Variable costs are those that vary with changes in production level. Hourly labour, gasoline, oil, repair and maintenance expenses and hours needed for each field activity affect variable costs. The labour rate of ₹/h was used to compute the cost of labour for the operator. The consumption rate was used to determine the expenses of gasoline and oil, which were subsequently multiplied by the prices for each.

Operating cost (OC)

There were two categories of annual operating costs for the machinery employed in this study: fixed and variable. Following converting the computed fixed and variable costs into ₹/ha (Rs/h), the total of the fixed and variable costs was supplied OC in ₹/ha (₹/h). Following is the computation of the OC:

OC, ₹/ha = Fixed cost +Variable cost

Break Even Point (BEP)

Many farmers want assistance selecting or purchasing all the equipment needed for farming. This is frequently due to a need for more resources, labour, tiny land holdings, or other factors. These farmers get the necessary machinery services for their farms by employing bespoke services. Compare the fixed and variable costs of owning and running the machinery to the overall expenses of bespoke service to determine if owning or engaging a client operator is more cost-effective. The break-even point (Gutierrez and Dalsted, 2020) is found faster and more accurately with the following formula:

where,

F: Annual fixed costs

V: Variable costs per unit of operation

R: Custom hiring charge/rent per unit

Payback period

The time frame whereby revenues can offset the costs of the investment is referred to as the payback. Stated differently, it is the amount of time needed for the cash flow generated by an investment to match the initial outlay made. The desirability of an investment is directly related to its payback period. Shorter paybacks mean more attractive investments (Mohammad *et al.*, 2019). This can be computed by applying the following formula:

Benefit-cost ratio (BCR)

The present value of the benefit stream divided by the present value of the expense stream is known as the benefit-cost ratio. In theory, the benefit-cost analysis approach is straightforward. Equation following provides it and it follows the methodical process of choosing amongst economic investment options (Guttinger, 1994):

A BCR greater than one indicates a profitable investment. To avoid duplicate accounting, depreciation and investment interest are not included in the costs. Including the investment cost accounts for depreciation, while the discount factor accounts for the interest of investment.

Utility index

It is an exact representation of the hours of labour machine interaction. The operation cost and the non-operating hours reduce as the utility index rises. This ultimately leads to a net gain in the overall electricity that may be used for agricultural tasks. One may compute the utility index (K) as follows:

Results and Discussions

For an entrepreneur, custom operator, or progressive farmer, the business of collecting paddy straw using baler technology and providing custom hiring services is a cyclical venture that takes place during the combine harvesting of rice crops. The total cost

of baler technology operations at the farm level comprises variable and fixed costs. Depreciation of the machine was calculated using the straight-line method and taken as a fixed cost. The findings indicated that investing in baler technology proved to be profitable for entrepreneurs. The subsequent section outlines the significant cost and return elements associated with operating a baler technology business in custom hire entrepreneurship:

Economic analysis

The economic analysis of using the baler technology and various assumption made during the analysis for both systems is given in **Table 1**. The financial analysis was calculated from the perspective of the machine owner, who may be a progressive farmer or a custom hired operator. Based on field data, the baler technology total operating cost for the system I and II were estimated as ₹ 4285.74 per hour and ₹ 2374.34 per hour. The actual field capacity of the baler, rake and stubble shaver machine was 0.53, 0.79 and 0.51 ha per hour having fuel consumption of 6.6, 4.8 and 4.25 per hour respectively. Fixed and variable cost for the machine operation were calculated as ₹ 629.2 and 3656.54 per hour for system I and 609.4 and 1764.94 per hour for system II based on the average field data collected through personal interviews of custom-hire service providers. The amount of twine used was 6.35 kg per ha costing ₹ 622.62 per hour. In case of system I, the transportation cost including loading the bales on the trolley and transport to the buying point (biomass power plant) was 1514.48 ₹ per hour. In operating the baler machine for system I, the total per hour operating cost was estimated as ₹ 3313.39, which includes a total fixed cost of ₹ 484, total variable cost of ₹ 866.54 and twine cost of ₹ 622.62 and transportation cost of ₹ 1514.48 respectively. This showed that the bale transportation cost (from the collection point to the selling point) was the major contributor (45.70%) in the baling system I, followed by the variable, twine and fixed costs. In system II, however, the bale transportation cost was not included as the farmers kept the bales. The total per-hour operating cost for operating the baler machine in system II was ₹ 1798.91, which includes the maximum contribution (38.48%) from variable cost followed by twine and fixed cost. The total per hour operating cost was computed as ₹ 575.43 for both the system and the major contributor of cost (78.21%) in operating the rake machine was variable cost followed by fixed cost. The total per-hour operating cost of the stubble shaver machine (for system I only) was ₹ 396.93 and the significant contribution (95.01%) was from variable cost followed by the fixed cost. The various itemized cost per hour for both systems were analysed and presented (**Figures 4 and 5**).

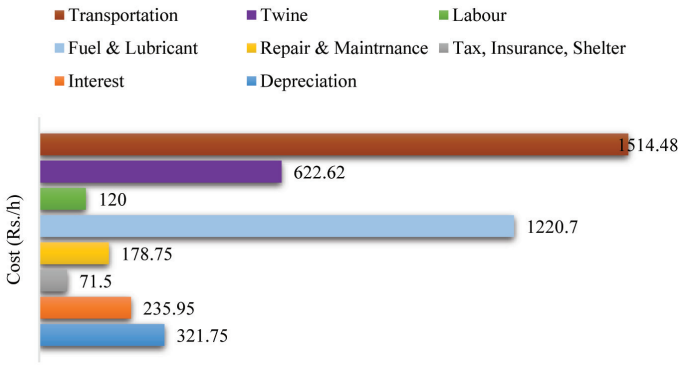


Figure. 4: Itemized cost per hour of operation for system I

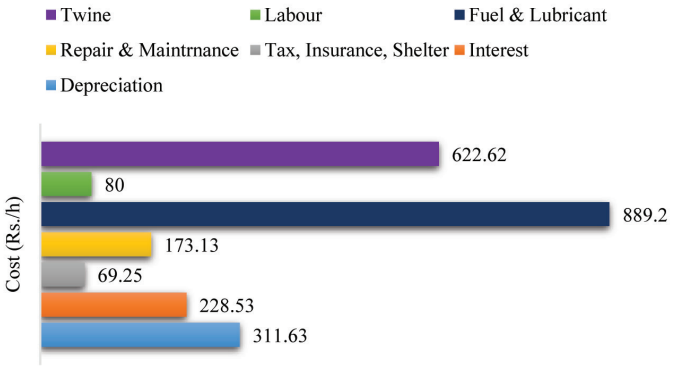


Figure 5: Itemized cost per hour of operation for system II

Table 1 Economic analysis of system I and II

System I: Operator retaining the bales and selling to power plants				System II: Farmer retaining the bales		
Particulars	**Assumption**	**Baler**	**Rake**	**Stubble shaver**	**Baler**	**Rake**
Purchase price, ₹	P	1100000	285000	450000	1100000	285000
Salvage (S), ₹	10% of P	110000	28500	4500	110000	28500
Life, yr	-	10	10	10	10	10
Economic life, h	-	400	400	400	400	400
Depreciation, ₹/yr	-	99000	25650	4050	99000	25650
Interest cost, ₹/yr	Rate of interest, 12%	72600	18810	2970	72600	18810
Tax, insurance, shelter, ₹/yr	2% of P	22000	5700	900	22000	5700
Fixed Cost, ₹/yr (₹/h)	-	193600	50160	7920	193600	50160
Total fixed cost (FC), ₹/yr (₹/h)	-	251680 (629.2)			243760 (609.4)	
Repair & maintenance, ₹/h	5% of P/Avg/yr	137.5	35.63	5.63	137.5	35.63
Fuel cost, ₹/h	@ ₹ 87/litre	574.2	399.18	369.75	574.2	399.18
Lubrication cost, ₹/h	20% of Fuel Cost	114.84	79.836	73.95	114.84	79.836
Labour Cost, ₹/h	-	40	40	40	40	40
Variable cost (VC), ₹/h	-	866.54	554.646	489.33	866.54	554.646
Twine cost, ₹/h (Twine used 6.35 kg/ha)	₹ 185/kg	622.62	-	-	622.62	-
Transportation cost, ₹/h	₹ 4.5/ton	1514.48	-	-	-	-
Operating cost (OC), (₹/h)		3313.39	575.43	396.93	1798.91	575.43
Total operating cost, ₹/h	-	4285.74			2374.34	

Economic worth assessment

The details of all economic parameters for assessing the economic worth of implementing baler technology were presented (**Table 2**). The rental charges for using baler technology by a customer operator is ₹ 1346.2 per hour for the system I and 3365.5 per hour for system II. The net benefit comes out to be ₹ 998.09 and 991.16 per hour (**Table 2**) for the system I and II. Considering 150 hours of annual use of baler technology according to the custom operators the net annual benefit or revenue was observed to be ₹ 399237 and 396463 for the system I and II.

After a detailed economic analysis of systems I and II, it has been observed that the net benefits per ha were ₹ 1883.19 and 1870.11, which showed that the net benefit was almost at par for both systems. Therefore, both systems followed by the machine owner or baling service provider gave at-par financial benefits. Therefore, if a new entrepreneur or progressive farmer wants to start a new venture of collecting and selling paddy straw, they can choose systems I and II. Considering the capital cost involved in the purchase of baler technology for both the systems and the assumption made for economic analysis in this study, the break-even point comes out to be 81.97 ha or 154.66 ha per year and 80.72 ha 152.23 hours per year for the system I and System II (**Figures 6 and 7**). In contrast, the actual use of baler technology is approximately 400 hours per year by the custom operator. Considering the actual annual use of baler technology, the custom operator or progressive farmer shall be able to recover his cost in 3.58 and 3.49 years (payback period). Mangaraj and Kulkarni (2011) have reported a payback period of 5 years while studying the techno-economic perspectives of baler machines. Both systems are profitable from the viewpoint of custom operators. The payback period of both the systems is

less than the life (10 years) of the baler technology machinery and also, the benefit-cost ratio for both systems I and II are found to be 1.23 and 1.42, which is greater (>) than unity. Pal *et al*., (2019) reported a benefit-cost ratio 1.39 for collecting paddy straw with a baler machine after harvesting paddy crops with a combine harvester. So implementing baler technology for managing paddy straw by its collection, is an acceptable venture from the business point of view. The utility indexes obtained were 2.58 and 3.64 for system I and II which are greater than unity. This indicates efficient utilization of baler technology.

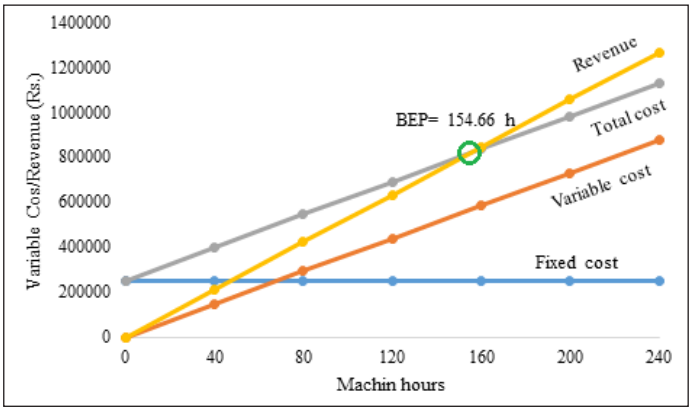


Figure 6: Economic use of baler technology for system I

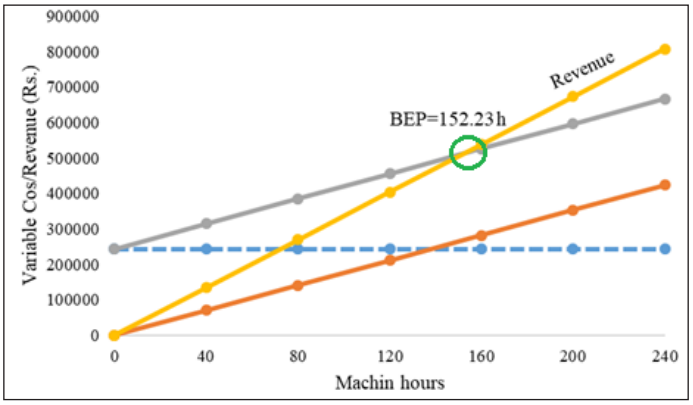


Figure 7: Economic use of baler technology for system II

Table 2: Baler technology economic worth assessment

System I: Operator retaining the bales and selling to power plants			System II: Farmer retaining the bales	
Items	**Value**	**Remarks**	**Value**	**Remarks**
Actual field capacity, ha/h	0.53	Field capacity of straw baler after operation of rake	0.53	Field capacity of straw baler after operation of rake
Rental revenue, ₹/ha (₹/h)	2540 (1346.2)	Rent for cleaning the field by making and collecting bales	6350 (3365.5)	Rent of making bales only
Straw collected, ton/ha	6.32	Average amount of straw collected from one ha	-	-
Revenue form straw sale, ₹/ha (₹/h)	8255 (4375.15)	Sold at the rate of ₹ 130 per quintal	-	-
Revenue after moisture cut, ₹/ha (₹/h)	7429.5 (3937.64)	10% moisture cut generally applied by buyer	-	-
Total revenue, ₹/ha (₹/h)	9969.5 (5283.84)	-	6350 (3365.5)	-
Net Benefit, ₹/ha (₹/h)	1883.19 (998.09)	-	1870.11 (991.16)	-
Annual Benefit (₹)	399237	-	396463	-
Actual Payback period (yr)	3.58	Less than economic life of machine (<6 yr)	3.49	Less than life of machine (<10 yr)
Break-even point ha/yr (h/yr))	81.97 (154.66)	More than the actual covered area	80.72 (152.23)	Less than the actual covered area
Benefit-cost ratio (BCR)	1.23	Greater than unity (>1)	1.42	Greater than unity (>1)
Utility index	2.58	Greater than unity (>1)	3.64	Greater than unity (>1)

It was observed that, although both the system of implementing baler technology is acceptable, system II is a little bit more beneficial as it is having benefit-to-cost ratio and less payback period than system I. This is due to the absence of cost involved in the operation of the stubble shaver machine and the absence of capital cost required to purchase the stubble shaver machine. In system II, farmers retain the bales, which they can sell to some other buyer at a higher price to get additional benefits or can use them for another purpose, such as the production of bioenergy and use in the packaging as a mushroom growth medium and paper industry, as natural manure (worm-compost), etc. Implementing baler technology also generates employment for the rural youth by engaging the youth in loading and unloading, transporting the bales, etc.

Limitation in Implementing Baler Technology

This study's budgeting process only permits the consideration of variables that can be measured and for which accurate estimates are available. Therefore, when employing the baler technology, the potential restrictions of the situational elements are not considered. The profit or revenue generated from using baler technology largely depends upon the sale price of the straw. If the sale price of paddy straw goes down or machine operators do not get the appropriate price, then the implementation of baler technology is considerably affected. There are also hidden costs, such as twine, labour and bales transportation costs, including using baler technology. The significant variation in these hidden costs may affect the implementation of the baler technology. The number of machinery and their high initial cost can also be hindrances in choosing the baler technology. The sole thing contributing to rising expenses per unit is the tardiness of field operations. On the other hand, management is responsible for operations scheduling. Only until a predetermined pattern of operations - including the dates and orders of each field operation - is defined can the budgeting approach be applied. Any disruption to this pattern results in untimeliness losses. But managing each circumstance to maximize gains or prevent losses is the manager's job. Depending on the situation, an observant owner or management may alter this operation pattern. The output from the baler technology also depends upon the skill of the machine operator. While operating the straw collection machinery, an unskilled operator can cause damage to the machinery, thereby halting the collection process and ultimately resulting in revenue loss. Biomass power plant operators apply 10% of the moisture cut if the bales come to them, which is moister than the desired level, which further reduces the income from selling the straw bales. So, keeping the moisture level of paddy straw within the limit while selling to the buyer is another challenge to the machine operator/ owner to avoid an unnecessary reduction in revenue.

Therefore, it is worth mentioning that before implementing baler technology, a machine owner/ progressive farmer/custom operator must ensure where they will sell the bales or their end-use. This exercise must be done before adopting the baler technology. Further, the help of government aid, such as providing subsidies on the machinery involved in the baler technology or developing more power plants or other practical industries which can utilize the paddy straw, can enhance the decision to use baler technology by the progressive farmer or service provider. Machine custom hiring centres or societies can be developed to enhance the availability of machinery to the individual or end user. The grouping of farmers can be done so that they can buy the costly baler technology machinery collectively and can implement this technology at the village or block level to earn and avoid straw burning issues. This will enhance the economic condition of farmers/entrepreneurs/service providers along with the avoidance of the infield burning of paddy straw problems, which will safeguard the overall ecosystem.

Conclusion

According to the study, implementing baler technology for paddy straws management by straws collection is profitable. The additional benefit is that paddy straw burning (on-farm) can be avoided, which is beneficial and much needed for the environment, agriculture and living beings. The economic worth assessment showed

that the total operating cost and net benefit for systems I and II were estimated as ₹ 4285.74, 2374.34, 998.09 and 991.16 per hour for systems I and II. The benefit-cost ratio of systems I and II of baler technology was found to be 1.23 and 1.42 (greater than unity), which makes it a profitable and acceptable venture for an entrepreneur. The break-even usage of the baler technology was appraised at 154.66 and 152.23 hours per year of machine operation for systems I and II. The utility indexes obtained in system I and II were 2.58 and 3.64 which are more than unity.

The economic indicators determined in the present study indicates the efficient and beneficial baler technology venture. The owners of baler technology or progressive farmers/service providers can embrace this profitable venture and get monetary benefits while contributing to the reduction of paddy straw burning and the associated environmental pollution.

Acknowledgements

Author highly acknowledged the cooperative farmers of Moga district, Punjab, India for their sincere help in completing the work.

References

Barnard CS and Nix JS. 1980. Farm Planning and Control (2nd ed.). Cambridge University Press, Cambridge, United Kingdom.

Bhattarai P, Dhakal DR, Neupane K and Chamberlin KS. 2012. Straw bale in construction of building and its future in India, *International Journal of Modern Engineering Research,* 2(2): 422-426.

Bhuvaneshwari S, Hettiarachchi H and Meegoda J. 2019. Crop residue burning in India: policy challenges and potential solutions. *International Journal of Environmental Research and Public Health*, 16:5, 832. DOI: 10.3390/ijerph16050832.

Chang CH, Liu CC and Tseng PY. 2013. Emissions inventory for rice straw open burning in Taiwan based on burned area classification and mapping using Formosat-2 satellite imagery, *Aerosol and Air Quality Research*, 13(2): 474-487. DOI: 10.4209/aaqr.2012.06.0150.

Dobie JB, Miller GE and Parsons PS. 1977. Management of rice straw for utilization, *Transactions of the ASAE.* 20(6): 1022-1028. DOI: 10.13031/2013.35695.

Dobie JB. 1980. Collection and handling of rice straw for energy use. ASAE Paper Number PR80-036, ASAE, St. Joseph, MI 49085.

Engling G, Lee JJ, Tsai YW, Lung SCC, Chou CCK and Chan CY. 2009. Size-resolved anhydrosugar composition in smoke aerosol from controlled field burning of rice straw, *Aerosol Science and Technology*, 43(7): 662-672. DOI:10.1080/02786820902825113.

Guttinger JP. 1994. Economic Analysis of Agricultural Projects. John Hopkins University Press. Baltimore, Maryland, U.S.A.

Gutierrez PH and Dalsted NL. 2020. Break-even method of investment analysis. Available online:http://www.ext.colostate.edu/pubs/farmmgt/03759. pdf.

Guerrieri A, Anifantis AS, Santoro F and Pascuzzi S. 2019. Study of a large square baler with innovative technological systems that optimize the baling effectiveness, *Agriculture,* 9(5): 86. DOI: 10.3390/agriculture9050086.

Gupta PK, Sahai S, Singh N, Dixit CK, Singh DP, Sharma C and Garg SC. 2004. Residue burning in rice-wheat cropping system: Causes and implications. *Current Science*, 87(12): 1713-1715.

Hira GS 2015. Water management in northern states and the food security of India. *Journal of Crop Improvement*, 23(2): 136-157. DOI: 10.1080/15427520802645432.

Jenkins BM, Mehlschau JJ, Williams RB, Solomon C, Balmes J, Kleinman M and Smith N. 2003. Rice straw smoke generation system for controlled human inhalation exposures, *Aerosol Science Technology*, 37(5): 437-454, Doi:10.1080/02786820300977.

Jenkins BM, Toenjes DA, Dobie JB and Arthur JF. 1985. Performance of large balers for collecting rice straw, *Transactions of the ASAE*, 28(2): 360-363.

Kumar P, Kumar S and Joshi L. 2015. Socioeconomic and environmental implications of agricultural residue burning A Case study of Punjab, India. *Springer Open*, New Delhi. DOI:10.4209/aaqr.2013.01.0031.

Lemos SV, Denadai MS, Guerra SPS, Esperancini MST, Bueno OC and Takitane IC. 2014 Economic efficiency of two baling systems for sugarcane straw, *Industrial Crops and Products*, 55: 97-101. DOI: 10.1016/j.indcrop.2014.02.010.

Malik A, Kumar V, Sharma A and Kumar A. 2017. Performance evaluation of strip till seed drill for wheat crop, *International Journal of Scientific and Engineering Research,* 8(7): 81-100.

Mander M. 2018. Rice Straw Management is Need of the Hour. Technical Bulletin. The Tribune, Ludhiana.

Mangaraj S and Kulkarni SD. 2011. Field straw management-a techno economic perspectives, *Journal of the Institute of Engineering*, 8(1): 153-159. DOI: 10.3126/jie.v8i1-2.5107.McLaughlin O, Mawhood B, Jamieson C and Slade R. 2016. Rice straw for bioenergy: The effectiveness of policymaking and implementation in Asia. 24th European Biomass Conference and Exhibition, Amsterdam, The Netherlands. DOI: 10.5071/24thEUBCE2016-4AV.3.20

Mohammad AM, Mohammed AH, Mohammad IH, Mohammad NA, Mohammad MA, Chayan KS. 2019. Assessment of cost-benefit parameters of conservation agricultural machinery for custom hires entrepreneurship in the southern region of Bangladesh, *Agricultural Engineering International: CIGR Journal*, 21(3): 94-103.

Nghi NT, Canh ND, Hoa HD, Hung NV and Gummert M. 2015. Technical, economic and environmental evaluation on mechanical rice straw gathering method. *Journal of Environmental Science and Engineering,* B4, 614-619, DOI:10.17265/2162-5263/2015.11.006.

Oanh NT, Ly BT and Tipayarom D. 2011. Characterization of particulate matter emission from open burning of rice straw, *Atmospheric Environment*, 45(2): 493-502. DOI: 10.1016/j.atmosenv.2010.09.023.

Pal R, Kumar R, Jalal R K and Kumar A. 2019. Economic and environmental performance of straw baler for collection of rice residue generated after mechanical harvesting by combine harvester. *Current Journal of Applied Science and Technology*, 37(6): 1-6. DOI: https://doi.org/10.9734/cjast/2019/v37i630338.

Rahman A, Matifunnahar M and Monjurul Alam Md 2013. Financial management for custom hire service of tractor in Bangladesh. *International Journal of Agricultural and Biological Engineering,* 6(3):28-33. http://dx.doi.org/10.3965/j.ijabe.20130603.004

Sharma A, Bhattu BS and Singh G. 2014. Baler-A need based technology for rice straw management. *Indian Farming*, 64(8): 33-34.

Sharma A and Chandel R. 2016. Comparative field and economic evaluation of baler for baling paddy straw. *Agricultural Engineering*, 3(2016): 69 - 76.

Shafie SM, Mahlia TMI, Masjuki HH and Chong WT. 2013. Logistic cost analysis of rice straw to optimize power plant in Malaysia, *Journal of Technology Innovations in Renewable Energy*, 2: 67-75. (PDF) Logistic Cost Analysis of Rice Straw to Optimize Power Plant in Malaysia (researchgate.net) [Accessed on August 25, 2022]

Singh S, Mehta V and Sharda A. 2005. Economics of using straw baler for paddy straw management*, Journal of Research of Punjab Agricultural University*, 42(1): 78-82.

Sarkar N and Aikat K. 2013. Kinetic study of acid hydrolysis of rice straw. Hindawi Publishing Corporation. ISRN Biotechnology. https://doi.org/10.5402/2013/170615.

Tabil L, Adapa P and Kashaninejad M. 2011. Biomass feedstock pre-processing-Part 2: Densification. In "*Biofuel's Engineering Process Technology*" Marco Aurelio Dos Santos Bernardes, BoD, ISBN: 978-953-307-480-1, 439-464. DOI: 10.5772/

Tathod DV, Mahatale YV, Chavan VK and Maski, D. 2015. Energy, time and cost of baler machine for harvested understory paddy biomass. *International Journal of Innovative Trends in Engineering*, 4(1): 15-18.

Van-Hung N, Duc-Nguyen C, Van-Tran T, Duc-Hau H, Thanh-Nguyen N and Gummert M. 2016. Energy efficiency, greenhouse gas emissions and cost of rice straw collection in the Mekong river delta of Vietnam, *Field Crop Research*, 198: 16-22.

RESEARCH ARTICLE https://doi.org/10.58297/QYPT6921

Status of Bacterial Leaf Blight in Major Rice Growing Districts of Gujarat

Ajay Chaudhary[1*], Gangwar RK[2] and Thorat SS[2]

[1]Department of Plant Pathology, BACA, AAU, Anand (Gujarat) 388 110

[2]Main Rice Research Station, AAU, Nawagam, Kheda (Gujarat) 387 540

*Corresponding author Email: ajchaudhary02@gmail.com

Received: 23rd July, 2024; Accepted: 22nd September, 2024

Abstract

Rice **(***Oryza sativa* L.), a staple food for over half of the global population, plays a crucial role in meeting nutritional needs, particularly in Asia, often referred to as the world's "Rice Bowl." Bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv. *oryzae* poses a significant threat to rice production. In response to the destructive nature of the pathogen, a survey was conducted during the *kharif* 2023 in Ahmedabad, Tapi, Anand, Kheda and Navsari districts of Gujarat. The survey aimed to assess the incidence of bacterial leaf blight, providing crucial insights into the current status of the disease. Among all the surveyed districts highest per centage incidence (49.54%) of bacterial leaf blight was observed in Kheda followed by Tapi (48.73%), Ahmedabad (46.53%), Navsari (12.74%) and the lowest incidence per centage was recorded in Anand (22.57%).

Keywords: Bacterial leaf blight, rice, survey, *Xanthomonas oryzae pv. oryzae*

Introduction

Rice **(***Oryza sativa* L.) belonging to the *Poaceae* family, is the world's most widely grown food crop (Ezuka and Kaku, 2000). In terms of its nutritional content, rice is becoming of paramount importance to more than half of the world's population. Asia is considered as the world's "Rice Bowl". It is a nourishing food because it has 6.89 g of protein, 78.2 g of carbohydrates, 0.5 g of fat, 0.2 g of crude fibre, 0.6 g of mineral matter, 10 mg of calcium and 160 mg of phosphorus per 100 g (Mangalarai and Mauria, 1999). In tropical and subtropical rural and urban settings, people get between 40 to 70 per cent of their calories from rice (Hossain and Fischer, 1995). The cultivation of rice is a significant source of income and employment in the rural areas of Asian countries (Hossain, 1997). Rice is a tropical plant and cultivated in hot and humid climate. It is primarily grown in the regions which are rain-fed and get good rain every year during *kharif* season. In India, rice occupies an area of 46.5 m ha with the production of 130.84 million tonnes and productivity of 2809 kg per ha (Anonymous, 2023). Whereas in Gujarat rice crop is cultivated on 0.89 million hectares with the production of 2.10 million tonnes and productivity of 2356 kg per ha (Anonymous, 2023). Rice is mainly grown in central and southern districts of Gujarat, which include Valsad, Dang, Kheda, Ahmedabad, Anand, Mahisagar, Panchmahal, Vadodara, Tapi and Navsari. The crop is cultivated in both irrigated as well as rainfed conditions during *Kharif* as well as summer season in Gujarat state. The productivity of rice in Gujarat is quite low due to several abiotic and biotic factors, which includes bad weather, diseases and insect-pests infestation.

Among the diseases bacterial leaf blight (BLB) or bacterial blight (BB) caused by *Xanthomonas oryzae* pv. *oryzae (Xoo)* is a serious problem and threat to rice production in both tropical and temperate rice growing regions due to its high epidemic potential (Mew,1987). The disease broke out in the epiphytotic form in Shahabad district of Bihar (Srivastava and Rao, 1966). The disease has become endemic on rice due to intensive and repeated cultivation in many Asian countries, (Mew *et al*., 1993). BLB has spread to many non-traditional areas in India, in addition to recurring incidence in the traditional areas under irrigated and rainfed shallow lands. The pathogen is highly variable in nature (Kumar *et al.,* 2016).

The disease causes up to 20 per cent of the yield losses when appear at the tillering stage (Thind and Bala 2002; Liu *et al*., 2006). The disease has the potential to cause 10-12 per cent yield losses under mild infection (Mew *et al*., 1993). Under severe conditions, bacterial blight of rice can cause significant yield losses. In Japan, yield losses have ranged from 25-35%, sometimes reaching up to 60% (Ou, 1985). In the Philippines and Indonesia, losses were also very high, with the Philippines recording losses of 24.50% in the moist season and 7.21% in the dry season for vulnerable crops (Exconde, 1973). In India and Bangladesh, heavy yield losses of 12-32% have been reported (Shah Jahan, 1992). Similarly, in East India, yield losses have ranged from 7- 62% and even up to 82% for the same genetic resources (Srivastava *et al.*, 1967; Singh *et al*., 1980; Srivastava and Kapoor, 1982).

Laha *et al*., (2016) reported in production-oriented survey 9-52% intensity of bacterial leaf blight during 2001 to 2014 in different rice growing districts of Gujarat. Laha *et al*., (2020) reported that a production-oriented survey conducted in 2020 found the incidence of bacterial leaf blight to be low to moderate in different rice growing districts of Gujarat. The disease occurs at the seedling, vegetative and reproductive stages but at the tillering stage it causes severe blighting of leaves resulting in yield loss. The pathogen, is seed-borne, residing in glumes and occasionally within the endosperm. Seeds collected from heavily diseased fields carry the pathogen and seedlings grown from such seeds typically exhibit disease symptoms and succumb at an early stage (Srivastava and Rao, 1966). The ability of the bacteria to persist in seeds contributes to the perpetuation and dissemination of the disease, further emphasizing the need for effective management strategies to safeguard rice crops from this destructive threat (Mondal *et al*., 2019).

The most effective approach to control these this disease is using resistant varieties. Development of disease resistant rice is one of the most important achievements rice breeders attempt to accomplish (Tejaswini *et al.,* 2016).

In view of the destructive nature of the pathogen, a roving survey on the incidence of bacterial leaf blight was carried out during *Kharif*, 2023 in major rice-growing districts of Gujarat.

Symptomatology

Bacterial leaf blight is a typical vascular disease that can be divided in three distinct phases of symptoms i) Leaf blight phase, ii) Kresek phase and iii) Pale yellow leaf phase. The leaf blight phase is characterized by water-soaked lesions starting at the leaf tips, which then extend downward. Initially, these lesions are pale green but later turn yellow to straw-colored with wavy margins. Water soaking can be observed where the lesions meet healthy tissue. Lesions can begin at one or both edges of the leaves and sometimes appear along the midrib or elsewhere on the leaf blade. As the disease progresses, the lesions can cover the entire leaf blade, turning white and eventually gray or black due to saprophytic fungi growth. In humid areas, yellowish, turbid drops of bacterial ooze may be seen on young lesions in the early morning, which dry into

small, yellowish beads. The most destructive phase, known as the 'kresek' or wilt phase, occurs in the tropics due to early systemic infection in the nursery or from seed infection. This phase causes leaves to roll, droop, turn yellow or gray and ultimately wither. In severe cases, the entire affected plant may die. And the last is pale yellow leaf phase, which was reported from the Philippines, this phase causes some of the youngest leaves in a clump to turn pale yellow or whitish. These diseased leaves then wither, turn yellowish-brown and dry up. This phase has not been reported in other countries (Laha *et al.,* 2009).

Materials and Methods

The roving survey was conducted during the *kharif* season of 2023 to estimate the incidence of bacterial leaf blight in rice in five major rice growing districts of Gujarat *viz.,* Anand, Kheda, Navsari, Ahmedabad and Tapi. To conduct this survey two talukas were selected from each district and two villages were chosen from each taluka, whereas total five fields were selected randomly from each village to ensure a broad and representative sample of the rice crops in these regions. The survey was conducted between panicle initiation to booting stage of the crop.

During the field surveys, positive sampling was conducted and infected leaves of rice plants exhibiting typical bacterial blight symptoms **(Figure 1)** were collected.

Figure 1: Bacterial leaf blight infected plants

For accurately record observations of the Per centage Disease Index (PDI) and Disease Incidence (DI) for (BLB) of rice, several key parameters were recorded.

For calculating the actual incidence of disease in a field, plants were observed at ten points along a diagonal transect (IRRI, 1996). Five quadrates were randomly selected from each field and ten plants were then observed for the disease symptoms.

$$DI\ (\%) = \frac{\text{Number of bacterial blight infected plants}}{\text{Total number of plants examined}} \times 100$$

Total number of plants examined within each quadrate, as well as the number of plants showing symptoms of BLB were counted and recorded. The per cent disease index (PDI) was assessed by evaluating the severity of the disease on individual plants, using a standardized scale (e.g., 1-9, where 1 indicates mild symptom and 9 indicates severe disease).

The PDI is calculated with the formula:

$$PDI\ (\%) = \frac{\text{Sum of all the disease rating}}{\text{Total no. of leaves examined}} \times 100 \frac{100}{\text{Max. disease grade}}$$

Observations recorded

Per centage disease index (PDI)

Disease incidence (DI)

Results and Discussions

A roving survey was conducted during September-October of *kharif* 2023 in major rice growing districts of Gujarat *i.e.,* Anand, Ahmedabad, Tapi, Kheda and Navsari which are known for their rice cultivation to assess the incidence of bacterial leaf blight of rice.

The data in **Table 1** revealed that the highest incidence (49.54%) of bacterial leaf blight was observed in Kheda followed by Tapi (48.73%), Ahmedabad (46.53%), Navsari (12.74%) and the lowest incidence per centage was recorded in Anand (10.56%).

Table 1: Per cent disease incidence and per cent disease index of bacterial leaf blight of rice in different rice growing districts of Gujarat

Sl. No.	District	Taluka	Village	Per cent Incidence			Per cent Disease index		GPS coordinates	Cultivar/ Varieties
				Village	Taluka	District	Village	District		
1.	Kheda	Kheda	Nawagam	87.30	84.4	49.54	47.30	31.31	22.797505° 72.573497°	GR11, Surya Moti,
2.			Lali	81.50			38.50		22.861302° 72.633431°	Punjab S, Moti Gold
3.		Matar	Radhvanaj	13.17	14.69		20.17		22.70970° 72.72390°	GAR13
4.			Ratanpur	16.21			19.27		22.73660° 72.71477°	GAR13
5.	Ahmed-abad	Daskroi	Devdi	71.92	74.65	46.53	35.92	28.56	22.901808° 72.660803°	GR11, Punjab S
6.			Nandej	77.38			37.55		22.908878° 72.673322°	Moti Gold, GR11, Gurjari
7.		Bavla	Kathwada	29.50	18.41		22.45		23.80799° 72.55299°	GAR 13, Moti Gold
8.			Bavla	7.33			18.33		22.842144° 72.363074°	Surya Moti, GAR13
9.	Anand	Anand	Lambhvel	21.45	15.06	10.56	22.50	17.50	22.577175° 72.924656°	GR21, Sonam, Moti gold
10.			Chikhodra	8.67			16.67		22.559579° 73.00783°	Masuri, Sonam
11.		Petlad	Morad	6.97	6.07		19.97		22.543975° 72.873618	Moti Gold, GAR13
12.			Ravipura	5.18			11.18		22.549936° 72.847512°	Sriram125, GAR13, Mahisagar
13.	Tapi	Vyara	Magarkui	79.31	81.43	48.73	39.31	26.44	21.070414° 73.394043°	Versha, US-312
14.			Panvadi	83.55			40.38		21.094584° 73.400135°	US-312, MC-13, Annapurna
15.		Valod	Borakhadi	15.55	16.03		12.55		21.094584° 73.400135°	US 2171, Masuri, GAR13
16.			Bajipura	16.52			13.50		21.10013° 73.291831°	Bayer 6444, GAR 13, US-312
17.	Navsari	Chikhli	Chikhli	9.18	18.17	12.74	11.18	16.63	20.76388° 73.06012°	GNR7, GAR13
18.			Rethvania	27.17			30.70		20.81083° 73.12391°	Nath Pawan, MC-13, US 312
19.		Navsari	Dhantej	7.13	7.32		14.13		20.92247° 72.93124°	US 2111, Gurjari
20.			Sisodra	5.51			10.51		20.93445° 72.98385	US 2111, GR15, GAR13

The incidence of bacterial blight varied across talukas in different districts. In Kheda district, the highest incidence was observed in Kheda taluka (84.4%), followed by Matar taluka (14.69%). In Tapi district, Vyra taluka recorded 81.43%, while Valod taluka had 16.03%. Ahmadabad district reported 74.65% in Daskroi taluka and 18.41% in Bavla taluka. In Navsari district, the incidence rates were 7.32% in

Navsari taluka, 18.17% in Chikhli taluka and 16.03% in Valod taluka. Meanwhile, Anand district showed 15.06% in Anand taluka and 6.07% in Petlad taluka, reflecting considerable variation in disease incidence across these regions.

The data on village wise incidence of bacterial leaf blight showed that the highest incidence (87.30%) was recorded in Nawagam of Kheda district followed by Panvadi (83.55%) of Tapi district, Lali (81.50%) of Kheda district, Mangarkui (79.31%) of Tapi district, Nandej (77.38%), Devdi (71.92) of Ahmedabad district and Kathwada (29.50%) of Ahmedabad district, Rethvania (27.17%) of Navsari district, Lambhvel (21.45%) of Anand district, Bajipura (16.52%) of Tapi district, Ratanpur (16.21%) of Kheda district, Borkhadi (15.55%) of Tapi district, Radvanaj (13.17%) of Kheda district, Chikhli (9.18%) of Navsari district, Chikhodra (8.67%) of Anand district, Bavla (7.33%) of Ahmedabad district, Dhantej (7.13%) of Navsari district, Morad (6.97%) of Anand district and Sisodra (5.51%) of Navsari district whereas the village with the lowest incidence was Ravipura of Anand district with a disease incidence of (5.18%) **(Table 1).**

As for the Per cent Disease Index (PDI) the highest PDI (31.31%) of bacterial leaf blight was recorded in Kheda followed by Ahmedabad (28.56%), Tapi (26.44%), Anand (17.50%) and the lowest PDI was recorded in Navsari (16.63%).

The PDI of BLB was also recorded during the survey in major rice growing districts of Gujarat. The highest PDI was observed in village Nawagam of Kheda district with a PDI of 47.30%, followed by Panvadi in Tapi district with 40.38% and Magarkui in Tapi district with 39.31%. Nandej and Devdi in Ahmedabad district also exhibited a high PDI (37.55 and 35.92%, respectively). Other significant observations in PDI were from Lali (38.50%) in Kheda district and Lambhvel (22.50%) in Anand district. Kathwada in Ahmedabad showed a PDI of 22.45% and Ratanpur in Kheda had a PDI of 19.27%. Whereas in Radhvanaj village of Kheda, the PDI was 20.17% and in Bavla of Ahmedabad it was 18.33%, showed moderate PDI. While the lower PDI was recorded from the village Chikhodra in Anand (16.67%), Borakhadi in Tapi (12.55%) and Morad in Anand (19.97%). The minimum PDI was recorded from the Ravipura village (11.18%) and Chikli village (11.18%) while the lowest PDI was recorded in village Sisodra (10.51%) of Navsari district. This comprehensive data highlights the varying severity of BLB across different regions and varieties in Gujarat.

The result found were in accordance to that recorded by Laha *et al*., (2016) who reported during production-oriented survey 09-52 *per cent* incidence of bacterial leaf blight during 2001 to 2014 in different rice growing districts of Gujarat. Laha *et al*., (2020) also reported that during production-oriented survey conducted of *kharif* 2020 that the incidence of bacterial leaf blight to be low to moderate in different rice growing districts of Gujarat. The results of this study align with the findings of Thimmegowda (2006), who observed during the *kharif* season of 2005 that Raichur had the highest disease incidence rate of 61.7 per cent, while Siruguppa had the lowest incidence 46.78 per cent. In the summer of 2006, the highest disease incidence was recorded in Sindhanur at 74.69 per cent, with Siruguppa again having the lowest at 46.78 per cent.

Our present study identified the hotspots of bacterial leaf blight (BLB) of rice in different ecosystems of Gujarat. This disease, caused by a dynamic pathogen that rapidly evolves new races, can be effectively managed through several strategies.

The widespread presence of bacterial leaf blight (BLB) across various regions of Gujarat suggests the critical need for improved management practices. In particular, high incidences in specific areas point to potential hot spots where targeted interventions could be most effective. The variability in disease incidence across different districts, talukas and villages suggests that local environmental conditions, agricultural practices and the choice of rice cultivars play significant roles in disease dynamics.

High incidence rates in districts such as Kheda (49.54%), Tapi (48.73%) and Ahmedabad (46.53%) indicate the urgent need for focused disease management strategies in these regions. Similarly, talukas with exceptionally high incidences, such as Kheda (84.4%), Vyara (81.43%) and Daskroi (74.65%), represent critical areas where targeted control measures could substantially reduce the disease burden. Village-level data, revealed the highest incidence in Nawagam (87.30%) and Panvadi (83.55%), further emphasize the importance of localized interventions.

Several factors contribute to the observed variability in BLB incidence, including climatic conditions, soil health, water management and the susceptibility of rice cultivars. For instance, areas with high humidity and frequent rainfall provide conducive environments for the spread of BLB. Poor soil health and improper water management practices can exacerbate disease conditions. Additionally, the use of susceptible rice cultivars in certain regions can lead to higher disease incidences. Research by Mew *et al*. (1993) and Gnanamanickam *et al*. (1999) highlights that high-yielding varieties and excessive nitrogen use are key factors in bacterial blight outbreaks.

To mitigate the impact of BLB and improve rice yields in Gujarat, region-specific integrated disease management strategies are essential. These strategies should combine both chemical and cultural practices. Chemical management could include the use of effective bactericides and antibiotics, while cultural practices might involve crop rotation, proper water management and the use of resistant rice varieties.

Studies have shown that integrated disease management, which combines various control methods, is more effective in managing BLB than relying on a single approach. For instance, Krishnakumar and Kumaravadivel (2018) reported that the incidence of BLB could be reduced through the adoption of integrated management practices that include timely application of bactericides, use of resistant cultivars and implementation of good agricultural practices.

Conclusion

Bacterial leaf blight (BLB) is a major issue in Gujarat's traditional rice-growing areas, with disease incidence ranging from 10.56% to 49.54% and PDI from 16.63% to 31.31%. It is severe in moderate rainfall areas with high humidity, driven by factors like strong winds, rain splashes and heavy monsoon rains. The widespread cultivation of susceptible varieties such as GR11 and Moti Gold, monocropping and excessive nitrogen fertilization have further increased its prevalence.

The significant variability in BLB incidence across Gujarat highlights the need for targeted, region-specific management strategies. By addressing the unique conditions and practices in each region, it is possible to effectively control BLB, thereby safeguarding rice production and enhancing food security in the state. Effective control can be achieved through proper cultural practices, resistant cultivars and timely antibiotic applications. Identifying high-risk areas is essential for implementing targeted interventions to reduce disease impact and improve yield.

Acknowledgements

The research was conducted as part of a M. Sc. research work titled "Studies on the variability of *Xanthomonas oryzae* pv. *oryzae* causing bacterial leaf blight in rice and its management" by the primary author at the B. A. College of Agriculture, Anand Agricultural University, Anand.

References

Anonymous. 2023. District-wise area, production and yield of important food & non-food crops in Gujarat state. Directorate of Agriculture, Krishi- Bhavan, Section 10A, Gujarat state, Gandhinagar, pp. 61.

Anonymous. 2023. Agriculture Statistics at a Glance. Directorate of Economics and Statistics, Department of Agriculture, Cooperation and Farmer Welfare, Ministry of Agriculture and Farmer Welfare, Govt. of India, pp. 48-50.

Ezuka A and Kaku H. 2000. A historical review of bacterial blight of rice. *Bulletin of the National Institute of Agrobiological Resources*, 15: 1-207.

Exconde OR, Opina OS and Phanomsawarn K. 1973. Yield losses due to bacterial leaf blight of rice. *Philippine Agricultural Scientist*, 57: 128-140.

Gnanamanickam SS, Priyadarisini VB, Narayanan NN, Vasudevan, P and Kavitha S. 1999. An overview of bacterial blight disease of rice and strategies for its management. *Current Science*, 1435-1444.

Hossain M. 1997. Rice supply and demand in Asia: a socioeconomic and biophysical analysis. In *Applications of Systems Approaches at the Farm and Regional Levels,* Springer Netherlands, pp. 263-279.

Hossain M and Fischer KS. 1995. Rice research for food security and sustainable development in Asia: Achievements and future challenges. *Geo Journal*, 35(3): 286-298

IRRI 1996. Standard Evaluation System for Rice. *International Rice Testing Program*, Manila, Philippines, pp. 0-40.

Krishnakumar R and Kumaravadivel N. 2018. Marker-assisted selection for biotic stress (Bacterial leaf blight and gall midge) tolerance in Bc4F4 generation of rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 9(1): 275-282.

Kumar A, Swati, Kumar A, Kumari P and Patel B. 2016. Virulence Profile of *Xanthomonas oryzae* pv. *oryzae* Strains from Bihar. *Journal of Rice Research*, 9(1): 60-63.

Laha GS, Reddy CS, Krishnaveni D, Sundaram RM, Srinivas Prasad M, Ram T, Muralidharan K and Viraktamath BC. 2009. Bacterial blight of rice and its management. *DRR Technical Bulletin*, 41: 30-37.

Laha GS, Sailaja B, Srinivas Prasad M, Ladhalakshmi D, Krishnaveni D, Ram Singh, Prakasam V, Yugander A, Kannan C, Valarmathi P and Ravindra Babu V. 2016. Changes in Rice Disease Scenario in India: An analysis from Production Oriented Survey, ICAR-IIRR, Rajendranagar, Hyderabad, pp. 69-78.

Laha GS, Srinivas Prasad M, Krishnaveni D, Kannan C, Ladhalakshmi D, Prakasam V, Basavaraj K and Jasudasu GS. 2020. Production Oriented Survey 2020, All India Coordinated Rice Improvement Programme, ICAR-IIRR, Rajendranagar, Hyderabad, pp. 12-39.

Liu DO, Ronald PC and Bogdanove AJ. 2006. *Xanthomonas oryzae* pv. *oryzae*: Model pathogen of a model crop. *Molecular Plant Pathology*, 7: 303-324.

Mangalarai and Mauria S. 1999. The Hindu Survey of Indian Agriculture. Pub. M/s Kasturi and Sons Ltd., Chennai, p. 55.

Mew TW. 1987. Current status and future prospects of research prospects of research on bacterial blight of rice. *Annual Reviews Phytopathology*, 25: 359-382.

Mew TW, Alvarez AM, Leach JE and Swing J. 1993. Focus on bacterial blight of rice. *Plant Diseases*, 77: 5-12.

Mondal S, Hossien ME, Akter MA, Haque MM, Ali MA and Islam MR. 2019. Survival and transmission of *Xanthomonas oryzae* pv. *oryzae* in rice seeds. *Fundamental and Applied Agriculture*, 4(1): 680-688.

Ou SH. 1985. Bacterial leaf blight in Rice diseases. Commonwealth Microbiological Institutes, Cambrian News, Aberystwyth, U.K. 70-74.

Shah Jahan AKM. 1992. Development of technologies and their transfer to farmers in Bangladesh. *Crop Science Society,* Bangladesh, p. 34.

Singh RA, Das B, Ahmed KM and Pal V. 1980. Chemical control of bacterial leaf blight of rice. *International Journal of Pest Management*, 26(1): 2 1-25.

Srivastava DN and Rao YP. 1966. Can Taichung Native 1 stands up to bacterial blight. *Indian Farming*, 16(2): 15-17.

Srivastava DN and Kapoor TR. 1982. Yield loss due to bacterial leaf blight. *International Rice Research News,* 1(7): 7.

Srivastava DN, Rao YP, Durgapal JC, Jindal, JK and Singh W. 1967. Screening Rice varieties for resistance to bacterial blight. India. *Phytopathology,* 17: 25-28.

Tejaswini KLY, Krishnam R, Kumar R, Mohammad LA, Ramakumar PV, Sayanarayana PV and Srinivas M. 2016. Screening of rice F5 families for sheath blight and bacterial leaf blight. *Journal of Rice Research*, 9(1): 4-10.

Thind BS and Bala GS. 2002. Effect of cultural practices on seed plant transmission of *Xanthomonas oryzae* pv. *oryzae* in rice. *Journal of Mycology and Plant Pathology*, 32: 90-91.

Thimmegowda PR. 2006. *Studies on bacterial leaf blight of paddy*. M. Sc. (Agri.) Thesis, University of Agriculture Science, Dharwad, India.

RESEARCH ARTICLE https://doi.org/10.58297/PEVT5581

Evaluation of Donor and Advanced Lines for Blast Resistance Across Agroclimatic Zones of Andhra Pradesh and Telangana

Eden Georgia Karedi[1*], Srinivas Prasad M[2], Jesudas GS[2], Bhuvaneswari V[3], Madhusudhan P[4], Udayababu P[4], NVSR Ravi Kumar B[5] and Manoj Kumar V[6]

[1]Agricultural College, ANGRAU, Bapatla, AP,
[2]Indian Institute of Rice Research, Rajendranagar, Telangana,
[3]Regional Agricultural Research Station, ANGRAU, Maruteru, AP,
[4] Agricultural Research Station, ANGRAU, Nellore, AP,
[5]Regional Agricultural Research Station, ANGRAU, Nandyal, AP,
[6]Regional Agricultural Research Station, ANGRAU, Guntur, AP

*Corresponding author Email: *karedi.eden@gmail.com*

Received: 4th November, 2024; Accepted : 13th December, 2024

Abstract

Rice blast, caused by the fungal pathogen *Pyricularia oryzae*, is a major threat to rice production worldwide. As *P. oryzae* is a highly evolving and dynamic pathogen and adapting host plant resistance is the most significant way of managing the blast disease. The present study aims to assess the performance of rice genotypes across different locations to understand their adaptability and also to monitor the virulence patterns of the blast pathogen population. A multi-location trail was carried out with 39 cultivars consisting of near-isogenic lines, international differentials, donors and commercial cultivars possessing different genes for blast resistance by adopting Uniform Blast Nursery (UBN) at six locations in different agroclimatic zones of Andhra Pradesh and Telangana during *Kharif* 2023. There was significant variation in disease pressure among locations, with ARS, Nellore exhibiting the highest Location Severity Index (LSI) of 4.44 and ARS, Uttukur showing the lowest LSI of 2.76. The susceptibility Index (SI) 7.45 was recorded highest in the susceptible check (HR-12) while the resistant check Tetep showed the lowest SI of 2.16. Several genotypes carrying the *Pi-1*, *Pi-12*, *Pi-z+Pi-a+Pi-i*, *Pi-54*, *Pi-9* and *Pi-kh+* genes demonstrated consistent resistance across different locations. The study highlights the importance of considering gene combinations for durable resistance and the need for site-specific adaptation in rice breeding programs to combat rice blast effectively.

Keywords: Agroclimatic zones, Blast disease, Differential lines, Rice, Telangana

Introduction

Rice is one of the most significant edible cereal grains. Rice is a rich source of carbohydrates, which is essential for providing energy. It also contains vitamins and minerals, contributing to a balanced diet and it serves as a primary staple food for more than two-thirds of the world's population (Fukagawa and Ziska, 2019). Although rice output has expanded to meet global demand, productivity has not increased appreciably. One of the major constraints faced by the rice growers for low productivity is biotic stress. Among the biotic factors, diseases remain a persistent challenge in rice cultivation. The rice crop suffers

from diseases caused by fungi, bacteria, viruses, phytoplasma, nematodes and other non-parasitic disorders. Among the fungal diseases blast disease is caused by *Pyricularia oryzae* Cavara which is a significant threat to rice production worldwide (Anand Kumar *et al*., 2023). It can cause severe loss in yield to the extent of 70-80% in various rice ecosystems (Aruna *et al*., 2015). *P. oryzae* is constantly evolving and is regarded as a threat to global food security. Management of blast disease is carried out using various strategies, including crop rotation, fungicide application and planting of resistant varieties. Among the various methods for managing plant diseases, genetic resistance is widely regarded as the most effective and sustainable, providing both economic and environmental benefits (Bonman, 1992). Rice blast resistance is a classic gene-for-gene interaction, where a major resistance gene in the host plant effectively counters *P. oryzae* strains carrying the corresponding avirulence gene (Silue *et al*., 1992). Developing rice cultivars with durable resistance to blast is crucial for ensuring food security. This study aimed to evaluate the resistance of various rice genotypes containing of near-isogenic lines, international differentials, donors and commercial cultivars possessing different genes for blast resistance under different agro-climatic conditions in Andhra Pradesh and Telangana, India.

Materials and Methods

The present study was carried out to evaluate blast disease in different agro-climatic regions of Andhra Pradesh and Telangana during *kharif* 2023.These lines were evaluated in Uniform blast nurseries at six different locations *viz.*, IIRR Hyderabad, RARS Maruteru (A.P.), ARS Nellore (A.P.), ARS Ragolu (A.P.), RARS Nandyal (A.P.) and ARS Uttukur (A.P.). The details of the locations were presented in the **Table 1**. Thirty-nine cultivars consisting of near-isogenic lines, international differentials, donors and commercial cultivars possessing different genes for blast resistance including appropriate susceptible (HR-12, Co-39) and resistance (Tetep, Rasi and IR 64) checks were evaluated for blast resistance. The fungus was isolated by tissue segmentation method (Bonman *et al.*, 1987). Single spores were located and picked up microscopically and transferred to fresh sterilized Petri plates containing Oat Meal Agar (OMA) medium. The Petri plates were incubated at 28 °C for 7 days and the fungus was identified following mycological description (Ou, 1985). After 14 days of incubation at 28 °C, petri plates (90 mm) of *P. oryzae* isolate was washed with 20 ml of sterile distilled water to produce spore suspension. The concentration of the conidial suspension was adjusted to 1×10^5 conidia ml^{-1} using a haemocytometer.

Uniform Blast Nursery (UBN) was a 10x1 m bed. The soil was pretreated with FYM, NPK and commercial sulphuric acid before tilling to distribute the manure uniformly in the soil. Highly susceptible variety (HR 12) was sown as a border row on either side of the bed and between the test material rows. After every 10 rows of test materials HR 12 was planted which acts as spreader rows. Test material was sown in 50 cm rows perpendicular to the border row with 10 cm spacing between the rows (**Figure 1**).

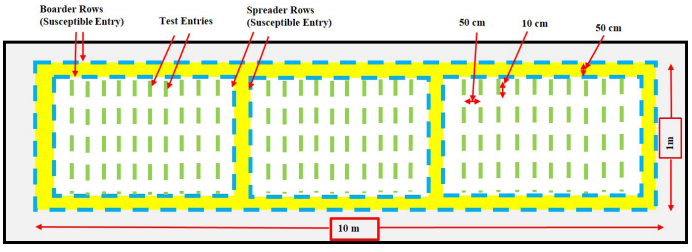


Figure 1: Layout of Uniform Blast Nursery

25 days after sowing these nursery beds were sprayed with spore suspension of local blast isolate using a hand-operated atomizer. Relative humidity was maintained by sprinkling water as mist with

30 min time interval depending on the intensity of temperature. The UBNs were covered with polythene sheets during night to maintain the humidity to build up more spore load and in turn to increase the disease pressure on the varieties. Scoring was done after 10-15 days of post infection depending on the severity of the infection on the susceptible check using SES scale (IRRI, 1996) (**Table 2**). Scoring was done after 10-15 days of inoculation depending on the severity of the infection on the susceptible check using SES scale (IRRI, 1996). The data thus obtained from field experiments in a Randomized Block Design were analyzed statistically by Two-way ANOVA (Gomez and Gomez, 1984).

Table 1: Details of different locations of Andhra Pradesh and Telangana

Agro climatic zone	Location	Research Station/ Institute	State	Latitude	Longitude	Ecosystem
Godavari Zone	Maruteru	Regional Agricultural Research Station (RARS)	Andhra Pradesh	16.6299° N	81.7457° E	Irrigated, Lowland
Southern Zone	Nellore	Agricultural Research Station (ARS)	Andhra Pradesh	14.4303° N	79.9987° E	Irrigated, Lowland
North coastal Zone	Ragolu	Agricultural Research Station (ARS)	Andhra Pradesh	18.16412°N	83.5010° E	Irrigated, Lowland
Scarce rainfall Zone	Nandyal	Regional Agricultural Research Station (RARS)	Andhra Pradesh	15.4786° N	78.4831° E	Rainfed, Upland
Southern Zone	Uttukur	Agricultural Research Station (ARS)	Andhra Pradesh	14.4373° N	78.8050° E	Rainfed, Upland
Southern Telangana Zone	Hyderabad	Indian Institute of Rice Research (ICAR-IIRR)	Telangana	17.3871° N	78.4916° E	Irrigated, Lowland

Results and Discussions

The results revealed that the intensity of rice blast disease incidence varied at different test locations. Among the locations, the Location Severity Index (LSI) was recorded high at ARS, Nellore (4.44) located in the Southern region of the agroclimatic zone of Andhra Pradesh followed by RARS, Maruteru (3.70) located in the Godavari zone and the least disease incidence was recorded at ARS, Uttukur (2.76) located in the Southern region of the agroclimatic zone of Andhra Pradesh (**Figure 2**). HR-12 showed susceptibility to blast in all the regions (**Plate 1a** and **1b**). HR-12 showed highest susceptibility index (7.31) and resistant check Tetep recorded lowest susceptibility index (2.06) while, Rasi and IR-64 recorded an average score of 2.95 and 3.10 respectively (**Table 2**).

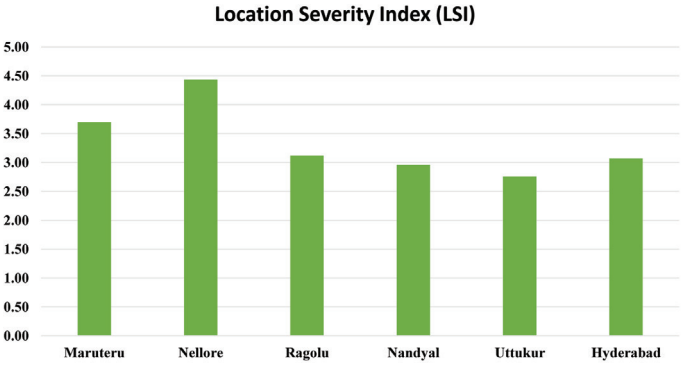


Figure 2: Location Severity Index (LSI) of different test locations

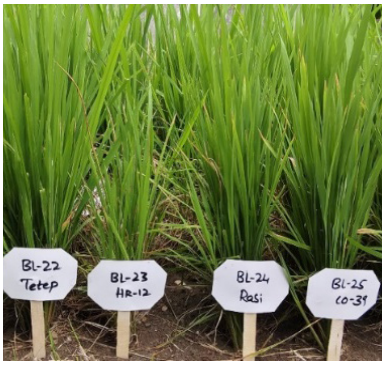
The differential lines RP Biopatho-3 (*Pi-2*), RP Biopatho-4 (*Pi-54*) and PRS-59 (*Pi-9*) showed resistant

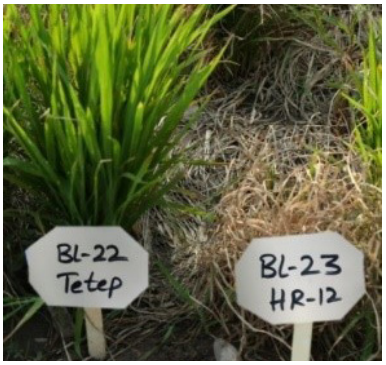



RARS, Maruteru **ARS, Nellore** **ARS, Ragolu**

Plate 1a: Multilocation evaluation of differential lines carrying different blast resistant genes





RARS, Nandyal **ARS, Uttukur** **IIRR, Hyderabad**

Plate 1b: Multilocation evaluation of differential lines carrying different blast resistant genes

reaction (<3) to blast disease in all the locations. PRS-17 (*Pi-9*+*Pi-54*) exhibited resistant reaction (<3) in four locations, whereas at IIRR, Hyderabad and ARS, Uttukur it showed moderately resistant reaction of 3.15 and 3.52, respectively. Differentials with combinations of genes BL-122 (*Pi-1*+*Pi-2*) and A57 (*Pi-1*+*Pi-2*+*Pi-4*) showed resistant reaction in all the locations except at RARS, Maruteru and ARS, Nellore. Differential line Zenith (*Pi-z*+*Pi-a*+*Pi-i*) showed resistant reaction in all the locations except in ARS, Nellore. C104 PKT (*Pi-3*) recorded susceptible reaction in RARS, Maruteru, ARS, Nellore and ARS, Ragolu. Tadukan (*Pi-ta*) showed susceptible reaction only in ARS, Nellore and it showed resistant reaction in all other locations.

The susceptible check (HR-12) succumbed to blast in all the locations except at ARS, Uttukur it showed moderately resistant reaction (5.04). The resistant check Tetep (*Pi-k*$^{h+}$) showed resistant reaction (<3) to blast disease in all the test locations. Resistant check IR 64 was found resistant (<3) only at RARS, Nandyal, while it showed moderately resistant reaction in the remaining locations. Another resistant check Rasi showed resistant reaction (<3) in four locations and at ARS, Nellore and IIRR, Hyderabad it exhibited moderately resistant reaction. The susceptible check Co-39 showed resistant reaction (<3) at ARS, Ragolu and ARS, Uttukur while it exhibited moderately resistant reaction at RARS, Nandyal and IIRR, Hyderabad. It exhibited a moderately resistant reaction at RARS, Maruteru and susceptible reaction at ARS, Nellore.

Table 2: Details and performance of the differential lines to *Pyricularia oryzae* under different agro climatic regions during *kharif* -2023

S. No.	Desig-nation	Entry No.	Resistance Gene	Disease reaction to blast 0-9 Scale (IRRI, 1996)*												
				Maruteru	R/S	Nellore	R/S	Ragolu	R/S	Nandyal	R/S	Uttukur	R/S	Hyderabad	R/S	SI**
1	BL1	C101 LAC	*Pi-1*	2.80	R	5.53	MS	3.43	MR	2.43	R	3.22	MR	3.45	MR	3.48
2	BL2	C101 A51	*Pi-2*	3.69	MR	5.61	MS	3.18	MR	3.50	MR	3.01	MR	3.88	MR	3.81
3	BL3	C104 PKT	*Pi-3*	5.37	MS	4.87	MS	5.10	MS	3.17	MR	3.21	MR	3.58	MR	4.22
4	BL4	C101 TTP	*Pi-4b*	4.91	MS	5.62	MS	2.35	R	2.25	R	2.35	R	2.78	R	3.38
5	BL5	RIL - 10	*Pi-12*	2.74	R	5.48	MS	2.14	R	3.50	MR	3.11	MR	2.65	R	3.27
6	BL6	RIL - 29	*Pi-7*	5.31	MS	3.61	MR	3.54	MR	3.63	MR	2.28	R	3.60	MR	3.66
7	BL7	O. minuta	*Pi-9*	3.63	MR	4.82	MS	2.30	R	3.77	MR	2.10	R	2.27	R	3.15
8	BL8	BL-122	*Pi-1 + Pi-2*	4.07	MS	4.12	MS	2.69	R	3.12	MR	3.36	MR	2.26	R	3.27
9	BL9	BL-245	*Pi-2 + Pi-4*	4.25	MS	3.62	MR	2.27	R	3.21	MR	3.04	MR	3.07	MR	3.24
10	BL10	A 57	*Pi-1 + Pi-2 + Pi-4*	4.60	MS	5.22	MS	2.17	R	2.57	R	2.15	R	2.53	R	3.21
11	BL11	C101 PKT	*Pi-4a*	3.87	MR	4.56	MS	3.24	MR	3.22	MR	3.23	MR	2.07	MR	3.36
12	BL12	Raminad-STR-3	-	3.32	MR	5.68	MS	3.47	MR	2.53	R	3.02	MR	2.76	R	3.46
13	BL13	Zenith	*Pi-z + Pi-a + Pi-i*	2.75	R	4.43	MS	2.67	R	2.16	R	2.22	R	2.42	R	2.77
14	BL14	NP - 125	-	2.28	R	5.91	MS	3.48	MR	3.32	MR	3.02	MR	3.20	MR	3.54
15	BL15	USEN	*Pi-a*$^{+}$	3.47	MR	3.97	MR	3.57	MR	3.15	MR	3.10	MR	4.89	MS	3.69
16	BL16	Dular	*Pi-k*$^{a+}$	3.28	MR	3.88	MR	2.88	R	2.22	R	3.31	MR	2.63	R	3.03
17	BL17	Kanto - 51	*Pi-k*	5.21	MS	4.64	MS	2.18	R	2.80	R	3.14	MR	2.79	R	3.46
18	BL18	Shi-tia-tao	*Pi-k*^{s}	5.44	MS	3.92	MR	2.42	R	2.25	R	2.30	R	5.30	MS	3.60
19	BL19	Calaro	*Pi-k*^{s}	5.22	MS	3.78	MR	2.48	R	3.23	MR	2.37	R	3.17	MR	3.37
20	BL20	Tadukan	*Pi-ta*	3.69	MR	5.66	MS	2.82	R	2.20	R	2.20	R	2.77	R	3.22
21	BL21	IR - 64	Resistant	3.85	MR	3.89	MR	3.05	MR	2.22	R	3.12	MR	3.05	MR	3.20
22	BL22	Tetep	*Pi-k*$^{h+}$	2.47	R	2.97	R	2.71	R	1.97	HR	1.83	HR	1.02	HR	2.16

23	BL23	HR - 12	Susceptible	7.98	S	8.69	HS	7.44	S	6.54	S	5.04	MS	9.00	HS	7.45
24	BL24	Rasi	Resistant	2.87	R	3.95	MR	2.78	R	2.14	R	2.22	R	3.67	MR	2.94
25	BL25	Co - 39	Susceptible	4.25	MS	6.92	S	2.35	R	3.12	MR	2.43	R	3.18	MR	3.71
26	BL26	RP Patho-1	*Pi-1*	2.70	R	4.73	MS	2.64	R	2.37	R	3.10	MR	2.33	R	2.98
27	BL27	RP Patho-2	*Pi-2*	3.90	MR	4.96	MS	3.46	MR	3.05	MR	2.07	R	2.69	R	3.36
28	BL28	RP Patho-3	*Pi-54*	2.54	R	3.80	MR	2.32	R	3.12	MR	3.05	MR	3.66	MR	3.08
29	BL29	RP Patho-7	*Pi-1*	2.70	R	3.60	MR	3.48	MR	3.57	MR	3.01	MR	2.45	R	3.14
30	BL30	RP Patho-8	*Pi-2*	3.60	MR	3.78	MR	3.78	MR	2.48	R	2.35	R	2.53	R	3.09
31	BL31	RP Patho-9	*Pi-54*	3.73	MR	5.67	MS	3.50	MR	3.73	MR	3.07	MR	2.22	R	3.65
32	BL32	RP Biopatho-1	*Pi-2*	3.96	MR	4.69	MS	4.58	MS	2.67	R	2.14	R	2.13	R	3.36
33	BL33	RP Biopatho-2	*Pi-54*	2.59	R	3.86	MR	2.82	R	3.11	MR	3.15	MR	2.66	R	3.03
34	BL34	RP Biopatho-3	*Pi-2*	2.62	R	2.90	R	2.88	R	2.28	R	2.13	R	2.71	R	2.59
35	BL35	RP Biopatho-4	*Pi-54*	2.77	R	2.47	R	2.85	R	2.42	R	2.08	R	2.56	R	2.52
36	BL36	PRS-17	*(Pi-9 + Pi-54)*	2.49	R	2.65	R	2.50	R	2.98	R	3.52	MR	3.15	MR	2.88
37	BL37	PRS-50	*Pi-54*	3.74	MR	2.80	R	3.69	MR	3.44	MR	2.15	R	3.67	MR	3.25
38	BL38	PRS-58	*Pi-9*	2.71	R	2.75	R	3.44	MR	3.87	MR	3.22	MR	2.47	R	3.08
39	BL39	PRS-59	*Pi-9*	2.93	R	3.02	R	2.85	R	2.12	R	2.12	R	2.59	R	2.60
	Location Severity Index (LSI)			**3.70**		**4.44**		**3.12**		**2.96**		**2.76**		**3.07**		

*Blast scale (IRRI, 1996), 0- HR, 1-R, 2 to 3-MR, 4 to 5-MS, 6 to 7-S, 8 to 9-HS; R/S- Resistant/Susceptible, HR-Highly Resistance, R-Resistance, MR-Moderate resistant, MS- Moderate Susceptible, S- Susceptible, HS- Highly Susceptible, ** SI-Severity Index

Statistical analysis was carried out using Two way Anova (RBD), the results obtained are presented in the **Table 3**.

Table 3: LSD of test lines and locations

LSD	Differential lines	Locations
C.D.	0.81	0.32
SE(m)	0.29	0.11
SE(d)	0.41	0.16
C.V.	10.07	10.07

The difference in disease reaction scores of susceptible and resistant checks reveals the shift in the pathogen population. The results also reveal that the disease severity and the performance of genes varied in different agroclimatic zones. Apex and minimal disease severity were recorded in the southern zone alone due to varied climatic conditions. Similar trial was also conducted by Muralidharan *et al*., (2004) and evaluated rice genotypes carrying resistance genes to blast disease in multi-environment tests (METs) Tadukan carrying resistance gene *Pi-ta* showed small lesions infecting <2% leaf area indicating a very high level of durable resistance to blast disease. The METs clearly demonstrated the expression of a high degree of resistance in A57 carrying three resistance genes (*Pi-1*, *Pi-2* and *Pi-4*). A 57 was identified as the best line that exhibited resistance to blast across the country in all rice growing environments irrespective of ecosystems.

Similar results were observed by Jahaar *et al*., (2018) screened 23 Near Isogenic Lines (NILs) at four different agroclimatic locations and reported that NILs with combination of resistant genes *i.e*., BPT5204×C101LAC×C101A5×Tetep (*Pi-1*, *Pi-2* and *Pi-54*), Swarna×C101LAC×Tetep (*Pi-1* and *Pi-54*) and Swarna×C101LAC×C101A5×Tetep (*Pi-1*, *Pi-2* and *Pi-54*) showed complete resistance to blast disease in all the locations.

In the same way, Abamu *et al*., (1998) studied effects and Multiplicative Interaction Models which are widely used for analyzing main-effects and genotype by-environment (G×E) interactions in multilocation variety trials to gain insight into G×E in rice blast and

identify genotypes with high and stable resistance to the disease. Divya *et al*., (2013) also reported that lines with gene combinations *Pi-1+Pi-2+Pi-33+Pi-54* and *Pi-1+Pi-2+Pi-33* were highly resistant to blast disease than those with single genes indicating that these non-allelic genes have a complementary effect.

The present study offers valuable insights into the genetic factors underlying blast resistance in rice. The Southern Zone saw the highest and lowest LSI values at ARS, Nellore and ARS, Uttukur, respectively, reflecting changes in pathogen virulence and environmental factors. The resistant genes *Pi-1*, *Pi-12*, *Pi-z* + *Pi-a* + *Pi-i*, *Pi-54* and *Pi-9* and the demonstrated effectiveness of combining these genes provide promising avenues for breeding programs to develop cultivars that are more resilient to this devastating disease.

References

Abamu FJ, Akinsola EA and Alluri K. 1998. Applying the AMMI models to understand genotype-by-environment (GE) interactions in rice reaction to blast disease in Africa. *International Journal of Pest Management*, 44(4): 239-245.

Anand Kumar ADVSLP, Nanda Kishore M, Bhuvaneswari V, Srinivas Rao N, Anusha B and Jogi Naidu G. 2023. Studies on Compatibility of Insecticides and Fungicides against Brown Plant Hopper and Blast in Rice. *Journal of Rice Research*, 16(2): 108-113.

Aruna J, Vijay Kumar S, Rambabu R, Ramesh S, Madhavi KR, Abhilash V, Laha GS, Krishnaveni D, Ladha Lakshmi D, Prakasam V, Ravindrababu V and Prasad MS. 2015. Variability in Aggressiveness of Rice Blast (*P. oryzae*) Isolates originating from resistant and susceptible cultivars. *Journal of Rice Research,* 8(1): 82-83.

Bonman JM, Vergel de Dois TI, Bandong JM and Lee EJ. 1987. Pathogenic variability of monoconidial isolates of *Pyricularia oryzae* in Korea and in Philippines. *Plant Disease,* 71(2): 127-130.

Bonman JM. 1992. Durable resistance to rice blast disease-environmental influences. *Euphytica*, 63 (1-2): 115-123.

Divya B, Robin S, Rabindran R, Manjunath H, Valarmathi P and Joel AJ. 2014. Resistance reaction of gene introgressed lines against rice blast (*Pyricularia oryzae*) disease. *Australasian Plant Pathology,* 43: 177-191.

Gomez KA and Gomez AA. 1984. *Statistical Procedures for Agricultural Research*, p-683, (2 Ed.), John Wiley and Sons Ltd., Singapore.

IRRI. 1996. Standard Evaluation System for Rice (SES), pp-15-16, (4 Ed.). International Rice Research Institute, Philippines.

Muralidharan K, Krishnaveni D, Laha GS, Reddy CS, Srinivasprasad M and Sridhar R. 2004. Performance of rice blast resistance genes in multi-environment tests in India. *Indian Phytopathology*, 57(3): 260-266.

Fukagawa NK and Ziska LH. 2019. Rice: Importance for Global Nutrition. *Journal of Nutritional Science and Vitaminology,* 65 (Supplement): S2-S3.

Ou SH**.** 1985. Rice Diseases, p-380, (2 Ed.), Commonwealth Mycological Institute, Kew.

Silue G B, Notteghem J L and Tharreau D. 1992. Evidence for a gene-for-gene relationship in the *Oryza sativa Magnoporthe gresea*- pathosystem, *Phytopathology,* 82(5): 577-580.

RESEARCH ARTICLE https://doi.org/10.58297/NBMY7147

A Sustainable Approach to Rice Cultivation in Punjab-Direct Seeding of Rice (DSR)

Sangeet Ranguwal[1*], Raj Kumar[2] and Gurpreet Singh[3]

[1]Agricultural Economist, Department of Economics and Sociology, Punjab Agricultural University, Ludhiana, Punjab;

[2]Principal Extension Scientist (Agricultural Economics), Department of Economics and Sociology, Punjab Agricultural University, Ludhiana, Punjab;

[3]Senior Research Fellow, Crop Residue Management, Agricultural Technology Application Research Institute (ATARI) ICAR, Zone I, Ludhiana

*Corresponding author Email: sangeet@pau.edu

Received : 15th September, 2024; Accepted: 13th November, 2024

Abstract

Considering sustainable agriculture as the keystone of social and economic prosperity, promotion of Direct Seeded Rice (DSR) has been one of the pioneer steps in the Punjab Government's 2023-24 Budget. In the present study based on field survey of it was found that use of all the inputs was lower on DSR farms as compared to conventional Puddled Transplanted Rice (PTR) farms except seed, plant protection chemicals and some micro-nutrients. Though the yield in DSR (2769 kg per acre) was marginally lower than PTR (2801.3 kg per acre), the net returns over variable cost were higher by about 13 per cent in DSR (Rs 31482.14 per acre) than PTR (Rs 27788.41 per acre) because of lower variable costs involved in DSR. The cost in production of one kg grain using DSR was found to be lower (Rs 8.43 per kg) by about 15 per cent than in PTR (Rs 9.88 per kg) and the input energy involved in the same was Rs 7.84 MJ as compared to 8.86 MJ indicating that DSR has the potential to increase farmer's income and save scarce resources. DSR technology is a viable alternative to overcome the problems of rising cost of cultivation, labour and water shortages for sustainable rice production yet it has not been adopted at a very large scale. There is need for more research in development of high yielding rice cultivars suitable for DSR along with ensured and timely availability of agro-inputs and machinery. Also, there is a need to [3]generate more awareness of recommended DSR production practices among the farmers for its speedy adoption and thus achieving sustainable production.

Keywords: DSR, social and economic prosperity, farmers income, high yield rice, sustainable production

Introduction

Rice is one of the most important food crops of India. About 70 per cent Indians use rice as their primary food source and it occupies 40-45 per cent of all the land under cereal crops in India. The growing demand of rice has to be met by producing more rice with less agricultural input usages. Different challenges like lowering of water table, labour shortage during peak times and declining soil quality necessitate an alternative establishment approach to maintain rice production as well as natural resources. When the future of rice production is in jeopardy due to worldwide water constraint, Direct Seeded Rice (DSR) presents a desirable alternative. The conventional Puddled Transplanting of Rice (PTR) is water, capital, energy and labour-intensive practice. There is an urgent need to switch from the traditional PTR to DSR because it is not only cost, input, energy and time saving but is also environment

friendly (Bandumula *et al.,* 2018; Jat *et al.,* 2022; Singh *et al.,* 2023a).

Punjab state has been playing a leading role in the agricultural transformation of the country. A sustainable production of rice in the state is crucial for the food security of India. The state has contributed about 25-30 per cent rice and 35-40 per cent wheat to the central pool during the last one decade (PAU, 2022). Water guzzling paddy is a dominant crop in the cropping pattern of the Punjab state and is putting the groundwater resources in a jeopardy situation. Out of 153 water blocks of Punjab, only 17 are safe and the remaining 136 (89%) are in alarming condition (Anonymous, 2022). Further, electricity demand is increasing for irrigating the paddy crop which undermines the viability of the power sector as power for agricultural use is fully subsidized in the state. In addition, yield stability and assured marketing of paddy makes it the most remunerative rainy (kharif) season crop.

During the COVID-19 lockdown, the return of migrant labour who were working in Punjab, to their native places, created a severe shortage of labour during the *kharif* season of 2020 in Punjab. During that time the DSR, which was being promoted in the State for a long time as a more water and labour efficient alternative of paddy cultivation, seemed more attractive to the farmers. They perceived that the economic losses of shifting to DSR were significantly less than shifting to alternative crops due to larger market risk and disruption of supply chains for alternative crops. Further, the Government of Punjab encouraged DSR by distributing about 4000 DSR machines at subsidized rates along with large-scale efforts on extension activities to promote this technology. Reportedly, about 5 lakh hectares (ha) area under paddy was sown through DSR during that time (Vatta *et al.,* 2021). But the results were not encouraging during the subsequent years as the paddy area cultivated with DSR technology was much lesser than the targets. During 2022 *kharif* season despite announcing incentives for farmers, the Punjab government missed its DSR target by a huge margin . Against the target of 30 lakh acres (12 lakh hectares), the government managed to bring only 1.68 lakh acres (5.6% of target) under DSR (HT 2022).Various studies (Kaur and Kaur 2017, Kaur and Singh 2017, Kaur *et al.,* 2017, Sidana *et al.,* 2020, Vatta *et al.,* 2021; Singh *et al.,* 2023b) listed poor initial germination, poor crop look, high weed infestation, problem of rodents, lesser yield, high risk to crop in DSR and non-availability of DSR drill as the reasons for shifting back to traditional technique of PTR cultivation. Further, there were considerable variations in the practices of cultivation followed by the farmers from the recommended practices (Kamboj *et al.,* 2022). Due to this they faced plenty of technical issues regarding the establishment of the crop and ploughed back the crop. Keeping all this in view, the present study was carried out in Punjab state with the following objectives.

Objectives

1. To examine the extent of DSR adoption in Punjab
2. To compare input use and energy consumption pattern in DSR and PTR
3. To study the reasons for non-adoption of DSR in the state.

Materials and Methods

To study the extent of adoption of DSR in the Punjab state, secondary data for the year 2023-24 was gathered from the Department of Agriculture, Punjab. Further, to accomplish the objectives of the study, primary data was collected by using multi-stage random sampling technique. At the first stage, one district namely Sri Mukatsar Sahib having the highest area under the DSR technology for paddy cultivation was identified through consultation with officials of the Punjab

State Department of Agriculture. Keeping in view the concentration of DSR technology, two blocks namely Gidderbaha and Mukatsar were selected at the second stage **(Figure 1).** From each selected block, two villages were selected for the study, as shown in **Figure 1.**

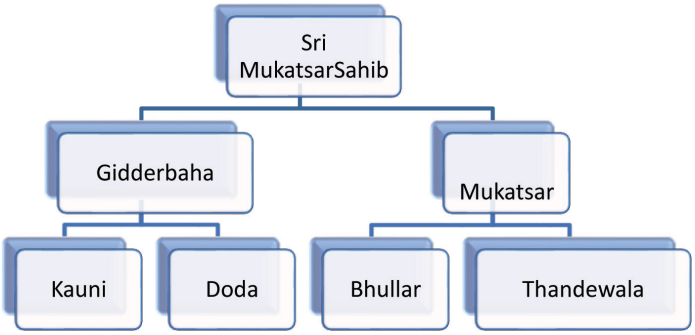


Figure 1: Distribution of survey sample

20 DSR farmers were chosen from each selected village for the study using simple random sampling technique. In order to undertake impact assessment of the DSR technology, ten PTR farmers from the same vicinity were also taken as a control group in the analysis. Thus, the total sample for the study comprised of 120 farmers (80 DSR and 40 PTR farmers) spreading over different farm size groups based on operational holding i.e. small (up to 5 acres), medium (>5 to 15 acres) and large (more than 15 acres).

The primary data pertaining to the two systems of rice cultivation i.e. DSR and PTR were collected from the sample farmers for the agricultural year 2021-22 through personal interview method. Requisite information relevant to various inputs used in paddy cultivation such as seed, diesel fuel (consumed for various farm operations viz. seed bed preparation, inter-culture operations, harvesting, transport on farm etc.), fertilizers, Farm Yard Manure (FYM), chemicals (insecticides, fungicides, herbicides), total working hours of labour (men and women hours) as well as draught power used for different farm operations along with total working hours of agri-machinery were recorded. The information on capacity of the pumps used by the farmer for irrigating in terms of horse power (Hp) was also collected from the respondents. Data on paddy grain yield was used for the estimation of straw yield using crop to residue ratio method (Chauhan, 2012).

The data on inputs used in paddy cultivation and output (grain and straw) were converted to energy units using embodied energy equivalents for each input and output energy type and expressed in Mega Joules (MJ) using specific energy coefficients taken from the Research Digest on Energy Requirement in Agriculture Sector, Department of Farm Power and Machinery, PAU (Singh and Singh, 2002) as mentioned in **Table 1.**

Table 1: Energy coefficients for energy calculation in paddy cultivation

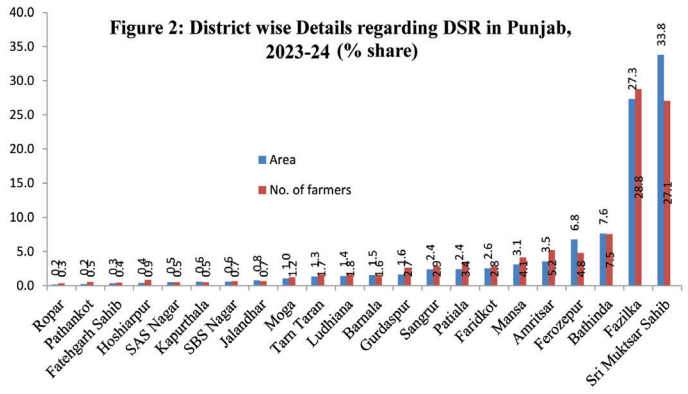
Sr. No.	Energy source	Energy coefficient (MJ/unit)
1	Human labour (h)	1.96
2	Animal labour (h)	14.05
3	Fertilizer (kg)	
	N	60.6
	P_2O_5	11.1
	K_2O	6.7
4	Farmyard manure (FYM) in kg	0.3
5	Chemicals (kg and litre respectively)	120 and 102 respectively
6	Machinery (h)	62.7
7	Diesel (litre)	56.31
8	Seed/Grain (kg)	14.57
9	Straw (kg)	12.5
10	Electricity (KWh)	11.93

Source: Singh and Singh, 2002

Status of adoption of DSR in Punjab

Considering sustainable agriculture as the keystone of Punjab's social and economic prosperity, promotion of DSR remained one of the pioneer steps in the Punjab Government's 2023-24 Budget.

About 17026 thousand famers have been provided with an incentive Rs1500 per acre for adopting the practice of DSR, for which Rs 19.92 crore has been paid during 2023-24. During 2023-24, the area under DSR was 53 thousand hectares forming only about 2 per cent of the total area under paddy. District wise analysis of the data revealed that the highest proportion of area under DSR was in Shri Mukatsar Sahib (33.8%) followed by Fazilka (27.3%), Bathinda (7.6%), Firozpur (6.86%) and Mansa (3.1%) while in other districts it was below 3 per cent as shown in **Figure 2.**



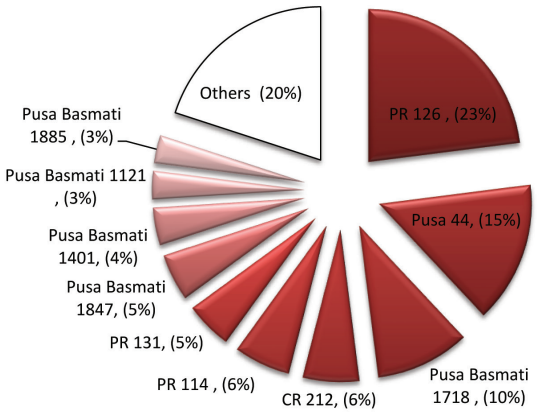
Source: Department of Agriculture, Punjab

In terms of number of farmers availing the subsidy, the maximum belonged to Fazilka (28.8%) followed by Shri Mukatsar Sahib (27.1%), Bathinda (7.5%), Amritsar (5.2%), Ferozepur (4.8%) and Mansa (4.1%).

Thus, DSR paddy adoption rate was higher in the south western districts of the state. One major reason behind this is that ground water is not fit for irrigation in most of the villages in this area. According to an earlier study, the adoption of DSR was higher amongst the farmers with relatively lower access to irrigation (Vatta *et al*, 2021).

According to estimates of Department of Economics and Sociology PAU, it was observed that maximum area under DSR during 2023-24 was under recommended non-basmati paddy variety PR126, requiring 120 days to mature followed by un-recommended Pusa 44 (15%) which is a long duration variety of paddy needing 155-160 days to mature (**Figure 3**). Among basmati varieties, Pusa Basmati 1718 occupied about 10 per cent of the DSR area followed by un-recommended Pusa Basmati 1847 (5%) and Pusa Basmati 1401 (4%) with rest being on less than three per cent of the DSR area.

Figure 3: Variety wise area under DSR in Punjab, 2023-24 (% share)



Source: Department of Economics and Sociology, PAU

Comparison of DSR to PTR in terms of input use energy consumption

The resource use in paddy cultivation on different farm sizes under DSR method of cultivation selected for the present study is given in **Table 2**. Analysis of the data revealed that use of human labour worked out to be 101.03 hours per acre on an average and machine labour (use of machinery for various cultural operations comprising mainly land preparation, irrigation, harvesting and on farm post-harvest operations) ranged between 7.85 - 8.67 hours per acre and it was 8.3 hours per acre on an average.

Table 2: Input use pattern, energy consumption and returns for paddy cultivation by DSR in Punjab

(Per acre)

Sr. No.	Input/Farm category	Small	Medium	Large	Overall (DSR)	PTR	Mean difference for DSR with traditional paddy cultivation	
							Input use	Energy consumption
1	Human Labour (h)	100.05	101.01	102.09	101.03	169.90	-68.87**	-122.38**
2	Animal Labour (h)	1.11	0.75	0.40	0.75	1.00	-0.25	-3.51
3	Machine Labour (h)	7.85	8.38	8.67	8.3	9.50	-1.20**	-18.73**
4	Diesel (litre) #	39.8	42.45	46	42.75	46.50	-3.75*	-211.15**
5	Seed (kg)	7.48	7.9	8.29	7.89	5.30	2.59**	38.07**
6	Fertilizers, micro nutrients and FYM							
a	Urea (kg)	143.0	141.0	147.5	143.80	170.62	-26.82**	-1696.63**
b	Phosphatic (kg)	6.21	6.53	6.90	6.54	6.80	-0.26	-2.89
c	Muriate of Potash (kg)	5.62	6.30	6.50	6.14	6.80	-0.66	-4.42
d	**Zinc (kg)**	4.50	5.20	5.70	5.13	6.50	-1.37*	-28.63*
e	**Iron Sulphate (kg)**	4.90	5.90	6.66	5.82	4.60	1.22	12.23
f	Others (kg) ##	2.50	3.20	3.60	3.18	2.70	0.48	4.80
g	FYM (Ton)	5.30	5.82	6.10	5.74	5.90	-0.16	-78
7	Plant Protection Chemicals							
a	Rodenticide (kg)	1.20	1.62	1.80	1.54	0.50	1.04**	125.98**
b	Insecticide (litre andkg)	2.30	2.60	3.20	2.70	2.23	0.47	47.98
c	Weedicide (litre)	2.80	3.30	3.55	3.21	1.20	2.01**	205.22**
8	Electricity for irrigation (KWh)	**603.03**	**609.01**	618.16	610.05	725.40	-115.35**	-1376.12**
9	Output							
A	Grain (Qtls)	**27.20**	**28.01**	27.88	27.69	28.01	-32.30	-1.15
B	Straw (Qtls)	**36.72**	**37.81**	37.63	37.38	37.81	-43.61	-1.15

Non-significant differences were observed among farm categories

#includes use of tractor for land preparation, irrigation, transport on farm and harvester combine

##includes seed treatment chemicals and growth regulators; ** and * significant at one and five per cent level of significance

Source: Field Survey

Thus, with farm size the use of human as well as machine labour increased. Consequently, the diesel fuel used in prime movers and oil engines/generators for running pumps on small farms (39.80 litre per acre) was lesser than on large farms (46.00 litre per acre) with average figure being 42.75 litre per acre. On the contrary, the animal labour use for on farm transportation showed inverse relationship with the farm size. The use of animal labour was reported to vary between 0.40 hours on large to 1.11 hours per acre on small farms and average figure worked out to be 0.75 hours per acre. In a similar kind of study for Punjab, maximum value for mechanization index was observed in the case of large farmers and maximum animal labour index was observed in the case of marginal farmers (Kaur *et al,* 2017).

Further analysis revealed that the seed rate increased with rise in the farm size. On an average, 7.89 kg/acre seed rate was followed by DSR adopters as against recommended seed rate of 8 kg/acre and it was the highest on large farms (8.29 kg /acre), followed by medium (7.90 kg/acre) and small farms (7.48 kg/acre). On the other hand, dose of urea applied was higher for small farmers than the medium category farmers. Two main reasons behind this pattern are lack of knowledge among farmers about the recommended package of practices and existing nutrient based subsidies on these chemical fertilizers. The DSR adopters were found to be using much higher dose of urea than recommended by the PAU (130 kg per acre). High magnitude of subsidies for nitrogen fertilizer extended by the government indirectly encouraged the farmers to apply larger quantities of nitrogen fertilizer for paddy crop. The average figures for the use of different chemical fertilizers namely urea, phosphatic fertilizers, muriate of potash and micro nutrients zinc, Iron sulphate and others (including seed treatment chemicals and growth regulators) were estimated to the tune of 143.80, 6.54, 6.14, 5.13, 5.82 and 3.18 kg per acre respectively on an average and their use was also found to increase with the farm size. Almost similar results were reported by Saha *et al.,* 2020.

The use of farm yard manure (FYM) was the highest on large farms (6.10 ton per acre) and the least on small farms (5.30 ton per acre) and this happened due to high availability of FYM from large livestock with the large farmers. As regards the use of plant protection chemicals (PPC) is concerned, the average use of rodenticides, insecticides (both liquid and granular) and weedicides turned out to be 1.54 kg, 2.70 (litre and kg) and 3.21 litres per acre respectively and their use was the highest by the large farm category. Similarly, the use of electricity for the irrigating one acre of DSR paddy turned out to be the highest on large farms (618.16 KW) as compared to small (603.03 KW) and medium farms (609.01 KW) though it was freely available to all the farm categories. The pumping of irrigation water from deeper layers of underground water through submersible electric pumps and electric motors has led to the high electricity consumption in the state. Further, on account of free of cost supply of electric power to agricultural sector in Punjab state, farmers had no incentive in saving electricity. The output from paddy cultivation in terms of grain and straw production of paddy was to 27.69 and 37.38 quintals on an average and it was the marginally high for the medium farm category (28.01 Qtls per acre) than small (27.2 Qtls per acre) and large farms (27.88 Qtls per acre). The analysis revealed that the input use in DSR paddy cultivation increased with the farm size, except use of animal labour. However the differences existed among the different farm categories in input use was non-significant.

The results for comparative input use pattern under DSR and PTR method revealed that human labour use was found to be about 41 per cent higher for PTR (169.9 hours) than for DSR (101.03 hours) as the human labour requirements in DSR were reduced due to no need for transplanting the paddy seedlings. Machine labour use was also higher by about 13 per cent for PTR (9.50 hours) than DSR (8.30 hours) and consequently about 8 per cent higher diesel use existed in PTR (46.5 litre) than DSR (42.75 litre). Compared to the average seed rate used by DSR adopters (7.89 kg), the PTR followers used only 5.30 kg of seed for sowing one acre of paddy because of self-confidence in their farming practices. Among different chemical fertilizers, the use of urea, phosphatic fertilisers, muriate of potash and micro nutrients-zinc and Iron sulphate, was higher for PTR than DSR except Iron sulphate (lower for PTR by 1.22%) and seed treatment chemicals and growth regulators (by 0.48%). On the contrary, the use of PPC was much higher by the DSR adopters. Due to huge weed infestation, almost double amount of weedicide

application per acre (3.21 litre) was observed for DSR than PTR (1.20 litre). Further, use of rodenticides to avoid rodent attack was three times higher side in DSR (1.54 kg) than PTR (0.50 kg). Insecticide application was also higher in DSR (2.70 kg) than PTR (2.23 kg) though the difference was statistically non-significant. The use of electricity for the irrigation was higher on PTR (725.40 KW) than the DSR farms (610.05 KW) by about 16 per cent because of lesser number of irrigations and water application in DSR.

The analysis revealed that use of all the inputs was lower on DSR farms as compared to PTR farms except seed, plant protection chemicals (PPC) and micro nutrient iron sulphate. The mean difference of major inputs such as human labour, machine labour, diesel fuel, seed rate, urea, rodenticides, weedicides, electricity differ significantly between DSR and PTR method of paddy cultivation. Accordingly, energy use was also lower in DSR system.

In terms of important economic parameters such as yield, total variable cost, gross returns, net income of DSR over PTR method of paddy cultivation the results are presented in **Table 3**.

Table 3: Economic benefits of DSR vs PTR in Punjab

(per acre)

Sr. No.	Particulars	DSR	PTR	Advantage in DSR (%)
1	Yield (kg)	2769.00	2801.30	-1.15
2	Total variable cost (Rs)	23344.06	27677.33	-15.66
3	Gross returns (Rs)	54826.20	55465.75	-1.15
4	Net returns over variable cost (Rs)	31482.14	27788.42	13.29
5	Cost of Grain production (Rs per kg)	8.43	9.88	-14.68
6	Energy (MJ per kg)	7.84	8.86	-11.51
7	Total Energy Input (MJ/Acre)	21708.61	24816.79	-12.52
8	Total Energy Output (MJ/Acre)	87431.18	88451.05	-1.15

Source: Field Survey

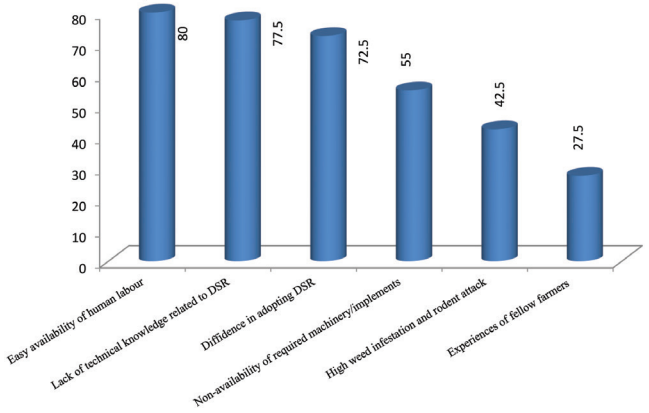
The results revealed that though the yield in DSR (2769 kg per acre) was marginally lower than PTR (2801.3 kg per acre), the net returns over variable cost were higher by about 13 per cent in DSR (Rs 31482.14 per acre) than PTR (Rs 27788.41 per acre). This is because of lower variable costs involved in DSR. The cost in production of one kg grain using DSR was found to be lower (Rs 8.43 per kg) by about 15 per cent than in PTR (Rs 9.88 per kg) and the input energy involved in the same was Rs 7.84 MJ as compared to 8.86 MJ.

Hence, the results of the present study indicated that DSR is an input saving as well as cost saving technology for paddy cultivation in comparison to traditional PTR method.

Perceptions of the respondents regarding non-adoption of DSR

Some genuine reasons and perceptions of the respondents for 'not adopting' the DSR has been presented in **Figure 4.** The results revealed that easy availability of labour for transplanting paddy emerged to be the major reason for not following the DSR by 80 per cent respondents. Other perceptions like lack of technical knowledge of DSR (77.5%), diffidence in adopting DSR (72.50%) and non-availability of required machinery/implements (55%) for sowing were the major reasons of not adopting the DSR.

Figure 4: Perceptions of respondents regarding non-adoption of DSR in Punjab (% share)



Source: Field Survey

Other reasons such as high risk of weed infestation and rodent attack and experiences of fellow farmers were reported by about 28 and 43 per cent, respectively. In a study by Kaur and Singh, (2017) at Punjab Agricultural University Ludhiana several constraints associated with shift from PTR to DSR included, high weed infestation, evolution of weedy rice, increase in soil borne pathogens (nematodes), nutrient disorders, poor crop establishment, lodging, incidence of blast, brown leaf spot etc.

Conclusions and Suggestions

Currently, DSR is emerging as an option for sustainable rice production, owing to limited water availability, shortage of labour and rising cost of cultivation. Though the method is economically advantageous and also farmer-friendly, yet it needs technological advancement to reap the full benefits and speedy adoption. It points towards need for more research in development of high yielding rice cultivars suitable for DSR in various agro-climatic situations along with ensured and timely availability of agro-inputs and machinery at affordable prices. There is a need to generate more awareness of recommended DSR production practices among the farmers along with the benefits of such practices. Embracing of such standard practices especially judicious use of inputs like fertilizers, underground water and plant protection chemicals will not only optimize the energy use but also will minimize the cost of cultivation. There is a need to focus more on capacity building by educating/training the young farmers for promotion of DSR. A campaign with the combined efforts of various stakeholders such as government agencies and non-government organisations as change agents will help in fast pacing the adoption process of DSR.

References

Anonymous 2022. *Ground Water Resources of Punjab State* (As on 31st March, 2022), Prepared by Ground Water Management Circle Water Resources Department, Punjab S.A.S Nagar and Central Ground Water Board North Western Region Chandigarh: 123.

Bandumula N, Mahajan G, Kumar R M. 2018. Farm Level and Aggregate Economic Impact of Direct Seeded Rice in Punjab. *Journal of Experimental Biology and Agricultural Sciences,* 6(1): 253-257.

Chauhan S. 2012. District wise agriculture biomass resource assessment for power generation: A case Study from an Indian state, Punjab. *Biomass Bioener,* 37: 205-12

HT 2022. Incentives fail to woo farmers, Punjab misses DSR target. Paddy sowing: Water level down, Punjab govt ups DSR drive. *Hindustan Times* 29th September, 2022. https://www.https://www.hindustantimes.com/cities/chandigarh-news/incentives-fail-to-woo-farmers-punjab-misses-dsr-target-101664398165382.html.

Jat RK, Meena VS, Kumar M, Jakkula VS, Reddy IR and Pandey AC, 2022. Direct Seeded Rice: Strategies to Improve Crop Resilience and Food Security under Adverse Climatic Conditions. *Land* 11(3): 382.

Kamboj R, Singh D and Kaur L. 2022. Adoption status of Direct Seeded Rice technology by the farmers

of Punjab. *Indian Journal of Extension Education,* 58(1): 76-80.

Kaur J and Singh A. 2017. Direct seeded rice: prospects, problems/constraints and researchable issues in India. *Current Agriculture Research Journal*, 5(1): 13-32.

Kaur K and Kaur P. 2017. Reasons for adoption and non-adoption of direct seeded rice in Punjab. *Indian Journal of Extension Education*, 53(1): 157-159.

Kaur K, Kaur P and Kaur T. 2017. Problems faced by farmers in cultivation of direct seeded rice in Indian Punjab. *Agricultural Research Journal*, 54(3): 428-431.

PAU 2022. *Package of Practices for Cultivation of Kharif Crops,* Punjab Agricultural University (PAU), Ludhiana: 1-21.

Saha S, Bandyopadhyay S, Mitra B, Patra PS and Paul T. (2020). Response of wet direct-seeded rice to methods of zinc application. *Journal of Rice Research* 2020, 13(1): 59 - 65.

Sidana BK, Singh JM, Kumar H, Singh J and Sachdeva J. 2020. Comparative economics of direct seeded rice technology and transplanted rice in Punjab. *Journal of Pharmacognosy and Phytochemistry*, SP6: 35-41.

Singh G, Ranguwal S and Kumar R. 2023b. Direct Seeding of Rice in Punjab: Current Status, Performance and Limitations. *Indian Farming* 73 (8): 36-38.

Singh G, Ranguwal S and Sachdeva J 2023a. Resource Use Pattern and Adoption of Direct Seeded Rice in Punjab. *Journal of Agricultural Development and Policy,* 33(1): 44-50.

Singh S and Singh J 2002. Research digest on energy requirement in agriculture sector, Department of Farm Power and Machinery, Punjab Agricultural University, Ludhiana 29: 1- 263.

Vatta K, Singh J, Kaur P, Bhardwaj S and Singh K. 2021. *Appraisal of Direct Seeding of Rice in Kharif 2020.* Department of Economics and Sociology, Punjab Agricultural University, Ludhiana-141004.

SHORT COMMUNICATION https://doi.org/10.58297/YQJH3827

BPT 2846 (IET 28737), A High Yielding Slender Grain Rice Variety Suitable for Krishna Zone of Andhra Pradesh

Krishna Veni B[1], Tushara M[2]*, Satyanarayana PV[3], Ramana JV[4], Suneetha Y[5], Roja V[5], Srinivas T[5] and Anny Mrudhula K[6]

[1]Agricultural Research Station, Bapatla, [2]Agricultural College, Bapatla, [3]Director of Research, ANGRAU, [4]Planning and Monitoring cell, ANGRAU, [5]Regional Agricultural Research Station, Maruteru, [6]Agronomy, SWS, Bapatla

*Corresponding author Email: m.thushara@angrau.ac.in

Received : 11th September, 2024;, Accepted: 10th October, 2024

Abstract

BPT 2846, developed through pedigree breeding at the Agricultural Research Station, Bapatla, is a result of the cross between MTU 1061 and IR78585-64-2-4-3-1. During the *kharif* seasons of 2015-2017, it underwent station yield trials, demonstrating an average grain yield of 6352 kg/ha. This marked a substantial 18.6% improvement over the reference variety BPT 5204. In the Multi-location Trial-Slender grain of *kharif* 2019, BPT 2846 showcased a noteworthy average grain yield of 6355 kg/ha, exhibiting a 23.0% improvement over the common check BPT 5204. Nominated in the AICRIP trial under the Initial Variety Trial-Medium Slender category as IET 28737 in 2019, BPT 2846 displayed adaptability across various locations in the country, recording a mean grain yield of 4420 kg/ha. The rice variety was further subjected to adaptive minikit testing in farmers' fields by DAATT Centres for three years, resulting in an average grain yield of 6513 kg/ha. This reflected an 11.8% improvement over BPT 5204. Similarly, minikit testing conducted by DAOs recorded an average grain yield of 6497 kg/ha for BPT 2846, demonstrating a 12% yield improvement over BPT 5204. Belonging to the late duration group with a 145-150 days duration in the *kharif* season, BPT 2846 is well-suited for irrigated wetlands in Andhra Pradesh. It possesses characteristics such as non-lodging, a semi-dwarf and erect plant type, dark green foliage, two weeks of seed dormancy, low shattering and high grain yield. Additionally, BPT 2846 exhibits moderate resistance to leaf blast, neck blast and leaf folder. It boasts excellent cooking quality, intermediate values of alkali spreading and amylose content, high head rice recovery (65.2%) with translucent grains and a Kernel Length to Breadth ratio of 2.85. These attributes make it highly desirable for obtaining a premium market price.

Keywords: Rice variety, medium slender grains, high yielding, late duration

Introduction

One of the main objective of the Agricultural Research Station, Bapatla is to create a high-yielding rice variety tailored for the *kharif* season, featuring a duration of 145-150 days. Even though, BPT 5204 possess good yield potential and excellent grain and cooking quality, it is susceptible to major pests/diseases due to which often farmers suffer heavy yield losses. Hence, there is a demand from the farming community for stable rice varieties with sustained production even under adverse climatic conditions with reduced cost of cultivation. Efforts are underway at Agricultural Research Station, Bapatla for the development of high yielding rice

varieties with 145-150 days duration (suitable for double cropped areas), non-lodging, low shattering of grains along with resistance to leaf blast, neck blast, plant hoppers coupled with good grain quality suitable for raw rice. Many varieties possessing high yield potential with tolerance to blast were released for replacement of Samba Mahsuri. But, many of them were not accepted by farmers due to their poor cooking quality traits. After years of dedicated efforts starting in 2009, BPT 2846, a rice variety with favorable features capable of replacing BPT 5204, was finally released by SVRC in 2023.

BPT 2846 possess excellent grain and cooking quality parameters similar to Samba Mahsuri. The cultivar BPT 2846 has the following desirable features.

- Duration: 145-150 days
- Erect plant type
- Strong culm, Non-lodging
- One-week seed dormancy
- Moderately resistant to leaf blast, neck blast and leaf folder
- Low shattering of grains
- Suitable for raw rice
- Medium slender grain with high market price and good consumer acceptability

The proposed cultivar, BPT 2846 is a high yielding, non-lodging, semi-dwarf, profuse tillering culture, possess medium slender grains with straw glume with 145-150 days duration suitable for double cropped areas also. It has two weeks seed dormancy. It is very much suitable for cultivation during *kharif* season in Krishna zone of Andhra Pradesh in realizing higher yields. Due to its non-lodging nature, the proposed culture is suitable for cultivation under direct sown conditions and for mechanical harvesting also.

Biotic stress resistance:

The screening trials data revealed that the suggested variety demonstrates moderate resistance to leaf blast, neck blast and leaf folder. This finding suggests that farmers may reduce pesticide sprayings, resulting in lower cultivation expenses and promoting sustainable yields **(Tables 1 and 2)**.

Table 1: Reaction of BPT 2846 to major diseases

Variety	National Screening Nursery-II (AICRIP) testing during 2019)		Variety	ARS, Nellore during, 2020-21			
	Leaf Blast	Neck Blast		Leaf Blast	Neck Blast	Sheath Rot	BLB
BPT 2846	5.2	3.0	BPT 2846	5.0	5.0	3.0	5.0
Check (BPT5204)	6.3	7.0	Check (BPT5204)	9.0	9.0	7.0	9.0
Resistant Check (Tetep)	3.0	2.0	Resistant Check	-	-	-	-
Susceptible Check (Pusa 44)	5.3	8.0	Susceptible Check (NLR34242)	9.0	9.0	9.0	9.0

Table 2: Reaction of BPT 2846 to major insect pests

Variety	National Screening Nursery - II (AICRIP) testing during 2019)
	Leaf Folder Score
BPT 2846	0.8
Check (BPT5204)	2.46
Resistant Check (W1263)	1.85
Susceptible Check (TN1)	3.36

BPT 2846 grain quality:

BPT 2846 exhibits outstanding cooking quality, along with intermediate and desirable values of alkali spreading value and amylose content. Additionally, it boasts high head rice recovery (65.2%) characterized by translucent grains and a Kernel Length to Breadth ratio of 2.85, making it highly sought after for obtaining a premium market price **(Table 3).**

Table 3: Physico-chemical and Biochemical quality characteristics of unpolished BPT 2846 and BPT 5204

S. No	Trait/ Character	Description of BPT 2846	Description of BPT 5204
1	Hulling (%)	76.6	75.8
2	Milling (%)	69.3	68.4
3	Head rice recovery	65.2	62.8
4	Kernel length (mm)	5.42	5.63
5	Kernel breadth (mm)	1.90	2.14
6	L/B ratio	2.85	2.63
7	1000 grain weight (g)	13.5-14.0	14.5-15.0
8	Gelatinization temperature	Intermediate	Intermediate
9	Keeping quality	Good	Excellent
10	Cooking quality	Excellent	Excellent
11	Alkali spreading value	4.5	5.0
12	Amylose content (%)	22.7	22.65
13	Protein content in unpoli-shed rice (%)	8.2	8.0
14	Fe content in unpolished rice (ppm)	6.2	8.7
15	Zn content in unpolished rice (ppm)	21.8	16.8

The organoleptic evaluation of BPT 2846 along with other rice varieties revealed that it recorded on par score with the popular BPT 5204 for overall acceptability and possess 8.2% protein content in brown rice. The unpolished rice of BPT 2846 possessed, 21.8 ppm Zn and 6.2 ppm iron content.

Performance in Multi-Location Trials and Adaptive minikit tests:

BPT 2846 was evaluated in station yield trials in *kharif* 2015-2017 and recorded an average grain yield of 6352 kg/ha in station trials with 18.6% yield improvement over the check variety BPT 5204. In Multi-Location Trial-Slender Grain conducted during *kharif* 2019, BPT 2846 recorded 6355 kg/ha and showed 23.0% yield improvement over common check BPT 5204. BPT 2846 (IET 28737) was nominated in AICRIP trial (Initial Variety Trial- Medium Slender) during 2019 and recorded a mean grain yield of 4420 kg/ha in different locations tested across the country.

The entry BPT 2846 was evaluated in adaptive minikit testing conducted by DAATT Centres in farmer's fields of erstwhile Krishna, East Godavari, Guntur, Kurnool, Darsi, Srikakulam, Vizianagaram, Visakhapatnam, Nellore, Ongole and Peddapuram districts in *kharif* season during the years 2019-20, 2020-21 and 2021-22. Across all the locations over three years, it recorded an average grain yield of 6513 kg/ha and exhibited 10.6% yield superiority overchecks *viz.,* BPT 5204/BPT 2782 and exhibited 11.8% improvement over BPT 5204.

Minikit testing conducted by the JDA's of erstwhile Guntur, Nellore, Krishna, East Godavari, Prakasam, Visakhapatnam and Vizianagaram districts of Andhra Pradesh, BPT 2846 recorded an average grain yield of 6497 kg/ha and 11.3% yield improvement over checks *viz.,* BPT 5204/BPT 2782. When compared with BPT 5204 it recorded 6545 kg/ha and 12% yield improvement.

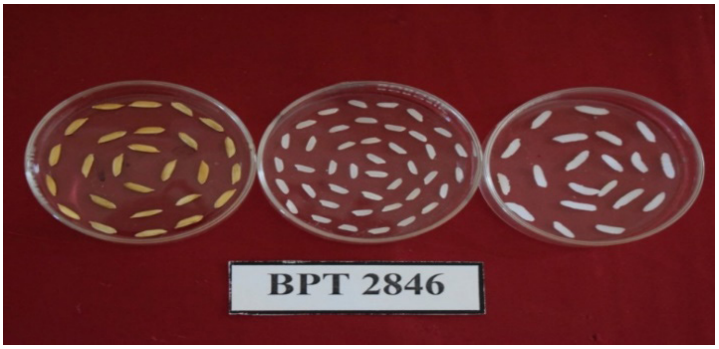
During 2021-22, BPT 2846 was tested against BPT 2782 in Guntur, Nellore, Krishna, Visakhapatnam and Prakasam districts and it recorded 6563 kg/ha grain yield and exhibited 8.6% yield superiority over the recently released variety *i.e.,* BPT 2782.

Agronomy trials were conducted for BPT 2846 at Agricultural Research Station, Bapatla. The results revealed that BPT 2846 recorded significantly superior grain and straw yield at 160 kg nitrogen/ha.

Conclusion

Farmers, industry (millers) and consumers alike have embraced BPT 2846. Over 50,000 acres in Krishna, Guntur, Nellore and Prakasam Districts were dedicated to planting BPT 2846 during the *Kharif* seasons of 2021 and 2022. Millers express great satisfaction due to its impressive milling capabilities and high head rice recovery, accompanied by minimal breakage (2-3%). Consequently, millers are offering a premium price for BPT 2846. Consumers are content with the cooking and eating quality parameters of BPT 2846.

Field View of BPT 2846



Paddy and Rice of BPT 2846

Panicles of BPT 2846

Paddy and Rice of BPT 2846

SHORT COMMUNICATION https://doi.org/10.58297/LSQC1623

DRR Dhan 74 (IET 30252) a Climate Resilient High Yielding Rice Variety with Low Soil Phosphorous Tolerance

Divya Balakrishnan*, Sarla Neelamraju, Sundaram RM, Swamy AVSR, Jyothi Badri, Padmavathi G, Anantha MS, Senguttuvel P, Aravind Kumar J, Sai Prasad SV, Neeraja CN, Kalyani MB, Suneetha K, Prasad MS, Ladhalakshmi D, Laha GS, Gireesh C, Jhansi Lakshmi V, Padmavathi Ch, Padmakumari AP, Latha PC, Mahendrakumar R, Sreedevi B, Tuti M, Mangrauthia SK, Brajendra P, Manasa V, Sanjeeva Rao D, Muthuraman P, Pranay G, Rao YV, Krishnamraju A, Kavitha B, Vijay Kumar M and Tahseen M

ICAR-Indian Institute of Rice Research (ICAR-IIRR), Rajendranagar, Hyderabad-500030

*Corresponding author Email: dbiirr23@gmail.com

Received: 4th December, 2024; Accepted: 11th December, 2024

Abstract

Changing climate conditions along with nutrient deficient soils adversely affect the environment and reduce rice production. Wild introgression lines derived from KMR 3 and *O. rufipogon* were evaluated in various environments to identify high yielding stress tolerant genotypes. DRR Dhan 74 (IET 30252) is a variety developed by IIRR, using parental lines from an Indian accession of *Oryza rufipogon* (IC22015/WR120) collected from Kerala, India, which was maintained at IIRR (erstwhile DRR) and was used as a donor parent. KMR 3, a restorer line for popular high yielding hybrid KRH 2 was used as recurrent parent and the variety was developed through advanced back cross breeding and selection. This short bold grain type variety is suitable for both normal irrigated and low soil phosphorous conditions in *kharif* and *rabi* seasons. An average yield of 7 t/ha under normal conditions with recommended dosage of fertilizers and 4.5 t/ ha under low Phosphorus condition was reported under AICRPR multi location trials. Variety possesses good cooking quality with short bold grain type and higher yield and moderately resistant reaction to leaf blast, neck blast, sheath rot and plant hoppers. It was released for cultivation in Karnataka, Maharashtra, Telangana and Jharkhand through Central Sub-committee on Crop Standards, Notification and Release of Varieties for Agricultural Crops vide S.O. 4027(E) dated 8th Oct 2024, CG-DL-E-14102024-257835.

Keywords: Rice variety, Low P tolerance, Climate resilience, Wild introgression

Introduction

Wild species are known for their stress tolerance and growth in resource-limited conditions. Several genes which contribute to yield and stress tolerance were lost during domestication and are not available in the existing gene pool of cultivars. Prebreeding programme at IIRR was initiated with the objective of bringing the lost valuable genes to cultivar background and enhance the allelic diversity for climate resilience. Phosphorus is the second most important key nutrient, vital for plant growth and development at all stages. Phosphorous deficiency is one of the factors limiting rice yields and farmer's profitability so it is necessary to identify genotypes with stable yield and tolerance to P deficiency. DRR Dhan 74 (IET 30252) is a

climate resilient rice variety developed by ICAR-IIRR using an interspecific cross (RP Bio 4919) between KMR 3 and *Oryza rufipogon* (IC22015/WR120). It is high yielding under both low soil phosphorus and normal irrigated condition. An advanced backcross strategy with repeated selections was followed to develop the variety as it is having a wild species in the parentage.

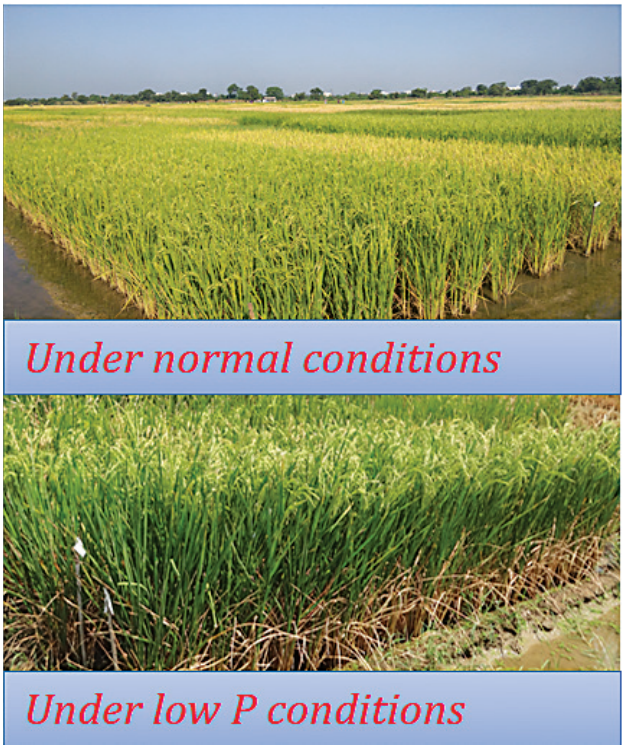
The high yielding lines in the genetic background of KMR 3 were characterized for 3 years and were further advanced based on single panicle selection up to BC_3F_{10} and the seed was multiplied. RP Bio 4919-NSR 5 is selected from a back cross introgression line derived from this cross, the genotype was tested rigorously in normal and low p conditions for several seasons and only tolerant line was advanced further. Interspecific introgression of *O. rufipogon* into *O. sativa* background helped to improve yield and tolerance to low Phosphorus in soil.

DRR Dhan 74 recorded an yield of 7 t/ha (under normal conditions; 60 kg/ha of P *i.e.,* recommended dose), 4.4 t/ ha (under low Phosphorus; 40 kg/ha of P) and 4.56 t/ha (under no Phosphorus; 0 kg/ha of P). It recorded average grain yield advantage of +14.43% and +2.96% (in terms of weighted average) over the positive check Swarna (late duration) under 0% and 50% application of phosphorous. It also showed a yield advantage of +79.56, +14.43%, +20.58 and +5.94 over Rasi, Swarna (Positive Check), Improved Samba Mahsuri (Negative check) and Qualifying check 1 (IET 30242) respectively considering weighted mean average of *kharif* 2021, 2022 and 2023 under no application of recommend dose of fertilizer (RDF) phosphorus. Similarly, at Low phosphorus condition it yielded with +14.44, +2.96, +14.78 and +8.13% advantage over Rasi, Swarna, Improved Samba Mahsuri and Qualifying check 1 (IET30242) respectively considering weighted mean average of *kharif* 2021, 2022 and 2023 under application 50% of recommend dose of fertilizer (RDF) phosphorus. Based on the performance under both 0% and 50% P of RDF. IET 30252 was found promising in zone 7, zone 3, zone 6 and also based on overall mean for all three testing years of 2021, 2022 and 2023 and promoted in AICRPR testing. In addition, entry was found superior to best check during 2021 in Karnataka and overall, it yielded 4.94 t/ha with 2nd rank and 16% yield advantage over best check. During 2022, recorded 1st, 4th, 6th and 9th rank in the states of Bihar, Telangana, Karnataka and Maharashtra. During 2023, recorded 2nd, 3rd and 5th rank in the states of Telangana, Jharkhand and Karnataka.

Variety possesses short bold grain type with high HRR (62.2%) and acceptable grain quality parameters of amylose content (23.7%), gel consistency (22) and alkali spreading value (7.0) and cooking quality parameters. Based on molecular marker analysis, it has shown > 95% recovery of recurrent parent genome. Considering better performance of the variety for yield in P deficit as well as under normal conditions and stress tolerance, grain and cooking quality traits IET 30252 was released in the states of Karnataka, Telangana andhra Pradesh and Jharkhand as DRR Dhan 74. Hon'ble Prime Minister of India dedicated DRR Dhan 74, a climate resilient variety to the farmers of the Nation on 11 August, 2024. This variety has potential to replace medium to late duration short bold varieties in low-input areas of the country with reduced cost of cultivation and making rice cultivation more economical.

Field view DRR dhan 74

Pot view DRR dhan 74



Normal and low P of field view DRR dhan 74

Grains **Decorticated grains** **Milled grains**

Rice Germplasm Registered during July to December 2024 at ICAR-National Bureau of Plant Genetic Resources, New Delhi

S. No.	Crop Name	Botanical Name	National Identity	Pedigree	INGR No.	Novel Unique Features
1	Rice	*Oryza sativa*	IC76013	IET-9854/ (Swarnadan/ veluthacheera)	24054	Possesses resistance to brown plant hopper at reproductive stage (damage score of 2.2)
2	Rice	*Oryza sativa*	IC75975	RP2068-18-2-9 (Swarnadhan/ Vellathachera)	24055	Novel donor for resistance to Brown plant hopper (damage score 2.3)
3	Rice	*Oryza sativa*	IR 75870-5-8-5-B-5-B-HWR-15	IR 64 x *O. glaberrima*//IR 64 in BC_1F_{11} generation	24056	Novel donor for resistance to Brown plant hopper (damage score is 4.2) Present in the background of IR64
4	Rice	*Oryza sativa*	IR73382-80-9-3-13-2-2-1-3-B-HWR-16	IR 64 x *O. rufipogon* acc. 106412//IR 64 in BC_1F_{11} generation	24057	Novel donor for resistance to Brown plant hopper (damage score <3) Present in the background of IR64
5	Rice	*Oryza sativa*	RP 6837- RMS- ISMA 13	Improved Samba Mahsuri (RP Bio 226)*4 / RP2068-18-3-5 in BC_3F_8 generation	24058	Novel donor for resistance to Brown planthopper (damage score <3) Present in the background of popular variety Improved Samba Mahsuri.

Source: Member Secretary, PGRC (Plant Germplasm Registration Committee), ICAR-NBPGR, New Delhi

Journal of Rice Research - Author Guidelines

Scope: Journal of Rice Research is a channel for publication of full length papers covering results of original research, invited critical reviews or interpretative articles related to all areas of rice science, rice based crop systems and rice crop management. The journal also publishes short communications, book reviews and letters to the editor.

Articles reporting experimentation or research in any field involving rice or rice based cropping systems will be accepted as original articles while critical reviews are generally invited. Short articles concerned with experimental techniques or observation of unique nature will be accepted as short communication. Letters to the editor concerning previous articles are welcome and are published subject to review and approval by the editorial board. The original authors will be invited to reply to the points raised in these letters for their response which are also published together.

General Requirement:

Submission to the journal must be reports of original research of at least two crop seasons and must not be previously published or simultaneously submitted to any other scientific or technical journal. At least one of the authors (in case of joint authorship) should be member of the Society for Advancement of Rice Research (SARR) and not in arrears of subscription. Authors of invited articles are exempted from this.

Submission of Manuscript:

Manuscripts should be sent by email to the chief editor (jrrchiefeditor@gmail.com) as an attachment. All the enclosed figures (as ppt/jpg files), graphs (as MS Excel worksheet with original data) and photographs (as jpg or ppt files with high resolution) may be submitted as separate files. Avoid using more than one font. The manuscript should be typed in double spaced times new roman font with margins of at least 2.5 cm. On the first page give the title, a byline with the names of authors, their affiliation and corresponding author's e-mail ID. Abstract should be followed by a list of key words. The usual order of sections to be included after title and abstract pages are: Introduction which includes literature review; materials and methods; results and discussion; conclusion (optional), acknowledgements and references followed by figures and tables.

Title should give a clear idea what the articles is about. It should be brief and informative (12-15 words).

Materials and Methods should include experimental design, treatment details, replications and techniques/ methods employed.

Results and Discussion should be supported by sound scientifically analysed data along with explanatory text with relevant tables and figures.

References should be quoted in author-year notation system only. All the references should be arranged alphabetically by author. All single author entries precede multiple author entries for the same first authors. Use chronological order within entries with identical authorship and add a low case letter a, b, c, etc., to year for same year entries of the same author. References should be presented in the format given below:

Research papers

1. Durvasula V. Seshu**.** 2017. Networking a Pivotal Strategy for Rice Genetic Improvement. *Journal of Rice Research*, 10: 1-8.
2. Kemparaju KB, MS Ramesha, K Sruti, AS Hari Prasad, RM Sundaram, P Senguttuvel and P Revathi**.** 2018. Breeding strategy for improvement of rice maintainer lines through composite population for short term diversity. *Journal of Rice Research*, 11: 27-30
3. Paul M and Keegstra K. 2008. Cell-wall carbohydrates and their modification as a resource for biofuels. *Plant Journal,* 54: 559-568.

Thesis

Bhuiyan MDAR. 2010. Phenotypic and genotypic evaluation of selected transgressive variants derived from *Oryza rufipogon* Griff. x *Oryza sativa* L. cv. MR219. Ph D. Thesis. University Kebaangsaan Malaysia, Malaysia, 150 p.

Book chapter

Scott JM 1984. Catabolism of folates. P. 307-327. In R.L. Blackley and S.J. Benkovic (ed.) Folates and Pterims Vol.1. John Wiley & Sons, New York

Book

Subba Rao LV, Shobha Rani N, Chiranjeevi M, Chaitanya U, Sudharshan I, Suneetha K, Jyothi Badri and Dipal R Choudhary 2013 DUS Characterization of Rice Varieties. Directorate of Rice Research, Rajendranagar, Hyderabad-500 030, AP, India. 524 pp

Figures: Photographs and drawings for graphs and charts should be prepared with good contrast of dark and light. Figure caption should be brief specifying the crop or soil, major variables presented and year. Give careful attention to the width of lines and size, and clarity of type and symbols.

Tables: Tables are used for reporting extensive numerical data in an organized manner and statistically analyzed. They should be self explanatory. Prepare tables with the word-processing tables feature and tabs or graphics boxes should not be used. Table head should be brief but complete and self contained. Define all variables and spell out all the abbreviations. An exponential expression (eg. x 10^3) in the unit's line is often needed to keep length of the data reasonably short, and referenced with an explanatory note. Unless otherwise required, two decimal place values are suggested.

Published by :

Dr. RM Sundaram, President, Society for Advancement of Rice Research, Hyderabad.

Printed at :

Balaji Scan Pvt. Ltd., Hyderabad - 500 004. Ph: 040-23303424 / 25 E-mail: bsplpress@gmail.com

Society for Advancement of Rice Research

ICAR-Indian Institute of Rice Research (ICAR-IIRR)

Rajendranagar, Hyderabad - 500 030 (India)

Phone No: +91 40 24591218; Fax: +91 40 24591217

www.sarr.co.in