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Society for Advancement of Rice Research

Society For Advancement of Rice Research

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The Society for Advancement of Rice Research is a registered society for researchers, research managers, extension personnel, institutions, development agencies, trade and industry who practice and promote activities for the advancement of rice science and development. The Society has been started with overall objectives of providing a platform for exchange of information and knowledge and to disseminate the latest developments in rice research and to bring together all persons / institutions working for the cause of rice.

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- To advance the cause of rice research and development in the country.
- To disseminate knowledge on latest development in rice research through publications, seminars, lectures and training programme.
- To provide a platform for exchange of knowledge and information on rice research and developments through organizing workshops, symposia, conferences, etc.
- 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.

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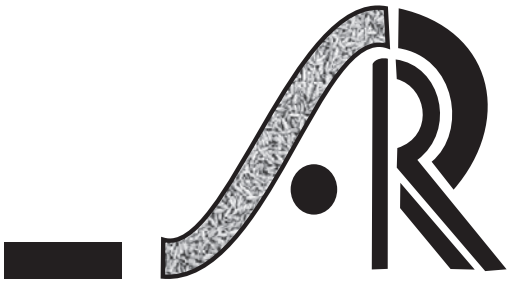

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REVIEW ARTICLE OPEN ACCESS

Networking a Pivotal Strategy for Rice Genetic Improvement

Durvasula V. Seshu*

Former Plant Breeder and Global Coordinator, INGER
International Rice Research Institute, Los Baños, Philippines
*Corresponding author:dvseshu@hotmail.com

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Abstract

Network approach for boosting efficiency in agricultural research has been widely accepted by various International and National research organizations, because of the wide-ranging benefits, most important of which is the acceleration of transfer of technology to the farmer. The International Network for Genetic Evaluation of Rice (INGER), the subject of this paper, is the world's largest agricultural research network participated by more than 75 countries in Asia, Africa, Latin America, the Caribbean and the Oceania. Through the cooperative exchange and evaluation of promising breeding lines, by end of 2015 a total of 1,120 INGER-tested lines were directly released as varieties to farmers in 74 countries. Further, several entries were used in crosses as genetic donors for important traits, and 1,129 elite lines from those progenies were released as varieties in 21 countries. Some entries have been successfully utilized as restorers in hybrid rice programs. For example, 36 hybrids released in India and 34 in China, owe their restorer source to INGER. The multi-location screening trials have provided valuable information on pathogenic variation in major disease causing organisms, and biotype variation in severe crop-damaging insect pests. Various aspects of interaction of rice with weather variables have been elucidated through special studies conducted at 23 INGER test sites in 16 countries. INGER now is at crossroads; some directions it has to pursue have been indicated for it to sustain its relevance to the national programs, and effectively address the emerging needs.

Introduction

Rice, the world's foremost food crop derived from a wild progenitor was born as a semi-aquatic plant in the hot humid tropics with a strong monsoonal pattern. However, it has gradually forayed into a diversity of habitats, breaking the environmental, as well as geographical barriers, and encompassing agroecosystems that reflect a wide range of water and temperature regimes, altitude levels and edaphic properties. Its cultivation extends to latitudes that circumscribe the tropical and semitemperate environments, ranging from 40^0 south in central Argentina to 51^0 north in northeastern China. Thus, rice is grown in more diverse environmental conditions than any other major crop. The flip side of such an ecological sprawl is its face-off with a plethora of biotic and abiotic stresses, posing a strong challenge for rice genetic improvement.

Prior to the Green Revolution era, rice scientists in the developing countries used to work in scientific isolation with limited experimental materials, paucity of research facilities including literature, inadequate training, and lack of opportunities to interact with fellow rice scientists at other locations. Moreover, the experimental stations in several instances were not quite representative of the ecosystems they were purported to serve. Progress in rice yields and thereby its production, thus remained at a pace that allowed it to be overrun by the rate of population growth. That was the post-world war II scenario in several developing countries, where rice is the main staple, and that situation has raised concerns and awareness at both national and international levels.

Because of the geographical and ecological diversity, a structured networking of rice breeding programs across the world is strategically vital for global genetic improvement of rice for cultivation in different ecosystems, and raising the world output of the grain. Such an approach is also effective within national programs with wide-ranging rice cultural systems. Networks are inexpensive and at the same time are effective catalysts for research. Collaborative networks help spread useful research results among regions with similar agroecologies.

Some national programs that gained experience in rice research turned towards pooling up their resources for a nationwide cooperative crop improvement program. An excellent example is the All India Coordinated Rice Improvement Project (AICRIP), a largest national rice research network, established by the Indian Council of Agricultural Research (ICAR) in 1965. AICRIP has successfully brought together scientists working at over 100 research stations across different states, and through its exchange platform, forged national cooperation on research on genetic enhancement, nutrition management, and protection against major insects and pathogens.

Shastry (1971) summarized the concepts, organization and implementation of the AICRIP program. AICRIP is one of the several nationwide networks launched by ICAR during the sixties, very thoughtfully, with focus on crops, fish, dairy and poultry.

Historically, at an international level, a limited and informal exchange of plant germplasm among scientists from few countries with common interest took place prior to World War II. The International Wheat Stem Rust Nursery established by the United States Department of Agriculture (USDA) in 1950 was the first formal and systematic nursery to transcend the national borders. This was necessitated by a serious outbreak of a new race of the stem rust in 1950's (Plucknett and Smith, 1984). The Rice Blast Nursery organized by IRRI in 1963, and the Spring Wheat Yield Nursery organized by the International Maize and Wheat Improvement Center (CIMMYT) in 1964 represent the first efforts by the International Agricultural Research Centres (IARCs) to work cooperatively with the National Agricultural and Extension Systems (NARES).

The establishment of a series of IARCs under the aegis of the Consultative Group of International Agricultural Research Centers (CGIAR) was a quintessential response to the emerging food crisis in early sixties of last century in the developing world. The first among those was the International Rice Research Institute (IRRI), originally funded by the Rockefeller and Ford Foundations, and established in the Philippines in 1960. IRRI in its first decade primarily focused on research and related activities at its own center, which resulted among other things in the development of a high-yielding semi-dwarf variety, IR8 (IRRI's flagship); establishment of a gene bank; development of screening techniques for resistance to major diseases and insects; establishment of a comprehensive training program, setting up of a library with world's largest collection of rice literature, and so on. To buttress the Varietal Improvement research, a multidisciplinary 'Genetic Evaluation and Utilization (GEU)' program was introduced in IRRI's second decade. Once equipped with the necessary research wherewithal, and having acquired the capacity to take a lead role, IRRI initiated the establishment of various research networks with the cooperation and commitment of the NARES. The International Rice Testing Program (IRTP) was the first among those networks. Initiation of the networks also reflects the concern and realization of IRRI, that while it has a mandate for rice improvement across the rice-growing world, its research facilities are located in but one of the several rice growing environments. For example, gall midge, a major insect pest in parts of South Asia does not occur in the Philippines, which limits IRRI's capabilities to carry research related to that pest without collaboration with scientists in the concerned national programs. Similar is the case with problems such as deepwater, low temperature *etc.* Thus networking involving NARES has become imperative for global rice improvement.

The author had the privilege to be associated with AICRIP for over 10 years and with the International Network for Genetic Evaluation of Rice (INGER, initially known as IRTP) for nearly 20 years. The experiences gained at AICRIP, the world's largest national rice improvement network proved to be of immense help to him in the implementation of INGER. To demonstrate the benefits of networking for rice breeding research, the procedures and impact of INGER have been chosen as the subject of this paper, because of its global nature.

Networking types and concepts

Cooperation through research networking has been widely adapted by various International Agricultural Research Centers in view of the wide-ranging benefits accrued by that approach. Contributions of spillover effects from regions where research is conducted to other regions with similar agroecologies has been determined to be substantial (Davis *et al.,* 1986). There are various types of networks, the design and formulations of which depend on the purpose and goals of the specified cooperative effort. Cummings and Martin (1986) proposed three types of networks:1) Information Networks that collate and disseminate research information to individuals on the mailing list, 2) Scientific Consultation Networks to share research information and ideas through discussions in meetings and workshops, and 3) Collaborative Research Networks involving joint planning and execution of research of common interest. Plucknett and Smith (1984) considered an addition of a fourth type, namely, the Material Exchange Network concerned with testing of varieties, machinery *etc*. However, in classifying the International Nurseries as typified by INGER, the author wishes to elaborate the Material Exchange Network as 'Material and Methodologies Exchange Network', where the evaluation procedures are jointly planned.

Plucknett and Smith (1984) outlined seven principles on which successful networks are grounded.

These are: Clearly defined problem and realistic research agenda; widely shared problem; strong self-interest; willingness of participants to commit resources; availability of outside funding; sufficient training and expertise of the participants to be able to make useful contributions; and a strong and efficient leadership to win the confidence of the participants. The author considers three additional requirements of importance: establishment of various mechanisms for interaction among the participants; unrestricted exchange of research materials and information; and treating the network trials as an integral part of the respective local research programs, instead of viewing them as separate and parallel entities.

International Network for Genetic Evaluation of Rice (INGER)

INGER framework

International Rice testing program (IRTP) was established by IRRI in 1975 with generous funding from the United Nations Development Program (UNDP).The network has been subsequently renamed by the author as 'International Network for Genetic Evaluation of Rice' (INGER) to better reflect the purpose and goals of the program. This cooperative program was initially implemented in Asia and later extended to rice-growing countries in Africa, Latin America and the Caribbean in cooperation with the international centers located in those respective regions, namely, International Institute of Tropical Agriculture (IITA), Africa Rice Center (formerly known as WARDA) and International Center for Tropical Agriculture (CIAT). The program which started with 12 Asian countries gradually expanded to more than 75 countries across the rice-growing world, and involves the participation of over 600 rice research stations and more than 1500 rice scientists of various disciplines – breeders, pathologists, entomologists, soil scientists, physiologists and agronomists. Thus the network reflects an international multidisciplinary approach to rice varietal improvement. Individual experimental stations assume financial responsibility for the conduct of trials at their respective locations, whereas IRRI defrays the costs involved in the logistics of processing and dispatch of seed; data analysis and preparation and distribution of reports; and in the organization of training programs, workshops and joint site visits. The coordinator located at IRRI assumes global responsibility for implementation of INGER, whereas the regional coordinators located at the respective international centers, plan the testing and evaluation in those specific regions. An advisory committee representing experienced rice scientists from selected countries meets annually to review the progress of INGER and provide suggestions to promote and sustain the relevance of the network to the national needs.

INGER objectives:

- To make the elite rice germplasm available to all rice scientists across the rice-growing world for direct use after proper evaluation, or for use in crosses as parental material.
- To provide rice scientists from the participating countries with an opportunity to assess their own advanced breeding lines over a wide range of climatic, cultural, soil, and pest and disease conditions.
- To identify genetic sources for resistance to major biotic stresses and tolerance for abiotic stresses.
- To monitor and evaluate the variation in pathogen strains and insect biotypes.
- To promote interaction and cooperation among worldwide rice improvement scientists.
- To serve as a Center for information exchange on how varietal characteristics interact with diverse rice growing environments.
- To accelerate the transfer of technology to the farmer.

The network addresses sustainability by 1) promoting genetic diversity in rice to reduce vulnerability to pest epidemics through exchanging a broad pool of genetic material, 2) identifying a range of genetic sources for durable resistance to diseases and insects that help lessen the use of chemicals, and 3) identifying genotypes with stable yields under rainfed and other unfavorable environments.

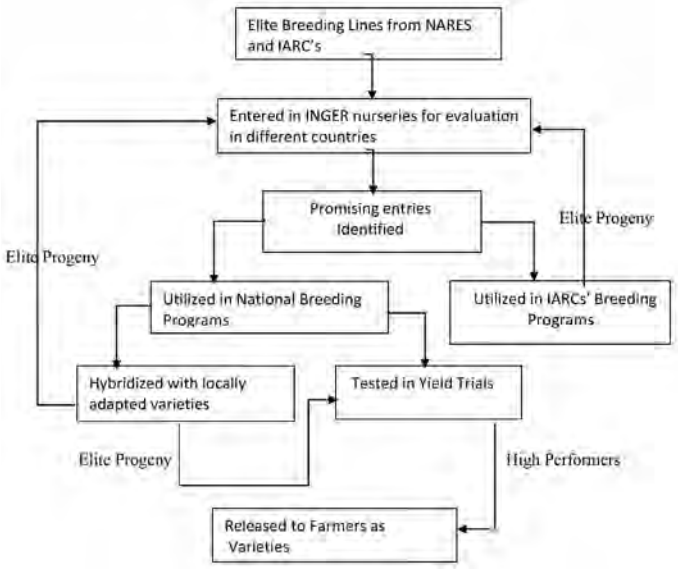
INGER logistics / procedures

Small quantities of seed of promising breeding lines from various NARES and International Centers (mainly IRRI) are obtained by the INGER Coordinator and multiplied at IRRI experimental farm to raise a required quantity of seed for experimentation at various cooperating stations. Obtaining small quantities for multiplication has been necessitated by two factors, 1) Breeders' seed of promising lines from various centers is generally limited in quantity, and may not be enough for multi-location testing, and 2) more importantly, seed increase at IRRI farm provides an opportunity to examine and ensure the seed quality in terms of both genetic purity and seed health, which in turn assures the reliability of test results. At the time of receipt of nominations and prior to distribution of nurseries, the seed is subjected to rigorous phytosanitary treatments to prevent the transfer of diseases and insect pests to the cooperating countries, and to retain the seed vigor during shipping to the test sites. The relevant phytosanitary certificate is enclosed in the seed boxes.

The pooled promising breeding lines and varieties from NARES and IARCs are organized into various types of nurseries primarily with focus on different ecosystems (irrigated, rainfed upland, rainfed lowland, tidal wetlands, deepwater *etc.*), and on different biotic and abiotic stresses. The ecosystem-oriented category involves both yield trials and observational nurseries. New nurseries have been added recently to address current issues like climate change. When the program started in 1975, over 80% of the test entries came from IRRI and the remaining from the NARES. In course of ten years after the start, the proportion of contribution of entries has significantly changed, with over 65% entries originating from NARES and 35% from IARCs, primarily from IRRI. This reflects on the strengthening of the national breeding programs, as resulting from active participation of its scientists in INGER, and in the network-sponsored joint site visits, workshops and training programs, with an opportunity to

interact with fellow rice scientists from other countries. Thus, with the strengthening of capabilities and institution building, the breeding researches of the NARES progressed from dependency to interdependency. NARES materials get fingerprinted to alleviate their concerns relating to intellectual property rights. A flowchart of international cooperative exchange and genetic evaluation of promising rice breeding lines through INGER is shown in Figure 1. Through that mechanism, over the past four decades, nearly three million seed samples representing around 55,500 entries of advanced lines have been shared for evaluation by hundreds of rice scientists at more than 600 research stations in 85 countries (Rice Today, 2015).

A Standard Evaluation System (SES) has been developed for the INGER nurseries to facilitate scoring of the morphological and physiological traits, and assessing the degree of damage caused by the major insects and pathogens. SES promotes uniform methodology in data collection lending comparability of test results from various network centers, and thus facilitating valid interpretation of the multi-location results. Specially designed field books are sent with the seed to secure a uniform reporting procedure. Data from different test sites are computerized, processed and stored for retrieval as and when needed. Results from the nurseries are analyzed by location, country and region, and across locations and years. Reports of the multi-location results with analyses are published annually and distributed to all the cooperators for follow-up research and extension activities. More recently an INGER website has been developed from which users can download reports, submit trial data and request nurseries and breeding lines.



NARES: National Agricultural Research and Extension Systems

IARCs: International Agricultural Research Centers

Figure 1: INGER Cooperative Rice Breeding Flow Chart

Monitoring visits are organized annually for a joint review of the INGER trials at selected sites by a group of scientists from NARES and IARCs. These reviews provide useful feedback for appropriate follow-up research. Also, the joint site visits along with the INGER advisory committee meetings mentioned above, and the periodic INGER and IRRI sponsored workshops provide excellent forums for interaction among rice breeders from different countries and organizations. For younger scientists they also serve as training avenues.

INGER utilization and impact

Over the past four decades, nearly three million seed samples representing around 55,500 entries of advanced lines have been shared for evaluation at more than 600 research stations in 85 countries. By end of 2015, a total of 1,120 INGER tested lines have been directly released as varieties to farmers in 74 countries in Asia, Africa, Latin America and the Caribbean for culture in different ecosystems. This signifies a true international cooperation, because several of those varieties were bred in one country and made available to farmers in another country. Further, cooperators from 51 countries made more than 20,000 crosses using genetic donors from 68 countries for incorporating various important traits, and 1,129 derivatives from those crosses were released as varieties in 21 countries (Rice Today, 2015). Some promising INGER lines have been successfully used as restorers in hybrid rice programs. For example, 34 hybrids released in China and 36 hybrids released in India to date have been developed utilizing entries from INGER.

Countries, big and small, irrespective of degree of development have been equally benefited by participation in INGER, while the network served as a two-directional conduit for those countries with greater experience in rice breeding research. According to the director of the Indian Rice Research Institute (IIRR), Hyderabad, V. Ravindra Babu, "In India, 43% of varietal releases (about 70 varieties) were directly introduced by INGER, while 250 varieties with INGER-derived parents have been released in 24 Indian states. In reciprocation, 35 Indian rice lines were released as 46 varieties in 28 countries". Shinhua Cheng, director-general of China National Rice Research Institute says "From 1981 to 2012, around 16.6 million hectares were cumulatively planted with INGER materials. These have resulted in the harvest of 6.2 million more tons of rough rice with an economic benefit of around USD 530 million. At least 2500 INGER entries were used as parents, restorers, and/or disease and pest-resistant donors in national and regional rice breeding programs. On the other hand, around 560 outstanding Chinese rice varieties have been nominated to INGER over the years for global evaluation and use in other countries" (Rice Today, 2015). According to Edgar Torres, head of the Rice Breeding Program at CIAT, "INGER has been a cornerstone for the development of rice varieties in Latin America and the Caribbean (LAC). Since 1976, this network has been

effective in disseminating improved materials. Around 115 rice varieties released in LAC originated from elite INGER lines. This germplasm also provided valuable donors for blast resistance and cold tolerance, among other key traits" (Rice Today, 2015). INGER's impact is even more pronounced in smaller and newer breeding programs according to Glen Gregorio, former IRRI plant breeder. According to him, varietal releases directly or indirectly traceable to INGER are 73% for Nepal, 72% for Myanmar, 61% for Indonesia, and 51% for Cambodia. Fifteen INGER-introduced entries were released to farmers in seven African countries: Benin. Burundi, Kenya, Mozambique, Malawi, Uganda and Zambia. Thus INGER had an impact on rice production in rice-growing countries around the world.

Apart from enabling identification of elite varieties and genetic donors for important traits, multi-location network of yield trials provide an excellent opportunity for studying Genotype by Environment (G x E) interactions of rice. When combined with data from over years, a time factor is added and a good continuum of multi-environmental variable data points are obtained to draw valid conclusions. For example, multi-location INGER rainfed lowland variety trials helped in identifying breeding lines with stable performance under rainfed culture. Figure 2 shows that the line BR 850-9-1 performed well under a wide range of environmental stresses related to rainfed culture, whereas the line BR 51-282-8 in the same set of trials gave higher yields only under favorable conditions (Seshu, 1986). Such useful information from just two or three seasons, would not have been possible, if the breeder concerned works in isolation at his/her own research station. Phenotypic stability of performance of the variety, Jaya, in irrigated yield trials was similarly determined through national multi-location trials of AICRIP in India (Seshu *et al*, 1974).

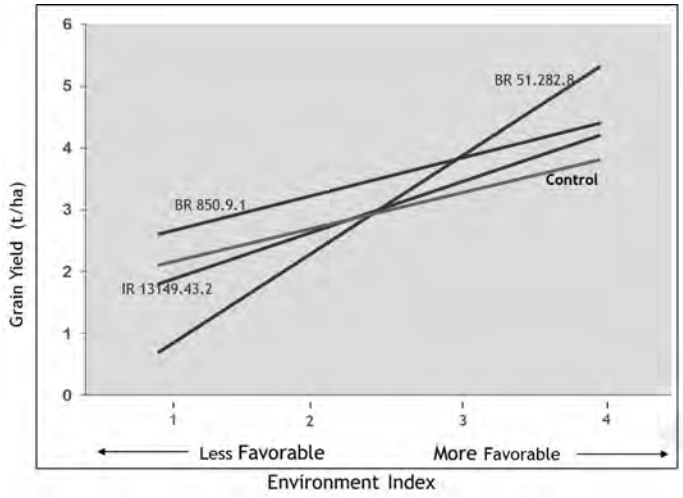


Figure 2: An example of utilization of multi-location Network Data-BR 850-9-1 shows a stable performance across a range of rainfed condition

In another G x E study, the response of rice to solar radiation and temperature was estimated from international irrigated rice variety trials conducted in 40 environments during 1976-1981 (Seshu and Cady, 1984). Both high and low levels of crop production could be explained by major weather factors. Figure 3 displays an isoquant plot for equal predicted yields (t/ha) for combinations of minimum temperature and solar radiation during ripening (30-day period after flowering). A significant negative correlation was evident between the mean temperature during the ripening stage and grain yield. In yet another study, through a special grant from UNDP, a nursery designated as International Rice-Weather Yield Nursery (IRWYN) was established and evaluated at 23 selected INGER sites in 16 countries representing a wide range of levels of temperature and solar radiation (Oldeman *et al*, 1987). That study yielded valuable information on the impact of major weather variables on the growth and yield of rice. Despite several studies in the past, it was difficult to find in the literature, estimates of rice-environment relationships with acceptably small standard errors based on field plot data, because of limited number and distribution of weather data points, and lack of time variables. INGER alleviated the problems by gathering data from a network of experiments over locations and years and thereby providing valid research information.

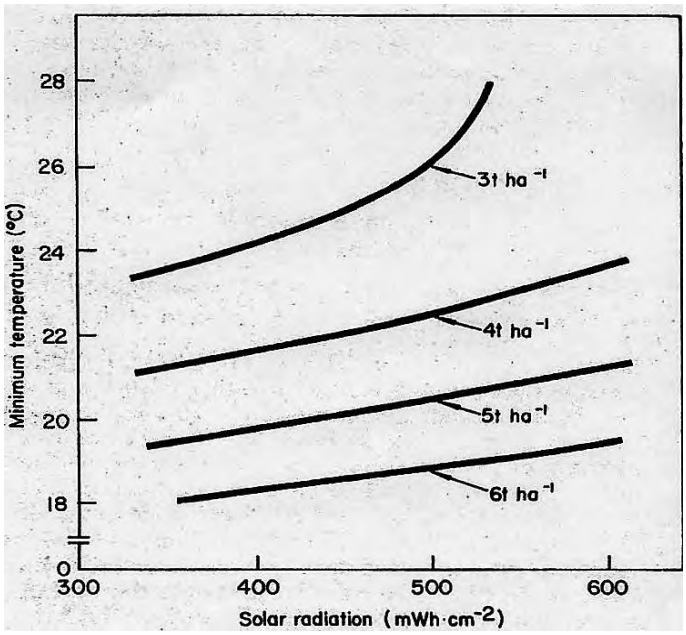


Figure 3: Isoquant plot for equal predicted yield for combinations of minimum temperature and solar radiation during ripening

Like with physical environment, INGER capitalized on the network approach in determining the G x E interaction in respect of biological environment. First, the variations within the disease causing organisms (pathogenic races/strains), and within the damage causing insect pests (biotypes) were evaluated through differential reactions of common set of varieties across the screening

sites. Following that, the genotypic responses to such variation patterns are determined under both field and greenhouse conditions. Significant information through INGER screening nurseries was obtained on pathogenic variation in the major disease causing organisms such as blast (Seshu and Kauffman, 1980) and bacterial leaf blight (Seshu, 1989); and on biotype variation in major insect pests such as rice gallmidge (Heinrichs and Seshu, 1981) and brown planthopper (Seshu and Kauffman, 1980). Sources of genetic resistance to major diseases and insects (both broad spectrum and location-specific) have been identified from the respective nurseries. For example, PTB 33 has been found to be resistant to all identified biotypes of the brown planthopper, and in all screening tests in Asia. Likewise, IR54 and RP633-76-1 showed resistance to bacterial leaf blight over several locations in Asia. The information on pathogenic and biotype variation was successfully utilized in various national breeding programs in choosing the location-specific genetic donors for resistance to relevant insects and diseases. Regional variations have become evident in respect of varietal reactions to some of the diseases and pests. As shown in Figure 4, variation was evident in the Brown Planthopper nursery in respect of percentage of entries susceptible to that insect among different regions of Asia (Seshu and Kauffman, 1980), with higher proportion of susceptible entries occurring at sites in South Asia.

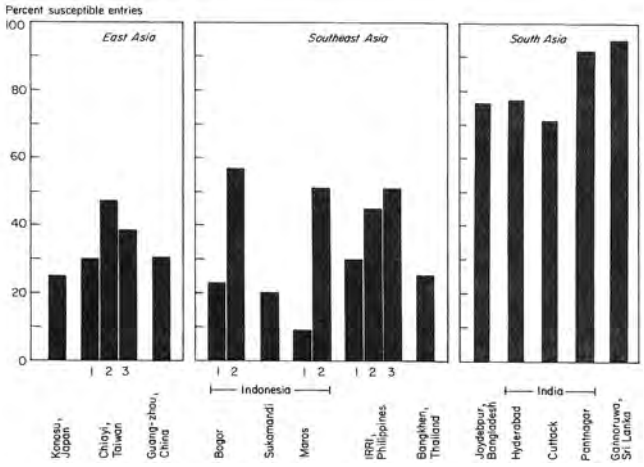


Figure 4: Percent susceptible entries at different test sites of International brown planthopper Nursery by regions of Asia (1, 2 and 3 refer to biotypes of BPH) (Seshu & Kauffmann, 1980)

Similar regional variation in Asia was observed in respect of reaction of entries to bacterial leaf blight (BLB), as evident from the results of the BLB nursery over years (Figure 5). A higher percentage of entries were found to be susceptible in South Asia, as compared to those in East and Southeast Asia, indicating possibly a higher degree of virulence of the pathogenic strains of BLB in South Asia.

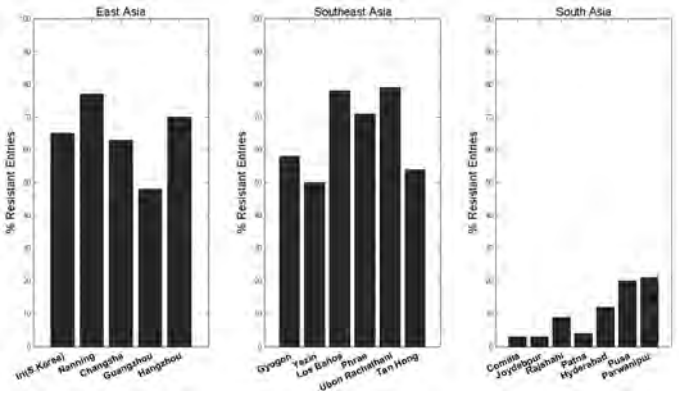


Figure 5: Region-wise variation in severity of bacterial blight strains in Asia as reflected by the percentage of resistant entries in Bacterial Blight Screening Nursery (Seshu, 1986)

The above are but few examples of the benefits accruing from multi-location cooperative networking for efficient and sustainable genetic improvement with savings on both time and costs.

From 1975, when INGER was established to 2015, the global rice production increased by about 30% (Source: Statista), whereas the acreage during that period increased by only 12%. The major contribution for the increase is from the improved varieties. INGER-tested and released varieties caused a significant part of that increase, as indicated by the number of varieties released through that mechanism. Yale University professors (Robert Evenson and Douglas Gollin) studied 591 INGER-derived high-yielding and pest-resistant varieties released in 64 countries. They estimated that each released variety contributes annually USD 2.5 million to the global economy at 1990's costs. Using that old figure on current data, the 1,120 INGER test lines released as varieties contributes annually USD 2.8 billion to the world economy.

Some comments by different organizations that reviewed INGER (IRTP)

IFDC: The International Rice Testing Program (IRTP) is well known with national agricultural research programs and has been very successful in providing genetic material for local breeding programs and as a forum for exchanging information on breeding methods and priorities.

ISNAR: The International Rice Testing Program (IRTP) has been widely recognized as one of the more successful research efforts of the IRRI scientists. Its impact has been enormous.

ICRISAT: The International Rice Testing and Improvement Program (IRTP) of the International Rice Research Institute is regarded as an excellent example of an inter-institutional, multidisciplinary approach for increasing rice yields in several countries in the developing world.

World Bank: International Rice Testing Program has made identifiable contributions to rice cultivation throughout the world.

Rockefeller Foundation: The International testing of rice varieties by national researchers under the conditions prevailing in their own research stations has probably been the single most effective dimension of IRRI's rice improvement work.

USAID: It is a project of the highest priority and worldwide importance.

CIDA: It is a corner-stone of IRRI's international network of rice scientists and the means whereby 'new' rice varieties are tested for their location-specificity, with improved varieties identified for specific environmental conditions.

UNDP Natural Resources Division: The network established has significantly increased agricultural productivity and furthered technical cooperation in adoption of rice improvement techniques.

Current Science (1986), Vol.55(9): 477-478: The major achievement of IRRI over the past two decades is in organizing and implementing large scale international testing of rice strains in different ecosystems. These studies involve extraordinary leadership qualities to work in close collaboration with scientists of different nations and cultural backgrounds. The achievements in this regard are highly commendable.

CGIAR / TAC External Review of IRRI, 1992. Assessment of IRTP / INGER: IRTP today is the largest single pathway for distributing, exchanging, and testing new rice varieties and breeding lines, worldwide. A large amount of valuable information has been gathered through IRTP on biotype and race differences among major pests and pathogens, on location-specific resistance genes, and on interaction of rice and major weather factors, which helped in the construction of simulation models. IRTP has allowed international seed exchange to be made unhampered by political restrictions. This major achievement together with the joint monitoring site visits involving NARS and IARC scientists, are services that are highly valued by the NARES. It is the panel's view that IRTP (INGER), with its sharp focus on germplasm and environmental characterization, has brought a great level of effectiveness in IRRI's germplasm exchange and evaluation activities. IRTP has made the germplasm exchange and evaluation activities more demand-driven, and less supply-driven.

Philippines Social Scientist: According to Gelia Castillo, a noted social scientist (designated as Philippine National Scientist), rice seeds share a common food value and speak a common language that transcends politics, geography, and culture. In Africa, for instance, INGER helped break a barrier in rice science between English and French-speaking countries. She maintains that "INGER is a beautiful illustration of humanity working together for our common future in a world filled with social conflicts, tribal wars, and fierce competition over the control of natural resources" (Rice Today, 2015).

Moving ahead with INGER

INGER has been established over a period of time as a strong cooperative platform for rice genetic improvement through the concerted efforts of the world community of rice scientists, breaking down social, cultural and political barriers. Every effort should be made to maintain and nurture such a well-proven excellent mechanism through both technical prowess and financial sustainability in order to uphold and validate the prodigious efforts that have gone into its establishment. In the larger interests of the world's food security, the research institutions concerned and the funding agencies should take cognizance of the need to enable INGER maintain its dynamism in addressing effectively the changing needs of rice improvement. The cooperative structure so carefully crafted should be efficiently utilized for all future challenges.

Several national programs have gained adequate strength in terms of research capabilities and facilities, and thus are in a position now to share some of the financial and organizational responsibilities to carry forward the successful network program. Delegation and assumption of technical responsibilities should be based on the respective ecosystem advantages with attending stresses. A comprehensive discussion with the concerned NARES will help set the stage for an effective and unhampered continuation of the network to meet the needs arising out of the new challenges.

Presently, as stated above, nurseries are being organized with orientation on important rice cultural ecosystems and on the major stresses encountered by the crop. The sets of nurseries, the composition of individual nurseries, and the type of data collection should reflect on the changing and practical needs of the participating countries. Varietal differences in respect of some important post-harvest traits like seed vigor and threshability should be included in the data collection as they have significant influence on the ultimate yield, and the recorded figures may not reflect on the true yields, if differences exist for those traits.

Shortage of water is probably the single most significant challenge that will confront the world's farmers in the coming years. Rice is a water guzzler when compared to other crops. It uses up to two to three times more water than other food crops such as maize or wheat and consumes around 30% of fresh water used for crops worldwide. Thus there is an urgent need to regulate the water footprints contributed by rice culture. While scientists from relevant disciplines may be pursuing research toward this goal, INGER should do its part by capitalizing on its cooperative base to evaluate varieties at selected representative sites for

their performance under a range of hydrological situations. Carefully planned testing should enable identifying varieties performing well with an optimal input of water under irrigated conditions. On the other hand, efforts should be intensified to screen for tolerance to water stress. Also, a systematic monitoring has to be done to elucidate the utilization of several INGER entries identified in the past for drought tolerance, and take stock of the progress made thereof. Promising progenies from those breeding efforts have to be recycled into the INGER system. Issues like climate change have more recently been built into the INGER testing.

When other network trials of relevance to INGER are conducted at a given station (say, cropping systems), it has to be ensured that they are appropriately linked, to derive maximum benefits from the combined information in choosing the more productive location-based varieties.

Finally, it should be noted that increased data-returns from systematically conducted trials underpin the success of the networks. In order for the purpose of establishment of INGER is duly served, the cooperators should also ensure that the data are returned promptly for timely analysis and utilization of the results. Reliability of information from well-conducted trials would accelerate the transfer of new technologies to the farmer, which is our ultimate goal.

Conclusions

Rice has evolved through very high levels of adaptation to various ecological habitats and has its cultivation spread across the continents. Genetic improvement remains a challenge when trying to maintain harmony between rice and its environment. This necessitates active cooperation of scientists within and between the rice growing countries to facilitate pooling and sharing of research materials and expertise through a structured network mechanism. Valuable bonuses from such an approach are savings in time and monetary inputs, and more importantly, acceleration of transfer of technology to the farmer. Pooling of materials from diverse sources also promotes the much needed genetic diversity. While the agro-ecological diversity of rice crop poses a 'challenge' for varietal improvement, the geographical diversity provides an 'opportunity' for cooperation. Individual strengths of the national systems may vary, but their collective strength is formidable. Meaningful fusion of those complementary strengths has powered INGER to effectively serve the needs of the various participating countries in fostering location-specific genetic enhancement of rice. INGER, thus proved to be an epitome of veritable synergy, and signifies the power of cooperation. Networks will continue to play a paramount role in agricultural research. In this context, it is important for the funding agencies to take cognizance of the fact that their financial support to cooperative networks such as INGER would yield very significant returns in terms of world's food security, paling the value of the investment.

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REVIEW ARTICLE OPEN ACCESS

Seed Systems and Supply Chain of Rice in India

J S Chauhan[1], S Rajender Prasad[2]*, Satinder Pal[1] and P R Choudhury[1]

[1]Indian Council of Agricultural Research, Krishi Bhawan, New Delhi 110 001, India.

Email:js_chau09@rediffmail.com

[2]University of Agricultural Sciences, GKVK Campus, Bangalore 560 065, Karnataka, India.

*Corresponding author: js_chau09@rediffmail.com

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Abstract

Rice accounts for 32.7% and 41.5%, respectively, of the acreage and production of food grains in India, during 2015-16. To meet the growing demand of 1.36 billion people, rice production needs to be increased by 20.8% by 2020 under declining and degrading land and water resources. Enhancing seed and varietal replacement rates coupled with integrating natural resource management is one of the important approaches to bridge the gap between potential and realized yields. Enabling the resource poor farmers with quality seed is still an imminent challenge. A strong and vibrant seed system is essential for food security of the country and accelerating growth in agriculture. This paper presents the various prevalent seed systems, seed chain, seed supply, quality seed status and its impact, issues and strategies to ensure continuous availability of quality seed of rice to farmers.

Introduction

Globally, India ranks first in acreage (26.6%) and 2nd in production (21.5%) of paddy. Its yield (3623 kg/ha) is only 80.8% of the world's average yield (Anonymous, 2016). Rice is an important food crop for the country accounting for 22.0% of the gross cropped area during 2012-13 (Anonymous, 2016). Further, it accounts for 32.7% and 41.5%, respectively, of the acreage and production of food grains during 2015-16 (Anonymous, 2017a). Green revolution was made possible by enabling public policies, good services (seed, water and fertilizers), hard working and innovative Indian farmers, besides input responsive dwarf varieties of wheat and rice. In the last 50 years of post green revolution, rice area, production and yield have increased by 1.24, 3.08 and 2.8 times, respectively (Anonymous, 2016). Quality seed played an important and critical role in bridging the yield gaps through improved productivity and it alone contributes about 15-20% to the crop yield. To meet the growing demand of 1.36 billion people, rice production needs to be increased by 20.8% by 2020 under declining and degrading land and water resources. This may be achieved by enhancing seed and varietal replacement rates coupled with integrating natural resource management, raising the ceiling to crop productivity; sustaining the gains achieved and also extending them to new niches. Enabling the resource poor farmers with quality seed is still an imminent challenge. A strong and vibrant seed system is essential for food security of the country and accelerating growth in agriculture. This paper presents various prevalent Indian seed systems, seed chain, seed supply, quality seed status and its impact and future strategies to ensure continuous availability of quality seed of rice to farmers.

Mile stones in the development of seed sector in India

Report of Royal Commission on Agriculture in 1928 was the beginning of the journey of seed sector development in India (Table 1). Presently, Indian seed sector comprises public sector institutions as well as private seed companies. Public seed sector includes various organizations, *viz.*, National Agriculture Research System (NARS) comprising 103 Indian Council of Agricultural Research (ICAR) Institutes/ Bureaux/National Research Centres, Project Directorates, 81 All India Coordinated & Network Projects and 11 Agricultural Technology Application Research Institutes, 3 Central Agricultural Universities and 5 Deemed Universities, 4 Universities having Faculty of Agriculture, 696 Krishi Vigyan Kendras (KVKs), National Seed Corporation Limited, New Delhi; 61 State Agricultural Universities, 15 State Seed Corporation and 24 State Seed Certification Agencies (Chauhan *et al.*, 2016a; ICAR Telephone Directory 2017; icar.org.in 26.7.2017). Private seed sector experienced rapid growth under liberalized government policy which resulted in establishment of around 500 seed companies across the country. Recently, Directorate of Seed Research Mau has been upgraded to Indian Institute of Seed Science (Table 1) highlights the important developments related to seed sector in the country.

Table 1. Milestones in the development of Indian seed sector

Year	Event	Objective/s
1928	Report of Royal Commission on Agriculture	First major milestone in the history of seed sector development.
1945	Famine Enquiry Commission	Emphasised need for multiplication and distribution of quality seed of improved varieties.
1952	Grow-More Food Program Committee	
During 50's	Seed Farms were established in Community Development Blocks	Department of Agriculture started Seed Farms to multiply foundation seed.
1961	First hybrid maize was released	Later hybrids of sorghum and pearl-millet were released.
1963	National Seeds Corporation Ltd was established	To develop a sound seed industry in the country.
1966	Enactment of Seed Act	To regulate quality of seed.
1967	Seed Review Team	Set-up to examine the seed situation in the country and to give suggestions.
1969	Tarai Development Corporation, Pantnagar	To develop 16,000 ha for seed production.
1969	State Farms Corporation of India	Production of certified seed having 38,325 ha in 14 farms.
1971	Report of National Commission on Agriculture	Stressed the need for maintaining purity of seed.
1974	Setting up of joint working party	To formulate National Seed program.
1976	National Seed Project	
1976	Phase I	Implementation in four states.
1978	Phase II	Five more states.
1990	Phase III	Four more states.
1987	Expert Group on Seed	To review the entire seed sector and to give suggestions.
1988	New Policy on Seed Development, Govt. of India.	To make available the best planting material in the world to the Indian farmers.
1983/ 1994	Seed Control Order under the Essential Commodity Act 1955	To regulate quality and pricing of seeds.
1991	New Industrial Policy	Opened doors for the foreign investors in the Indian seed industry.
2001/ 2003	PPV & FR Act / PPV & FR Act Rules	To protect plant breeder's and farmer's rights.
2002	National Seed Policy	To develop seed industry.
2004	Establishment of Directorate of Seed Research, Mau, UP	To undertake research and coordination on seed production.
2008	Joining of OECD seed schemes	To facilitate seed trade in international market.
2009-14	Export and Import Policy (New EXIM)	Liberalized export of seeds and planting materials with few exceptions.
2010	Seed Bill 2004 – pending in parliament	To produce quality seed and also protect Farmers' interests.
2011	Modified New policy on Seed Development / Modified policy on Seed Sector	Provision for import of wheat and rice.
2015	ISTA accreditation of first public sector laboratory	To produce quality seed matching international seed standards to promote seed export.
	Cotton Seed Price (Control) Order,2015	To provide an effective system for fixation of sale price for cotton seeds to ensure their availability to the farmers at fair, reasonable and affordable prices.

2016	Up gradation of Directorate of Seed Research, Mau to Indian Institute of Seed Science, Mau, UP	Conduct of basic, applied and strategic research on seed science, coordination of seed production and to capacity building in seed production, testing, quality assurance, certification and policy issues.
	Licensing and Formats for GM Technology Agreement Guidelines, 2016	To provide an effective system for fixation of sale price for cotton seeds to ensure their availability to the farmers at fair, reasonable and affordable prices.

Seed systems

Seed system can be defined as framework of institutions/ farmers group organized together by their involvement or influence on the seed multiplication, processing, quality assurance and marketing of seeds. There are three major seed systems: informal, formal and integrated.

Formal

Formal seed system is characterised by large scale production of seed of officially released varieties with strict quality assurance mechanism. The formal seed system is easier to characterize, as it is well organized and systematic involving a chain of activities leading to certified seed/ labelled seed of notified varieties. The chain usually starts with development of different types of varieties/ hybrids and formal variety release and maintenance. Guiding principles in the formal system are to maintain varietal identity and purity and to produce seed of optimal physical, physiological and sanitary quality (Reddy *et al*., 2007). There is a clear distinction between seed and grain.

Informal

Informal seed system is characterised by small scale supply of locally known varieties without any government interference in quality control. Activities tend to be integrated and locally organized, and the informal system embraces most of the other ways in which farmers themselves produce, disseminate and access seed: directly from their own harvest; through exchange / barter among friends, neighbours, relatives; and through local grain markets. Encompassing a wider range of seed system variations, flexibility characterizes the informal system most. Varieties may be landraces or mixed races and may be heterogeneous, modified through on farm breeding. In addition, the seed is of variable quality (diverse purity and physical/ physiological quality). The same general steps take place in the local system as in the formal sector (variety choice, variety testing, introduction, seed multiplication, selection, dissemination and storage) but they take place as integral parts of farmers' production systems rather than as discrete activities. There is not always necessarily a distinction between seed and grain. The steps do not flow in a linear sequence and they are not monitored or controlled by government policies and regulations. Rather, they are guided by local technical knowledge and standards and by local social structures and norms.

Integrated

In many cases, however, a farmer will use the formal system for some crops and informal system for others. He may buy seed from the formal system once in order to obtain a particular variety and produce own seed from there onwards and share the new variety with neighbours and relatives. Farmers, particularly, smallholding farmers, are involved in multiple seed systems, which help them to obtain the seed they need. Community based seed production of the varieties preferred by the farmers by themselves in their own locality by organizing themselves into small groups. These groups cultivate the same variety avoiding cross pollination and follow the recommended cultivation practices particularly seed selection procedures. These farmers are given the appropriate training, and supplied with good quality foundation seed for multiplication, so that they become the source of improved seed for the entire village (Figure 1). Each season the farmers are supplied with foundation seed of different crops.

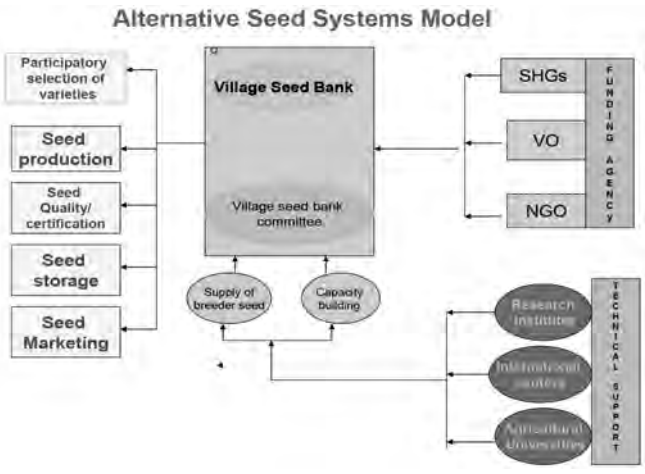

Figure 1. Integrated seed system

Seed supply chain

The ICAR is mandated to produce nucleus and breeder seed as per the indent received from Department of the Agriculture, Cooperation & Farmers Welfare (DAC & FW), Ministry of Agriculture and Farmers Welfare, Government of India. The production of breeder seed is demand driven and produced on the basis of indents received from private

as well as public sector organizations, by DAC which in turn consolidates the indents and forward to the ICAR. Crop Science Division of the ICAR coordinates the breeder seed production of field crops in the country with the cooperation of various SAUs and public sector crop based institutes. The breeder seed thus produced is supplied to indenting States Department of Agriculture as well as other public and private sector organizations for further multiplication in the form of foundation and certified seeds which is made available to the farmers (Figure 2). Production of quality seed (foundation and certified) of crops is primarily the responsibility of the States although ICAR institutes also produce limited quantity of certified/truthfully labelled (TL) seed. Each producing institute/agency fixes the price of foundation/certified/TL seed while price of breeder seed is fixed by the ICAR in consultation with DAC.

Figure 2. Stakeholders in the seed supply chain

Development of Varieties

The NARS as well as certain private seed companies have been continuously developing climate resilient varieties of seeds suitable for different agro-climatic regions and also engage in production of breeder/ basic seed, foundation, certified and TL seeds. This continuous variety improvement, led to release and notification of 4,615 varieties of field crops since 1969 till 75th meeting of Central Sub-Committee on Crop Standards, Notification and Release of Varieties for Agricultural Crops on August 12, 2016. Of these, 250 have also been de-notified (Chauhan *et al.,* 2016 b). These varieties are input-responsive, high yielding and show tolerance to major biotic and abiotic stresses. During the last 15 years, 1994 varieties were released and notified (Chauhan *et al.,* 2016 b), of which 986 were state releases (Figure 3) and a total of 231 rice varieties were released during 2009-16 (Figure 4) and maximum (63) were released during 2016.

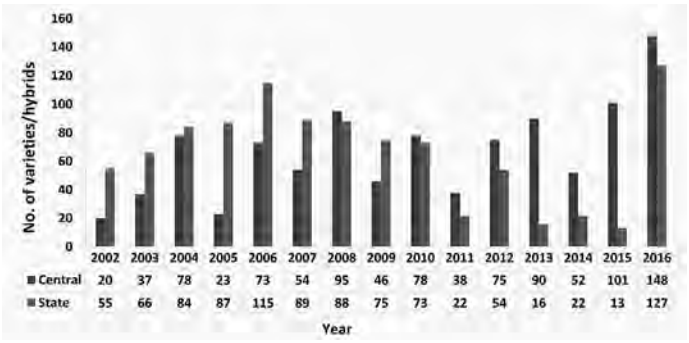

Figure 3. Central and state varieties of field crops released in India during 2002-2016 (Source: Chauhan *et al.,* 2016b)

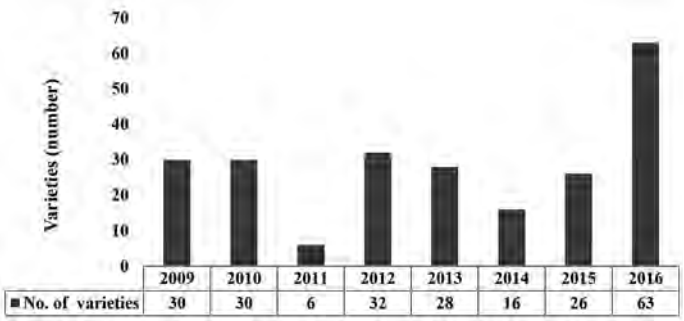

Figure 4. Rice varieties released during 2009-2016

Rice varieties in seed chain

Breeder seed is the first step of effective formal seed chain and only notified varieties as per section 5 of Seed Act, 1966 qualify for production of certified seed. Of the 900 varieties / hybrids of rice qualifying for such seed production, more than 300 were in the seed chain during 2016-17 (Table 2). The number of hybrids varied from 8-12 and their contribution to total breeder seed production of the crop was very low. Of the 4 years, Cottondora Sannalu (MTU1010) was the leading top most variety in three years while Swarnasub1 was the topmost leading variety during 2016-17. Only seven varieties occupied the first five positions in the seed chain and contributed from 28.6-34.8%.

Certified seed/Truthfully labelled seed marketing and distribution take place through a limited number of officially recognized seed outlets. There are adequate provisions under existing seed legislations to regulate the quality of seeds and the mechanisms for such regulations are in keeping with the federal structure of the country. The powers of enforcement and implementations of Seed Act, 1966 are appropriately vested in the State Governments. Besides, the provisions of Seeds Act 1966 and Seed Rules 1968, the Seeds (Control) Order 1983 are applicable to both notified and non-notified seeds. Seed certification is voluntary but labelling is mandatory. The business of selling, exporting and importing seeds can be carried out only under a license issued by the State government. Seed dealers are required to maintain books, accounts and

Table 2. Varieties (V) and hybrids (H) of rice in seed chain and their contributions to breeder seed indent (Anonymous, 2017b)

Year	Varieties / hybrids	Five top most varieties having highest indent	Indent (q)	Contribution (%)	Contribution of top most 5 varieties to total indent (%)
2013-14	V - 229 (99.87%) H- 12 (0.13%)	Cottondora Sannalu (MTU 1010)	485.0	10.2	30.9
		Swarna (MTU 7029)	443.1	9.3	
		Vijetha (MTU 1001)	193.6	4.1	
		Sahbhagi Dhan	181.4	3.8	
		IR 64	161.4	3.4	
		Total indent	**4745.0**		
2014-15	V - 219 (99.85%) H - 11 (0.15%)	Cottondora Sannalu (MTU 1010)	498.6	11.5	34.8
		Swarna-sub1	388.0	9.0	
		Vijetha (MTU 1001)	230.6	5.3	
		Swarna (MTU 7029)	202.0	4.7	
		Sahbhagi Dhan	188.3	4.4	
		Total indent	**4328.0**		
2015-16	V - 248 (99.69%) H - 11 (0.31%)	Cottondora Sannalu (MTU 1010)	427.1	8.5	28.6
		Swarna (MTU 7029)	359.4	7.2	
		Swarnasub1	232.9	4.6	
		Vijetha (MTU 1001)	210.1	4.2	
		Sahbhagi Dhan	206.1	4.1	
		Total indent	**5026.0**		
2016-17	V - 310 (99.94%) H - 8 (0.06%)	Swarnasub1	553.2	10.8	31.2
		Cottondora Sannalu (MTU 1010)	342.0	6.7	
		Sahbhagi Dhan	339.8	6.6	
		IR 64	183.3	3.6	
		Naveen (CR-749-20-2)	178.9	3.5	
		Total indent	**5119.0**		

display the stock position and sale price. State governments have powers in pursuance of section 13 of Seed Act, 1966 to appoint inspectors to regulate the seed trade. Seed Inspectors are vested with adequate powers for quality control, *viz.*, to draw the sample; enter and search; examine records, registers, and documents; seize the stock and issue 'Stop Sale' order in case the commodities under reference contravene provisions of law. Inspectors are also authorized to take punitive action / launch proceedings against dealers found to be selling sub-standard seeds. A dealer's license is liable to be suspended/cancelled for contravention of the Seed Act 1966. The seed in respect of which the contravention has been committed can be forfeited under Section 20 of the Seeds Act. The penalties are provided under Essential commodities Act, 1955 (Trivedi and Gunasekaran, 2014). The dealers can also be directed to distribute seeds in specified manner in public interest

Quality seed production of rice

Breeder seed: Breeder seed indent was highest (5,772 q) during 2011-12 and declined thereafter until 2014-15 (4,328 q) which was 8.7%, 16.2% and 25.7% during 2012-13, 2013-14 and 2014-15, respectively (Table 3). Since 2014-15, the breeder seed indent consistently increased to 5119 q during 2016-17. The increase was 17.3% in 2015-16 and 19.4% in 2016-17 (Table 3). The production of breeder seed was always higher than the indented quantity, nevertheless, varietal mismatch was invariably observed. The production was higher by 8.4% during 2015-16, a drought year, to 118.9% during 2013-14.

Table 3. Trends in indent and production of breeder seed of rice*

Year	Indent (q)	Production (q)
2011-12	5,772	6,828
2012-13	5,267	11,455
2013-14	4,837	10,586
2014-15	4,286	7,757
2015-16	5,026	5,449
2016-17	5, 119	8,765**

*Anonymous (2017b) and ** IIRR- AICRP on Rice Annual Report (2017)

Certified / quality seeds

It is the certified/quality seeds made available to the farmers/growers that could raise crop productivity by

enhancing seed replacement rate. In paddy, maximum dissemination of quality seeds was during 2011-12 (74.41 lakh q) showing an increase of 22.1% over that of 2009-10 and remained almost stagnant for the next two years. However, the quantity of paddy quality seed declined by 10.2% during 2014-15 over that of 2011-12. Nevertheless, it was higher by 9.7% over the base year, 2009-10 (Table 4). The reduction in dissemination of quality seed could be partly due to drought in 2014-15.

Table 4. Distribution of certified/ quality seeds of paddy (Anonymous, 2016)

Year	Quantity (lakh quintals)
2009-10	60.95
2010-11	69.34
2011-12	74.41
2012-13	72.14
2013-14	72.45
2014-15	66.84

Impact of quality seed use

Enhanced seed replacement rate leads to increased yields: During the last six years, availability of certified/ quality seed showed an inconsistent increase ranging from 9.7-22.1% over that of 2009-10. The increase in seed availability resulted into high seed replacement rates (SRR) in paddy until 2013-14 (57.6%). Due to severe drought during 2014-15, area and production coupled with SRR declined. Probably, there was less availability as well as demand for seed due to continuous drought since 2013-14 and about 0.55 million ha area was reduced during 2014-15 as compared to 2013-14 and the SRR was 32.8% (Chauhan *et al.*, 2016a). However, the increased SRR was, in general, associated with increased yield. The area under rice remained fairly consistent during the last five years, ranging from 42.75 (2012-13) to 44.14 million ha (2013-14) with about 2.95-1.50% decline during 2012-13 and 2015-16 as compared to that of 2011-12 (Anonymous, 2016).The rice cropped area was 43.39 million ha during 2015-16 (Figure 5). Similar was the trend for production which increased by about 1.28% during 2013-14 and decreased by 0.93% during 2015-16.Yield (kg/ha) during this period varied from 2391 (2014-15) to 2461 (2012-13) and it was 2404 during 2015-16 (Figure 5).

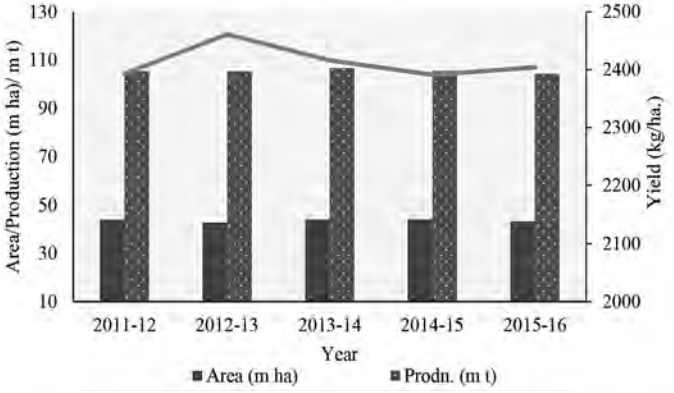

Figure 5. Recent trends in area, production and yield of rice

Increased rice export: India became food surplus country from food scarce as a result of green revolution in 70's, which enabled policy makers to enact Food Security Act in 2013 which ensures availability of food (rice, wheat, coarse cereals) to about 64% of the population at much reduced price. The increased seed replacement rate as a consequence of enhanced availability of quality seed could be one of the major reasons for high rice production despite two consecutive drought years (2014-15 and 2015-16) and sustaining continuous export of rice over 10 million tonnes (Table 5). India earned a sizeable amount of foreign exchange by exporting basmati and non-basmati rice. During the last six years, the export of basmati rice increased from 3.17 million tonnes in 2011-12 to 4.0 million tonnes in 2016-17, registering an increase of 26.2% (Table 5). Export of non-basmati rice during the corresponding period registered an increase of 105.8%

Table 5. Export of rice from India during the last six years

Year	Quantity (Million Tonnes)			Value (Billion US $)		
	Basmati	Non Basmati	Total	Basmati	Non Basmati	Total
2011-12	3.17	4.00	7.17	3.22	1.72	4.94
2012-13	3.46	6.69	10.15	3.56	2.65	6.21
2013-14	3.75	7.15	10.90	4.86	2.93	7.79
2014-15	3.70	8.23	11.93	4.52	3.32	7.84
2015-16	4.04	6.37	10.41	3.48	2.31	5.79
2016-17	4.0	6.81	10.81	3.22	2.55	5.77

Source: India export of principal commodities. http:// agriexchange. apeda. gov. in/ indexp /18 headgen report month_combine.aspx (24.7.2017)

until 2014-15 (8.23 million tonnes) over that of 2011-12 (4.0 million tonnes). Presently (2016-17), India exported 6.81 million tonnes of non-basmati rice which is 70.3% higher than that of 2011-12. Total (basmati + non-basmati) rice export increased consistently from 7.17 million tonnes during 2011-12 to 10.81 million tonnes during 2016-17, registering an increase of 50.8%. The foreign exchange earnings were 3.22-4.86 billion US $ and 1.72-3.32 billion US $ from basmati and non-basmati rice, respectively, during 2011-12 -2016-17 (Table 5).

Issues

- **Unrealistic demand for breeder seed:** Sudden big fluctuations in varietal demands in quick spans poses challenge to availability of breeder seed as nucleus seed for such unexpected unusual high demands may not be available. For example, to achieve a target SRR of 50.5% by 2019-20 even for all time high rice cropped area (45.5 million ha), only 919.1 q breeder seed is required while an indent of 5119.2 q for breeder seed production was received during 2016-17.
- **Varietal mismatch:** Although breeder seed production is invariably higher than the indented quantity, however, many a times seed of indented quantity of several rice varieties is not produced in sufficient quantity.
- **Non-lifting of breeder seed and weak seed chain:** The agencies such as States Department of Agriculture, States Seed Corporation, private seed producers and others responsible for conversion of breeder seed to foundation and certified seed do not lift the allotted quantity of breeder seed to take up effective conversion of indented breeder seed. Further, some agencies lift the breeder seed but sometime go for direct multiplication of certified seed which is not advisable.Traceability of breeder seed source in rice multiplication chain, thus, is a serious concern for quality seed production.
- **Over dependence on private-sector without any formal agreement:** Tendency of several states for not placing timely indents for requisite quantity of breeder seed. In fact, there is declining trend in many states for indents even for major rice varieties and procuring seed through tendering process, thus, quality of seed cannot be ensured.
- **Intellectual Property Rights:** In view of National/ International treaties such as CBD, ITPGRFA, Nagoya Protocol, PPVFRA and NBA restricting the easy access of quality seed of newly released hybrids and varieties and also restrict the free and easy exchange of germplam among the stakeholders from public as well as private sector involved in genetic enhancement and development of new rice varieties.
- **Climate change:** Deteriorating effects of climate change that has already affected the seed production programmes in many states.

Strategies

Inherent strengths of India are being the 2nd largest arable land with 46 soil types across 15 agro climatic zones favour seed production backed by strong national genetic enhancement and development programmes for new rice varieties, wide network of agriculture extension services. Growing demand for quality seed as SRRs in rice is consistently increasing and focus is on enhancing Varietal Replacement Rate, supportive public policies are the growth drivers for a vibrant seed systems and supply. Strategy development with focus on following issues would further strengthen the seed systems and rice seed supply chain in the country to address the demanding needs of ever increasing population of the country:

- Realistic assessment of breeder seed vis-à-vis strengthening of state seed rolling plan and seed chain.
- Need for development of rapid tests such molecular markers to replace grow out test, to establish genetic purity and seed health. Development of molecular markers to enable genetic purity testing and management of nucleus seed and its further maintenance.
- Focus should be on enhancing Varietal Replacement Rate with target Seed Replacement Rate, *viz.*, 35% for rice.
- To mitigate the adverse effects of climate change, search for identification of suitable alternate areas for seed production in non-traditional area/ season should be systematically pursued.
- Capacity building of various stake-holders in seed chain with focus on enhancing farmers' participation in seed production, development of seed villages and seed banks and main streaming of farmers protected varieties.
- Establishing seed hubs and National Seed Bank especially for meeting urgent demands of contingency planning.
- Marketing intelligence for increasing seed trade and encourage the export of seed by providing incentives to the exporters
- Introduction of bar code/ QR code for traceability of breeder seed source in multiplication chain.
- Establishment of rice advisory body/ referral lab for implementation of quality control system.

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ORIGINAL RESEARCH ARTICLE OPEN ACCESS

Genetic Divergence Studies for Yield and Quality Traits in Rice (*Oryza sativa* L.)

Ramesh Babu P and Sreelakshmi Ch

Agricultural Research Station, Nellore-524003, ANGRAU, AP
Email:ramesh_ars2004@yahoo.com

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Abstract

Genetic divergence was assessed among fifty genotypes of rice to study the nature and magnitude of genetic divergence using D^2 statistics. Based on the genetic distance the fifty genotypes were grouped into six clusters. Of the six clusters formed, cluster I having maximum number of genotypes (12) followed by cluster II with nine entries. Maximum intra cluster distance (746.9) was observed in cluster VI and minimum in Cluster III (327.8). Days to 50% flowering, gelatinization temperature score and water uptake together contributes around 72% to total divergence. Maximum inter cluster distance was recorded between clusters III and VI (827.45) followed by cluster III and IV indicating wide genetic diversity and it may be used in rice hybridization programme for improving grain yield.

Keywords: Divergence, Rice genotypes, Mahalanobis D^2

Introduction

Rice is the most important food crop of the world, providing over 21% of the calorific intake of the population of South East Asia. Genetic improvement of any crop mainly depends upon the genetic variability present in the population. The nature and magnitude of genetic divergence would help the plant breeder in choosing right choice of the parents in order to obtain high amount of heterotic expression in F_1s and broad spectrum variability in subsequent generations. Besides yield, improvement of physical, milling and cooking quality characters in rice is important factor to be considered in breeding. Hence, there is an imperative need for a shift in emphasis towards development of high quality rice. This is achieved by evaluating the available germplasm lines for quality traits, and by generation of knowledge regarding their inheritance pattern to use in further breeding programmes. Keeping this in view, the present investigation was undertaken to study the nature and degree of genetic divergence among fifty rice genotypes. A meaningful classification of experimental material depending upon different characters helps to distinguish genetically close and diverse genotypes which were a pre- requisite for any genetic study.

Several workers *viz.*, Ravindra Babu *et al* (2006), Subudhi *et al* (2009), Garg *et al* (2011) proposed to choose diverse parents for quality traits such as head rice recovery, kernel length after cooking, gel consistency, kernel elongation ratio and amylose content from the most divergent clusters so that they produce larger variability and desirable segregants. Similarly, Kumar *et al* (2015) for days to maturity, Senapathi and Sarkar (2005) for ear bearing tillers per plant, panicle length, Ramesh Chandra *et al* (2007) and Iftekharuddaula *et al* (2010) for test weight, Bose and Pradhan (2005) for grain yield, Suman *et al* (2005) for harvest index, Ramya and Kumar (2008) for number of filled grains per panicle, Raut *et al* (2009) for Kernal L/B ratio and Ubarhande *et al* (2009) for chlorophyll content contributes maximum towards total divergence.

Material and Methods

Fifty diverse genotypes from different geographic origin were transplanted in randomized block design with three replications during *rabi* season at Agricultural Research Station, Nellore, Andhra Pradesh. In each replication single seedling was transplanted per hill in 5 rows of 3 meters length with 15 x 15 cm spacing. Recommended package of practices were followed to obtain a normal crop. The observations were recorded on five randomly taken plants from each plot for days to 50% flowering, Plant height (cm), Number of ear bearing tillers, Panicle length (cm), Primary branches per panicle, secondary branches per panicle, filled grains per panicle, unfilled grains per panicle, test weight (g), grain yield per plant (g), kernel length (mm), kernel breadth (mm), kernel L/B ratio, hulling percentage, milling percentage, gelatinization temperature score, water uptake, volume expansion, and kernel elongation ratio. The analysis of genetic divergence was done using Mahalonobis D^2 (1936) statistics. The genotypes were grouped into different clusters by Tocher's method described by Rao (1952).

Results and Discussion

The analysis of variance revealed that significant differences among the genotypes for all the characters studied (Table 1). Based on D^2 analysis all the 50 genotypes could be grouped in to six clusters using Tocher's method (Singh and Chaudhary., 1977). However, with variable number of entries in each cluster revealing considerable amount of

Table 1. Distribution of 50 genotypes of rice in different clusters

Cluster	Number of genotypes	Identity of genotypes
I	12	NLR 33657, NLR 33656, NLR 33359, NLR 33637, NLR 33655, IR 50-15, IET 9994, IET 7563, W 1263, SUREKHA, ADT 39, CO 43
II	9	NLR 13969, NLR 33658, MTU 1005, MTU 1004, NLR 6802-1, WGL 20471, IET 10158, IET 10746, IR 60
III	5	BPT 5204, IET 10021, PANKAJ, IR 20, DV 85
IV	9	NLR 5050-13-1-1, NLR 5144-1-2-6, NLR 5110-16-2-1, NLR 5144-7-5-3, NLR 5144-5-3-1, NLR 30491, PR 164, MTU 1003, MTU 1002
V	5	NLR 145, NLR 5144-1-7, MTU 9992, KARJAT 1, WHITE PONNI
VI	10	NLR 33636, WGL 44645, RASI, POTTINALLAVARI, IET 4141, IET 7302, KHAO-DAWK-MALI, IR 72, IR 62, IR 64

genetic diversity in the material studied (Table1). It was observed that the cluster I had maximum number of 12 genotypes followed by cluster II with 10 genotypes and cluster II and IV with 9 genotypes each. Whereas, Cluster III and V had 5 genotypes in each cluster. The clustering pattern indicated that there was some degree of similarity of genotypes clubbed together in a cluster on the basis of their origin. The genotypes from Nellore, Warangal, Hyderabad, IRRI and Thailand were included in the same cluster (cluster X). Similar findings were reported by Singh *et al* (2008) and Allam *et al* (2014). Grouping of materials of similar origin into different clusters was an indication of broad genetic base of the genotypes belonging to that origin. So, genotypes originating from same place may have different genetic architecture or vice – versa as the genotypes developed at Agricultural Research Station, Nellore had fallen in clusters I, II, IV, V and VI Similar kind of results were also reported by Pradhan and Mani (2005), Sharma *et al* (2011) and Nirmaladevi *et al* (2015).

Average intra and inter cluster distance values among six clusters were presented in Table 2 and it revealed that the intra cluster average D^2 values ranged from 327.8 (cluster III) to 746.87 (Cluster VI). The maximum intra cluster distance was observed in cluster III revealed that existence of diverse genotypes that fell in these clusters. While the minimum distance was observed in the cluster VI indicating that the genotypes fell in this cluster was found similar. The average inter cluster D^2 value between clusters III and VI was maximum (827.45) followed by cluster III and cluster IV (760.71) which indicates that genotypes include in these clusters are genetically diverse and may give rise to high heterotic response. Minimum inter cluster D^2 values were observed between cluster I and II (223.86)

Table 2. Intra and inter cluster average distances (D^2) values of six clusters from 50 genotypes

Cluster	I	II	III	IV	V	VI
I	700.87	223.86	506.62	324.39	267.85	593.09
II		681.69	720.88	238.26	390.96	590.40
III			327.80	760.71	292.04	827.45
IV				536.20	504.02	690.91
V					582.80	645.08
VI						746.90

indicating the close relationship among the genotypes included in these clusters.

Considerable differences were found among the clusters for most of the characters studied (Table 3). The cluster I had the highest mean value for milling percentage (70.59), elongation ratio (1.64) and GT score (6.10). Clusters III, IV and VI had highest mean value for only one character each *viz.*, Days to 50% flowering (127.30), water uptake (264.40) and L/B ration of the kernel (3.18) respectively. On the other hand, cluster V had highest mean values for more number of characters *viz.*, primaries per panicle, secondary branches per panicle, grain yield per plant, hulling percentage and volume expansion. Thus, these genotypes hold great promise as parents for obtaining promising elite lines through hybridization and to create further variability for these characters (Mishra and Parvin 2004).

Percentage contribution of the each character towards total divergence is presented in table 4. The data revealed that maximum percentage of contribution came from the trait days to 50% flowering (41.5%) followed by G.T score (20.33), water uptake (9.84%), hulling percentage (7.76), elongation ratio (4.08%), L/B ratio of the kernel (3.18%), and number of primary branches per panicle (2.20%). The other traits had very low contribution to total

Table 3. Mean values of clusters from 50 genotypes of rice for different characters

Sl. No.	Character	I	II	III	IV	V	VI
1	Days to 50% flowering	102.92	91.11	127.30	105.58	113.20	89.0
2	Primaries per panicle	9.87	9.11	10.85	9.26	11.21	9.35
3	Secondaries per panicle	28.58	26.04	30.98	22.70	37.70	30.39
4	Grain yield per plant	13.97	17.93	18.33	16.45	21.50	19.43
5	L/B ration of the kernel	2.76	3.01	2.71	3.01	2.97	3.18
6	Hulling percentage	78.85	74.76	70.92	75.29	78.86	74.80
7	Milling percentage	70.59	66.69	64.33	69.71	68.83	69.76
8	G T score	6.10	5.64	4.10	5.55	4.60	2.22
9	Water uptake	233.29	29.17	230.5	264.40	240.45	245.64
10	Volume expansion	4.22	4.26	4.45	4.29	4.54	4.45
11	Kernal elongation ratio	1.64	1.50	1.53	1.49	1.50	1.54

Table 4. Relative contributing on (%) of individual trait to the divergence among genotypes

S. No	No. of times Ranked first	Contribution (%)
Days to 50% flowering	1	41.55
Primaries per panicle	7	2.20
Secondaries per panicle	8	0.73
Grain yield per plant	11	0.00
L/B ration of the kernel	6	3.18
Hulling percentage	4	7.76
Milling percentage	0	0.08
G T score	2	20.33
Water uptake	3	9.84
Volume expansion	9	0.24
Kernal elongation ratio	5	4.08

divergence. Relative importance of these parameters on these characters in inter varietal divergence on rice were reported by Patil *et al* (2005), Sandhya kishore *et al* (2007) and Garg *et al* (2011).

Contribution of each character towards genetic divergence has been estimated from the number of times that each character appeared in the rank first. Hence, days to 50% flowering, GT score, water uptake, hulling percentage, elongation ratio, L/B ratio of the kernel may be used as selection parameters in the segregating generations from the present material studied. The traits which had low or zero contribution towards divergence were of less importance as per the material studied in the experiment. Since genotypes with narrow genetic base are increasingly vulnerable to diseases and adverse climatic changes. Availability of genetically more divergent genotypes were important for hybridization programme. Since, days to flowering contributed maximum towards the genetic divergence, we may go for direct selection for this trait for diversity purpose.

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ORIGINAL RESEARCH ARTICLE OPEN ACCESS

Combining Ability Analysis for Yield and Yield Contributing Traits in Hybrid Rice (*Oryza sativa* L.).

B. S. Thorat, R. L. *Kunkerkar, B. L. Thaware, M. M. Burondkar and S.G. Bhave

Regional Agriculture Research Station, Karjat, Raigad.
Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli (MS), India.
* Corresponding author E mail :rlkramesh@rediffmail.com

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Abstract

Combining ability on grain yield and its components from line × tester analysis of 12 rice hybrids produced by crossing three CMS lines and four testers were studied. The additive gene action was observed for days to 50 per cent flowering, number of filled spikelets panicle^{-1} and days to maturity. Plant height, number of productive tillers plant^{-1}, panicle length, total number of spikelets panicle^{-1}, spikelet fertility, 1000 grain weight, grain yield plant^{-1}, straw yield plant^{-1} and harvest index showed the non-additive gene action. IR58025A was the good general combiner among the female parent for a total number of spikelets panicle^{-1} and number of filled spikelets panicle^{-1}. Male parent NPQ-49 was best general combiner for grain yield plant^{-1} and straw yield plant^{-1}. The crosses IR58025A x NPQ-49 and RTN12A x NPQ-49 were identified as most promising for yield and desired traits based on SCA effects, *per se* performance and GCA effects of parents for grain yield and its components in rice which could be exploited beneficially in future rice breeding program by adopting heterosis breeding strategy.

Keywords: CMS lines, testers, hybrids, GCA, SCA, rice, yield contributing traits.

Introduction

Rice is the staple food of more than 60% of Indian population. It accounts for about 43% of total food grain production and 46% of total cereal production in the country. Rice occupies a pivotal place in Indian Agriculture. In order to meet the domestic demand of the increasing population, the present day production of 107.40 million tonnes (Annonymous, 2015-16) of milled rice has to be increased to 125 million tonnes by the year 2030. Since the yield of high yielding varieties (HYVs) of rice is plateauing, it is rather difficult to achieve this target with the present day inbred varieties. Therefore, to sustain the selfsufficiency in rice, additional production of 1.17 million tonnes is needed every year. Among many genetic approaches being explored to break the yield barrier in rice and increased productivity, hybrid rice technology appears to be the most feasible and readily adaptable one. In a hybrid breeding program, choice of suitable parents is of primary importance since *per se* performance of parents is not always a true indicator of its combining ability in hybrid combination (Swamy *et al*., 2003). Therefore, performance of a F_1 hybrid depends on choice of parents. Several methods like *per se* performance, genetic diversity, combining ability *etc.*, have been attempted to select the parents. Among them combining ability analysis offers a powerful tool for estimating the value of a parent to produce superior hybrid. The combining ability studies of the parents provide information which helps in the selection of better parents for effective breeding. Its role is important to decide parents, crosses and appropriate breeding procedure to be followed to select desirable segregants (Salgotra *et al.,* 2009). Keeping this in view, the present investigation was carried out to study the combining ability in order to identify good combiners and superior hybrid combinations.

Materials and Methods

The experiment was conducted at the Experimental farm of Regional Agriculture Research Station, Karjat (Raigad). The identified parents were grown during December, 2015 and the crossing programme was under taken during April, 2016 and evaluation of F_{1s} along with parents and three standard checks were done during *kharif* 2016. Three CMS lines *viz*., IR58025A, RTN 12A and RTN17A were crossed with four testers *viz.*, Chedo Local, CR-2829-PLN-36, NPQ-49 and RP-5898-19-8-6-1-1-1 in a Line × Tester mating design and developed 12 hybrids. The experiment was laid out in a Randomized Block Design with three replications during *kharif*, 2016 at Regional Agriculture Research Station, Karjat (Raigad). The experimental material consisting of twelve F_{1s}, three CMS lines, four restorers and three standard checks were sown on 21st June 2016. Then twenty-five days old seedlings were transplanted in the main field at 20x15 cm spacing with single seedling per hill having plot size 3x0.60 m. The recommended fertilizers @ 100 kg N, 50 kg P_2O_5 and 50 kg K_2O along with 7.5 tonnes of FYM per hectare were

Table 1. Analysis of variance in Line x Tester analysis for twelve characters in Rice

Source of variation	DF	Characters											
		Days to 50 per cent flowering	Plant height (cm)	No. of productive tillers plant^{-1}	Panicle length (cm)	Total no. of spikelets panicle^{-1}	No. of filled spikelets panicle^{-1}	Spikelet fertility (%)	1000 Grain weight (g)	Grain yield plant^{-1} (g)	Straw yield plant^{-1} (g)	Harvest index (%)	Days to maturity
Replication	2	0.018	7.78	1.31	0.36	92.57	49.42	5.14	0.025	0.14	0.36	0.40	0.018
Parents	6	5.38**	370.27**	0.79	0.39	445.97**	370.02**	31.23**	9.15**	6.22**	88.1**	6.60**	5.38**
Male	3	9.33**	326.52**	0.83	0.67	722.92**	298.51**	39.64**	2.27	3.44	122.2**	57.56**	9.33**
Female	2	1.00	36.00**	0.05	0.12	22.46**	9.00	5.75**	4.78**	13.09**	6.88	3.21**	1.01
Male vs Female	1	2.28**	1170**	2.15	0.09	462.13**	1306.61**	56.96**	38.5**	0.82	148.1**	77.19**	2.27
Hybrids	11	54.45**	107.38**	1.15	8.55**	85.67**	234.96**	19.08**	4.74**	63.25**	55.15**	4.48**	54.46**
Parents vs. Hybrids	1	102.92**	7.86**	154.54**	112.6**	2725.1**	9036.16**	359.4**	87.15**	838.3**	221.1**	206.56**	102.91**
Line effect	2	22.75**	11.86**	0.475	0.510	196.82**	566.75**	19.33**	3.95**	10.42**	4.49**	8.08**	22.7**
Tester effect	3	155.00**	376.48**	2.77**	30.08**	104.21**	380.48**	35.24**	8.55**	224.29**	194.36**	9.21**	155.00**
Line vs. Tester effect	6	14.75**	4.67**	0.578	0.479	39.34**	51.59**	10.92**	3.10**	0.353	1.77	0.915	14.7**
Error	36	3.24	18.58	0.71	1.07	87.03	50.65	2.64	0.54	5.17	4.14	6.47	3.25
Variance component													
$б^2$gca		7.06	18.05	0.100	1.41	10.59	40.19	1.56	0.30	11.14	9.40	0.73	7.05
$б^2$sca		3.54	-6.40	-0.07	-0.12	-2.67	7.38	3.10	0.83	-1.73	-0.75	-1.54	3.58
$б^2$gca / $б^2$sca		1.99	-2.82	-1.43	-11.75	-3.97	5.45	0.50	0.36	-6.44	-12.53	-0.47	1.96

**p< 0.05, **p< 0.01*

applied. All standard agronomic recommended practices and plant protection measures were adopted for raising a healthy crop. Five sample plants were randomly selected from each plot excluding the border plants and the following data were recorded: Plant height, days to 50% flowering, number of productive tillers plant^{-1}, panicle length, total spikelet panicle^{-1}, filled spikelet panicle^{-1}, spikelet fertility, grain yield per plant, straw yield per plant, harvest index, 1000 grain weight and days to maturity. Collected data were subjected to statistical analysis using line × tester analysis by Kempthorne (1957).

Results and Discussion

The analysis of variance of Line X Tester analysis revealed that significant genotypic effect for all the characters under study for parents except for productive tillers plant^{-1} and panicle length. This provides evidence for the presence of sufficient genetic variability among lines, testers and test crosses indicating presence of diversity among treatments (Table 1). Significant variance due to females and males indicated the prevalence of additive variance whereas, non additive variance by line x tester. Variance due to interaction effect of male and female were found to be highly significant for all the traits under study except number of productive tillers plant^{-1}, panicle length and grain yield plant^{-1}. Variance due to hybrids were found to be highly significant for all the traits under study except number of productive tillers plant^{-1}. This indicated existence of the considerable amount of genetic variability among parents and hybrids for all the traits under study. The parents vs. hybrids comparison were found to be significant for all the characters indicating a substantial amount of heterosis in hybrids. Similar results reported by Sanghera *et al.,* (2012), Latha *et al.,* (2013), Islam *et al.,* (2015) and Khute *et al.,* (2015).

The general combining ability (GCA) identifies superior parents while specific combining ability (SCA) helps in identification of good hybrid combinations which may ultimate lead to the development of hybrids (Shiva Prasad *et al.,* 2011). Based on estimates of *per se* general combining ability effects for various characters (Table 2). It was observed that among three females, IR58025A was found to be good general combiner for the characters like total number of spikelets panicle^{-1} and number of filled spikelets panicle^{-1} and NPQ-49 were found to be good general combiner for the character plant height, grain yield plant^{-1} and straw yield plant^{-1}. The male parent, Chedo Local found to be good general combiner

Table 2. Crosses with SCA effects, Mean performance and GCA effects of parents for different characters of rice

Crosses	Days to 50 per cent flowering					Plant height (cm)				
	Mean performance	SCA Effects	GCA Effects		GCA Status	Mean performance	SCA Effects	GCA Effects		GCA Status
			Female parent	Male Parent				Female parent	Male Parent	
IR58025A x Chedo Local	103	0.33	-1.33	5.16**	A x P	104	0.86	-0.306	8.72**	A x P
IR58025A x CR-2829-PLN-36	93	0.00		-4.50**	A x G	95	-0.47		1.05	A x A
IR58025A x NPQ-49	100	1.33		1.16	A x A	89	0.30		-5.38**	A x G
IR58025A x RP-5898-19-8-6-1-1-1	94	-1.66		-1.83	A x A	90	-0.69		-4.38**	A x G
RTN12A x Chedo Local	104	0.08	-0.08	5.16**	A x P	106	1.11	1.11	8.72**	A x P
RTN12A x CR-2829-PLN-36	95	0.75		-4.50**	A x G	97	0.11		1.05	A x A
RTN12A x NPQ-49	101	1.08		1.16	A x A	90	-1.11		-5.38**	A x G
RTN12A x RP-5898-19-8-6-1-1-1	95	-1.91		-1.83	A x A	92	-0.11		-4.38**	A x G
RTN17A x Chedo Local	105	-0.41	1.41	5.16**	A x P	101	-1.97	-0.80	8.72**	A x P
RTN17A x CR-2829-PLN-36	95	-0.75		-4.50**	A x G	96	0.36		1.05	A x A
RTN17A x NPQ-49	99	-2.41*		1.16	A x A	90	0.80		-5.38**	A x G
RTN17A x RP-5898-19-8-6-1-1-1	102	3.58*		-1.83	A x A	91	0.80		-4.38**	A x G
	No. of productive tillers plant^{-1}					Panicle length (cm)				
IR58025A x Chedo Local	11.00	0.03	0.22	-0.48	A x A	25.63	-0.46	0.06	1.53	A x A
IR58025A x CR-2829-PLN-36	11.20	-0.16		-0.08	A x A	24.40	0.32		-0.48	A x A
IR58025A x NPQ-49	12.80	0.55		0.79	A x A	26.00	0.11		1.32	A x A
IR58025A x RP-5898-19-8-6-1-1-1	10.80	-0.42		-0.22	A x A	22.20	0.02		-2.38*	A x P
RTN12A x Chedo Local	10.80	0.11	-0.06	-0.48	A x A	26.37	0.56	-0.23	1.53	A x A
RTN12A x CR-2829-PLN-36	10.90	-0.18		-0.08	A x A	23.67	-0.11		-0.48	A x A
RTN12A x NPQ-49	11.97	0.00		0.79	A x A	25.48	-0.10		1.32	A x A
RTN12A x RP-5898-19-8-6-1-1-1	11.00	0.06		-0.22	A x A	21.53	-0.34		-2.38*	A x P
RTN17A x Chedo Local	10.43	-0.15	-0.16	-0.48	A x A	26.10	-0.09	0.16	1.53	A x A
RTN17A x CR-2829-PLN-36	11.33	0.35		-0.08	A x A	23.97	-0.21		-0.48	A x A
RTN17A x NPQ-49	11.30	-0.56		0.79	A x A	25.97	-0.01		1.32	A x A
RTN17A x RP-5898-19-8-6-1-1-1	11.20	0.36		-0.22	A x A	22.60	0.32		-2.38*	A x P
IR58025A x Chedo Local	261.90	0.67	3.73*	3.90**	G x G	245.75	-2.48*	6.29**	8.23**	G X G
IR58025A x CR-2829-PLN-36	261.03	1.93		1.77	G x A	237.30	-1.12		-1.57	G x A
IR58025A x NPQ-49	250.00	-4.11**		-3.20*	G x P	241.00	0.19		0.80	G x A
IR58025A x RP-5898-19-8-6-1-1-1	256.37	1.50		-2.46*	G x P	235.93	3.41*		-7.47**	G x P
RTN12A x Chedo Local	259.57	1.51	0.56	3.90**	A x G	241.00	-1.97	1.03	8.23**	A x G
RTN12A x CR-2829-PLN-36	256.05	0.12		1.77	A x A	235.00	1.83		-1.57	A x A
RTN12A x NPQ-49	249.00	-1.94		-3.20*	A x P	233.00	-2.54*		0.80	A x A
RTN12A x RP-5898-19-8-6-1-1-1	252.00	0.31		-2.46*	A x P	229.94	2.68*		-7.47**	A x P
RTN17A x Chedo Local	251.00	-2.18	-4.30**	3.90**	P x G	239.07	4.46**	-7.33**	8.23**	P x G
RTN17A x CR-2829-PLN-36	249.00	-2.05		1.77	P x A	224.08	-0.71		-1.57	P X A
RTN17A x NPQ-49	252.14	6.06**		-3.20*	P x P	229.52	2.34*		0.80	P x A
RTN17A x RP-5898-19-8-6-1-1-1	245.00	-1.82		-2.46*	P x P	212.80	-6.09**		-7.47**	P x P

	Spikelet fertility (%)					1000 Grain weight (g)				
IR58025A x Chedo Local	93.84	-1.30		1.84	A x A	22.80	-0.91		0.26	A x A
IR58025A x CR-2829-PLN-36	90.91	-1.14	1.14	-1.24	A x A	25.90	1.18	0.10	1.26	A x A
IR58025A x NPQ-49	96.41	1.59		1.51	A x A	22.47	-0.19		-0.78	A x P
IR58025A x RP-5898-19-8-6-1-1-1	92.03	0.84		-2.11	A x A	22.63	-0.07		-0.74	A x A
RTN12A x Chedo Local	92.88	-1.34		1.84	A x A	24.27	1.27		0.26	A x A
RTN12A x CR-2829-PLN-36	91.83	0.69	0.22	-1.24	A x A	23.70	-0.29	-0.61	1.26	A x A
RTN12A x NPQ-49	93.56	-0.32		1.51	A x A	21.53	-0.40		-0.78	A x P
RTN12A x RP-5898-19-8-6-1-1-1	91.24	0.98		-2.11	A x A	21.40	-0.58		-0.74	A x A
RTN17A x Chedo Local	95.29	2.65*		1.84	A x A	23.77	-0.35		0.26	A x A
RTN17A x CR-2829-PLN-36	89.99	0.44	-1.36	-1.24	A x A	24.23	-0.89	0.51	1.26	A x A
RTN17A x NPQ-49	91.04	-1.27		1.51	A x A	23.67	0.59		-0.78	A x P
RTN17A x RP-5898-19-8-6-1-1-1	86.84	-1.82		-2.11	A x A	23.77	0.65		-0.74	A x A
IR58025A x Chedo Local	33.00	0.06		0.78	A x A	39.80	0.07		0.77	A x A
IR58025A x CR-2829-PLN-36	27.40	-0.93	0.26	-6.01**	A x P	32.00	-0.92	0.27	-6.00**	A x P
IR58025A x NPQ-49	39.75	0.96		5.28**	A x G	45.20	0.90		5.24**	A x G
IR58025A x RP-5898-19-8-6-1-1-1	31.80	-0.09		-0.05	A x A	38.80	-0.08		-0.06	A x A
RTN12A x Chedo Local	32.00	-0.17		0.78	A x A	38.47	-0.18		0.77	A x A
RTN12A x CR-2829-PLN-36	25.44	0.13	-0.83	-6.01**	A x P	31.97	0.14	-0.84	-6.00**	A x P
RTN12A x NPQ-49	38.00	0.05		5.28**	A x G	43.19	0.06		5.24**	A x G
RTN12A x RP-5898-19-8-6-1-1-1	30.67	-0.01		-0.05	A x A	37.78	-0.02		-0.06	A x A
RTN17A x Chedo Local	31.31	0.11		0.78	A x A	40.15	0.12		0.77	A x A
RTN17A x CR-2829-PLN-36	26.00	0.80	0.56	-6.01**	A x P	34.03	0.82	0.57	-6.00**	A x P
RTN17A x NPQ-49	37.43	-1.01		5.28**	A x G	43.52	-1.00		5.24**	A x G
RTN17A x RP-5898-19-8-6-1-1-1	30.27	0.10		-0.05	A x A	39.29	0.11		-0.06	A x A
	Harvest index (%)					Days to maturity				
IR58025A x Chedo Local	45.27	-0.25		-0.29	A x A	133	0.32		5.14**	A x A
IR58025A x CR-2829-PLN-36	46.14	0.84	0.70	-0.52	A x A	123	0.01	-1.32	-4.51**	A x G
IR58025A x NPQ-49	46.81	-0.50		1.49	A x A	130	1.30		1.17	A x A
IR58025A x RP-5898-19-8-6-1-1-1	45.03	-0.09		-0.68	A x A	124	-1.67		-1.84	A x A
RTN12A x Chedo Local	45.38	0.36		-0.29	A x A	134	0.08		5.14**	A x A
RTN12A x CR-2829-PLN-36	44.32	-0.46	0.19	-0.52	A x A	125	0.74	-0.09	-4.51**	A x G
RTN12A x NPQ-49	46.80	-0.00		1.49	A x A	131	1.07		1.17	A x A
RTN12A x RP-5898-19-8-6-1-1-1	44.73	0.10		-0.68	A x A	125	-1.90		-1.84	A x A
RTN17A x Chedo Local	43.80	-0.11		-0.29	A x A	135	-0.42		5.14**	A x A
RTN17A x CR-2829-PLN-36	43.30	-0.38	-0.90	-0.52	A x A	125	-0.76	1.40	-4.51**	A x G
RTN17A x NPQ-49	46.21	0.50		1.49	A x A	129	-2.40*		1.17	A x A
RTN17A x RP-5898-19-8-6-1-1-1	43.51	-0.014		-0.68	A x A	132	3.56*		-1.84	A x A

G = Good parent having significant GCA effects in desirable direction; A = Average parent having either positive or negative but non-significant GCA effects; P = Poor parent having significant GCA effects in an undesirable direction.

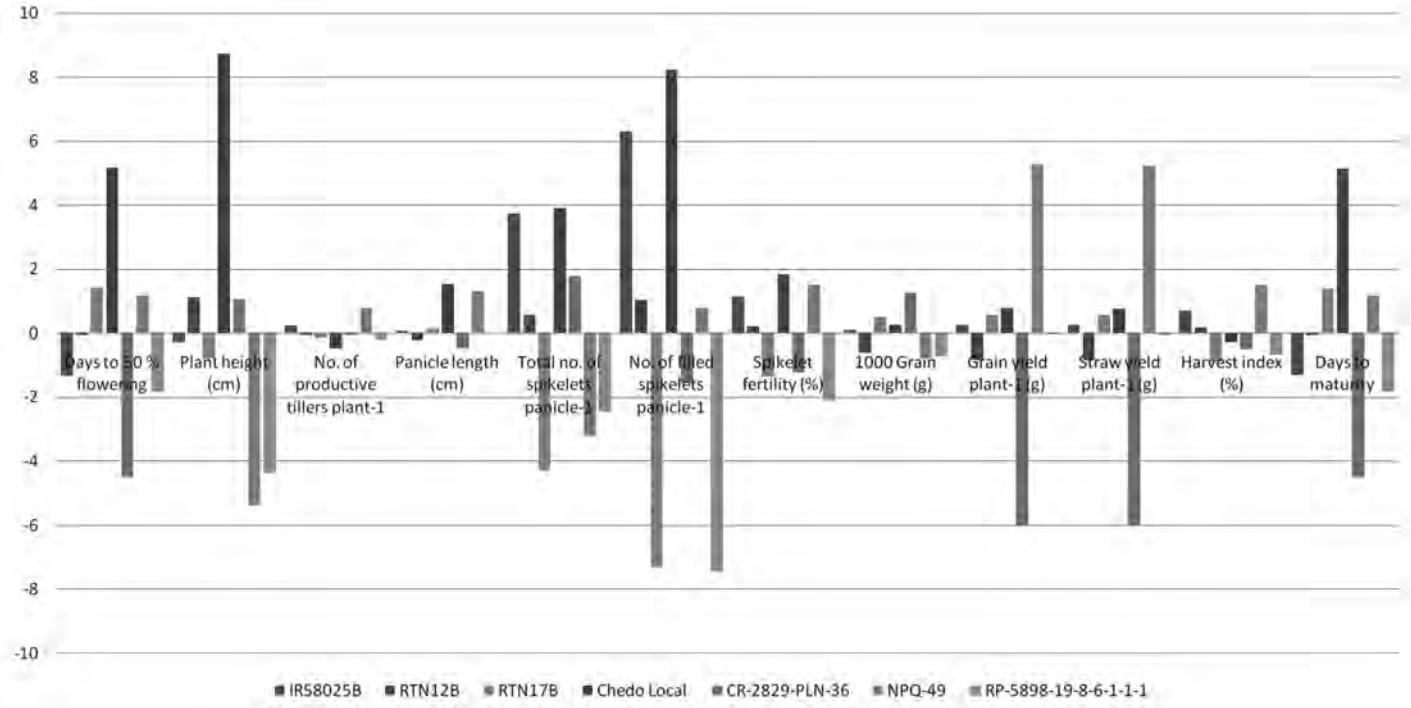

Figure 1. Multiple bar diagram – indicating GCA effects of seven parents for twelve characters

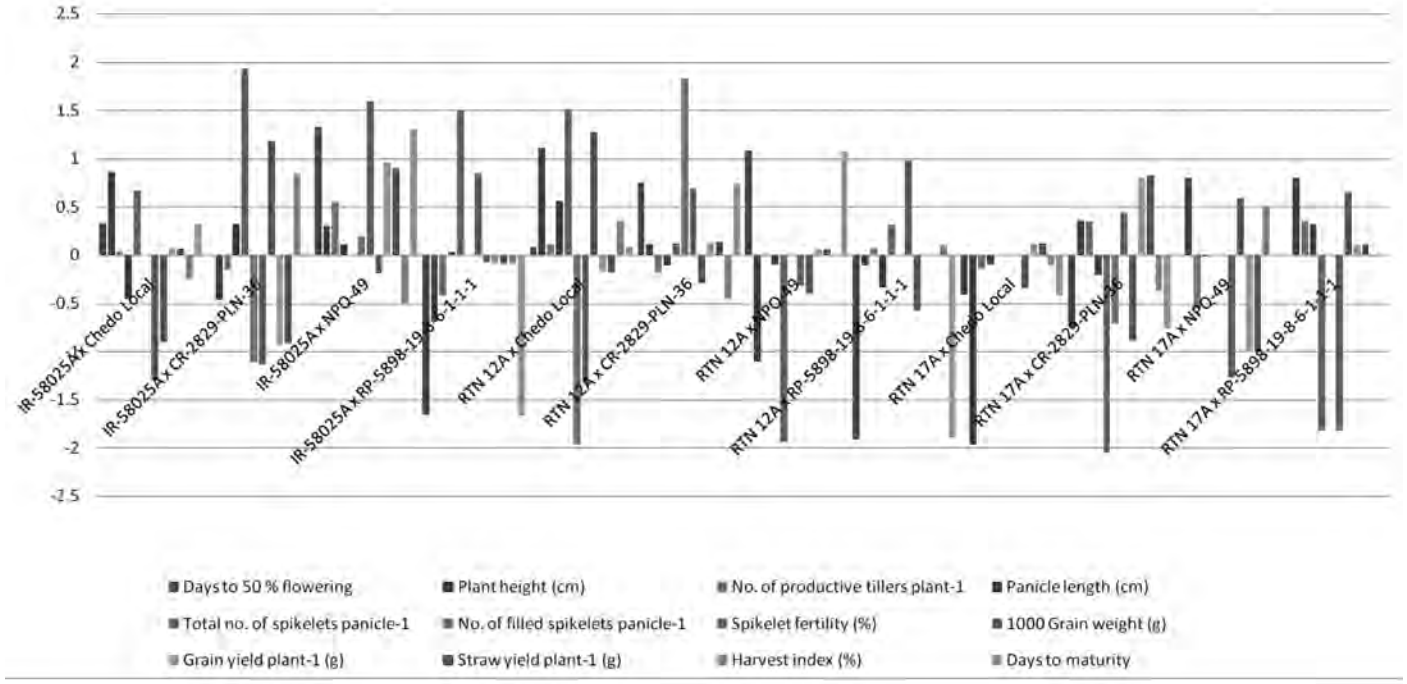

Figure 2. Multiple bar diagram – indicating SCA effects of twelve hybrids for twelve characters.

for the characters total number of spikelets panicle^{-1} and number of filled spikelets panicle^{-1}.

The three parents *viz*., IR58025A, NPQ-49 and Chedo Local was found to be good general combiner for the characters and may be extensively used in future hybrid rice breeding programme. These findings are in agreement with those reported by Sanghera *et al.,* (2012), Latha *et al.,* (2013), Islam *et al.,* (2015), Khute *et al.,* (2015) and Showkat *et al.,* (2015).

The specific combining ability (SCA) of crossess is the estimation and the understanding of the effect of non-additive gene action for a trait which is an indicator for the selection of a hybrid combination. The estimates of SCA effect revealed that none of the hybrids was consistently proved superior for all the traits. As many as 7 cross combinations exhibited positive SCA effect for grain yield plant^{-1}. Interestingly, two hybrids IR58025A x NPQ-49 and RTN12A x NPQ-49 exhibited positive SCA effect for this trait. These two crosses also manifested significant and desirable SCA effect for most of the yield attributing traits. Thus, hybrids with high SCA effect for grain yield plant^{-1} were also associated with high and desired SCA effect for yield contributing characters. Similar results were also reported by Thakare *et al.,* (2009), Sanghera *et al.,* (2012), Sharma *et al.,* (2013), Priyanka *et al.,* (2014) and Rahaman (2016).

On the basis of *per se* performance and combining ability three parents *viz*., IR58025A, NPQ-49 and Chedo Local were identified as good combiners for most of the traits. Hence they may be extensively used in future hybrid rice breeding programme and the hybrids *viz*., IR58025A x NPQ-49 and RTN12A x NPQ-49 was found to be the best crosses for yield contributing traits and may be evaluated critically to judge its superiority in performance and seed production technique for its utility on a commercial scale.

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ORIGINAL RESEARCH ARTICLE OPEN ACCESS

Morphological Characterization of Advanced Lines of Rice (*Oryza sativa* L.) Derived from Swarna x Ranbir Basmati at Seedling Stage

Komala, N. T*, Gurumurthy, R and Surendra, P

Department of Seed Science and Technology, College of Agriculture, Dharwad,
University of Agricultural Sciences, Dharwad, India
*Corresponding author: *ntkomala@gmail.com*

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Abstract

The present investigation entitled "Morphological characterization in advanced lines of rice (*Oryza sativa* L.) derived from Swarna x Ranbir basmati at seedling stage" was carried out during *kharif* 2016 at AICRIP, Agricultural Research Station, Mugad, UAS Dharwad. Segregation was observed in 30 different characters viz, basal leaf: sheath colour, Leaf: intensity of green colour, Leaf: anthocyanin colouration, Leaf: distribution of anthocyanin colour, Leaf sheath: anthocyanin colouration, Leaf sheath: intensity anthocyanin colouration, Leaf: pubescence of blade surface, Leaf: anthocyanin colouration of auricles, Leaf: colour of ligule, Leaf: length of blade, Culm: attitude, Flag leaf: attitude of blade, Spikelet: density of pubescence of lemma, Lemma: anthocyanin colouration of keel, Lemma: anthocyanin colouration of area below apex, Lemma: anthocyanin colouration of apex, Spikelet: colour of stigma, Stem: thickness, Stem: length and anthocyanin colourarion of internodes. There was no variation observed with respect to coleoptile: colour, Leaf: auricles, Leaf: collar, Leaf: anthocyanin colouration of collar, Leaf: ligule, Leaf: shape of ligule, Time of heading, Stem anthocyanin colouration of nodes and tem anthocyanin colouration of internodes.

Keywords: DUS, Ranbir Basmati, Swarna, morphological traits

Introduction

Rice (*Oryza sativa* L.) is the world's most important food crop and a primary food source for more than one third of world's population (Singh and Singh, 2008) Asia can be considered as 'Rice Basket' of the world, as more than 90 per cent of the rice is produced and consumed in Asia, a region with high population density. As the existing UPOV models of plant variety protection were not suitable for Indian requirements, the Government of India enacted our own legislation on the "Protection of Plant Varieties and Farmers Act" (PPV&FRA) in 2001 for providing protection to plant varieties based on distinctiveness, uniformity and stability (DUS) test apart from novelty. This is a unique and model act which gives equal importance to the farmers and breeders and treats them as partners in their efforts for sustainable food security (Patra, 2000). The concept of distinctness, uniformity and stability are thus fundamental to the characterization of a variety as a unique creation. Registration is allowed for three types of plant varieties viz., new varieties developed by breeders, extant varieties and farmer's varieties subject to their fulfilling the conditions of Distinctness, Uniformity, Stability and Novelty in case of breeder's variety. The uniqueness of a particular variety is to be established by the test called DUS.

Cultivar characterization is recommended based on the variations in seed and plant morphological characters, their response to chemical tests. In all cultivated crops, including agricultural and horticultural species varietal characterization was attempted by several researchers either for crop registration or to fix their utility in breeding and certification programmes. In a country like India, where contract farming is practiced at many places for seed production, with the active participation of private sector (Mishra *et al.*, 1996), monitoring of genetic purity at each stage of seed production becomes necessary and also cumbersome. In view of this, the study on varietal characterization is highly essential. Characterization is the most basic and important step in the process of evaluation and cataloguing of germplasm. It is essential for its evaluation, judicious use and protection against illegal utilization. Characterization of several morphological traits is helpful to develop distinctiveness among the genotypes.

Materials and Methods

The field experiment in 2016 was laid out at Agricultural Research Station, Mugad. It is situated at North latitude of 15^0 50′ and the East longitude of 75^0 40′, with an altitude of 697 m above mean sea level. The experimental material comprised of Swarna is a popular high yielding semi dwarf variety derived from cross between Vasistha x Mahsuri having low iron and zinc content (2.93 mg 100 g^{-1} and 2.28mg 100 g^{-1} respectively). While, Ranbir basmati selection from Basmati 370 possess high iron and zinc content of 4 mg 100^{-1} g and 5 mg 100^{-1} g respectively (details of the parents used are presented in Table 2). 160

segregating population were used as experimental material, were grown in a randomized complete block design with two replications to conduct DUS characterization during *kharif*, 2016, at All India Co-ordinate Rice Improvement Project (AICRIP, Mugad), University of Agricultural Sciences, Dharwad. Each entry was sown in three rows of two meter length at spacing of 20 cm between rows and 15 cm between plants. Crop was raised following recommended package of practices. Observations were recorded on five randomly chosen plants of each genotype per replication for thirty one morphological traits. The essential characters considered for the present study are mentioned in Table 1.

Table 1. Essential characters along with descriptor

Sl. No.	Characteristics	States	Note
1	Coleoptile: Colour	Colourless Green Purple	1 2 3
2	Basal leaf: Sheath colour	Green Light purple Purple lines Uniform purple	1 2 3 4
3	Leaf: Intensity of green colour	Light Medium Dark	3 5 7
4	Leaf: Anthocyanin Colouration	Absent Present	1 9
5	Leaf: Distribution of anthocyanin colour	On tips only On margins only In blotches only Uniform	1 2 3 4
6	Leaf Sheath: Anothhocyanin colouration	Absent Present	1 9
7	Leaf sheath: Intensity of anthocyanin colouration	Very weak Weak Medium Strong Very strong	1 3 5 7 9
8	Leaf: Pubescence of blade surface	Absent Weak Medium Strong Very strong	1 3 5 7 9
9	Leaf: Auricles	Absent Present	1 9
10	Leaf: Anthocyanin colouration of auricles	Colourless Light purple Purple	1 2 3
11	Leaf: Collar	Absent Present	1 9
12	Leaf: Anthocyanin colouration of collar	Absent Present	1 9
13	Leaf: Ligule	Absent Present	1 9
14	Leaf: Shape of lligule	Truncate Acute Split	1 2 3
15	Leaf: Colour of ligule	White Light purple Purple	1 2 3
16	Leaf: Length of blade	Short (<30 cm) Medium(30-45 cm) Long (>45 cm)	3 5 7
17	Leaf: Width of blade	Narrow (<1 cm) Medium (1-2 cm) Broad (>2 cm)	3 5 7
18	Culm: attitude	Erect Semi-erect Open Spreading	1 3 5 7
19	Time of heading (50% of plants with panicles) days	Very early (<71 days) Early (71-90 days) Medium (91-110 days) Late(111-130 days) Very late (> 131 days)	1 3 5 7 9
20	Flag leaf: Attitude of blade (early observation)	Erect Semi-erect Horizontal Drooping	1 3 5 7
21	Spikelet: Density of pubiscence of lemma	Absent Weak Medium Strong Very strong	1 3 5 7 9
22	Male sterility	Absent Present	1 9
23	Lemma: Anthocyanin colouration of keel	Absent or very weak Weak Medium Strong Very strong	1 3 5 7 9
24	Lemma: Anthocyanin colouration of area below apex	Absent Weak Medium Strong Very strong	1 3 5 7 9
25	Lemma: Anthocyanin colouration of apex	Absent Weak Medium Strong Very strong	1 3 5 7 9

26	Spikelet: Colour of stigma	White Light green Yellow Light purple Purple	1 2 3 4 5
27	Stem: Thickness	Thin (<0.40 cm) Medium (0.40-0.55 cm) Thick (>0.55 cm)	3 5 7
28	Stem: Length (excluding panicle; excluding floating rice)	Very short(<91 cm) Short (91-110 cm) Medium(111-130 cm) Long (131-150 cm) Very long(>150 cm)	1 3 5 7 9
29	Stem: Anthocyanin colouraiton of nodes	Absent Present	1 9
30	Stem : Anthocyanin colouration of internodes	Absent Present	1 9

Results and Discussion:

Qualitative and quantitative characters of rice seedlings derived from Swarna × Ranbir basmati are presented in Table 3. Among 160 rice inbred lines variation was observed, the characters coleoptile: colour was green in all 160 lines. Basal leaf: sheath colour showed segregation, of which 106 green, 19 light green, 33 purple lines and 2 lines showed unifrm purple colour. Similar results were obtained by Das and Ghosh (2010) they studied 431 traditional rice cultivars and reported that considerable variability was recorded for basal leaf sheath colour, awning and auricle colour. Characters like leaf blade colour, panicle excertion, stigma colour *etc*. showed moderate variability. Leaf: intensity of green colour showed segregation of which 28 light, 122 medium and 10 lines showed dark colour. Leaf: anthocyanin colouration was absent in 148 lines and present in 12 lines. Leaf: distribution of anthocyanin colour was observed on margins only in 9 lines, in blotches only in 3, uniform on 1 line and remaining all other lines were devoid 0f anthocyanin colour. Leaf sheath: anthocyanin colouration was absent in 113 and present in 47 lines. Leaf sheath: intensity anthocyanin colouration was weak in 2, medium in 39, strong in 5, very strong in 2 lines and absence of intensity anthocyanin colour in remaining lines. Leaf: pubescence of blade surface was weak in 1, medium in 61, strong in 63 and very strong in 35 lines. Leaf: anthocyanin colouration of auricles was colourless in 159 and purple in 1 line. Leaf: colour of ligule was white in 140, light purple in 19 and purple in 1 line. Leaf: length of blade was short (<30 cm) in 61, medium (30-45cm) in 78 and long (>45cm) in 21 lines. Rajanna *et al.,* (2011) observed more variation among the parents (IR-58025A, IR-58025B, KMR-3R, IR- 68897A, IR- 68897B, and DR-71-1-2R) and hybrids (KRH-2 and DRRH-2) for the characters such as leaf length and days to 50 per cent flowering exhibited. Leaf: width of blade was narrow (<1cm) in 119 and medium (1-2cm) in 41lines. Culm: attitude was erect in 32, semi erect in 80, open in 46 and spreading in 2 lines. Flag leaf: attitude of blade (early observation) was erect in 51, semi erect in 78 and horizontal in 31 lines. Spikelet: density of pubescence of lemma was absent in 29, weak in 125, medium in 5 and strong in 1 line. Male sterility was absent in 159 and present in 1 line. Lemma: anthocyanin colouration of keel was absent or very weak in 147, weak in 12 and medium in 1 line. Lemma: anthocyanin colouration of area below apex was absent in 136, weak in 21 and medium in 3 lines. Lemma: anthocyanin colouration of apex was absent in 117, weak in 1, medium in 20, strong in 19 and very strong in 3 lines. Spikelet: colour of stigma was white in 110, light green in 2, yellow in 47 and light purple in 1 line. Stem: thickness was thin (<0.40cm) in 52, medium (0.40-0.55cm) in 92 and thick (>0.55cm) in 16 lines. Stem: length (excluding panicle; excluding floating rice) was very short (<91 cm) in 83, short (91-110 cm) in 43, medium (111-130 cm) in 29 and long (131-150 cm) in 5 lines. Stem: anthocyanin colourarion of nodes was absent in 160 lines.

There was no variation observed with respect to coleoptile: colour was green in all 160 lines. Leaf: auricles were present in all 160 lines. Leaf: collar was present in 160 lines. Leaf: anthocyanin colouration of collar was absent in 160 lines. Leaf: ligule was present in 160 lines. Leaf: shape of ligule split ligule was observed in 160 lines. Time of heading (50% of plants with panicles) was very late (>131 days) in 160 lines. Stem: Intensity of anothocyanin colouration of nodes was not aberved in all 160 lines. Stem: anthocyanin colourarion of internodes was absent in

Table 2: Details of the parents used in the presents study

Sl. No.	Genotypes	Parentage	Grain type	50% Flowering	Iron content (mg/kg of brown rice)	Zinc content (mg/kg of brown rice)	Yield (t ha-1)	Year of release
1	Swarna (MTU 7029) IET 7041 Notif. 2103 (E) Dt.12/08/1980	Vasistha x Mahsuri	MS	125	7.8	22.8	3.5	1979
2	Ranbir Basmati IET 11348 Notif. 1(E) Dt. 01/01/1996	Selection from Basmati 370	LS	95	13.3	29.6	2.7	1994

Table 3: Qualitative and quantitative characters of rice seedlings derived from Swarna × Ranbir basmati

SN	Genotype		Coleoptile: Colour	Basal Leaf: Sheath	Leaf: Intensity of green	Leaf: Anthocyanin colouration	Leaf: Distribution of anthocyanin colour	Leaf Sheath: Anothhocyanin colouration	Leaf sheath: Intensity of anthocyanin colouration	Leaf: Pubescence of blade surface	Leaf: Auricles	Leaf: anthocyanin colouration of auricles	Leaf: collar	Leaf: Anthocyanin colouration of collar	Leaf: Ligule	Leaf: Shape of liigule	Leaf: Colour of ligule	Leaf: Length of blade	Leaf: Width of blade	Culm: attitude	Time of heading (50% of plants with panicles) days	Flag leaf: Attitude of blade (early observation)	Spikelet: Density of publiscence of lemma	Male sterility	Lemma: Anthocyanin colouration of keel	Lemma: Anthocyanin colouration of area below apex	Lemma: Anthocyanin colouration of apex	Spikelet: Colour of stigma	Stem: Thickness	Stem: Length (excluding panicle; excluding floating rice)	Stem: Anthocyanin colouration of nodes	Stem: Intensity of anothocyanin colouration of nodes	Stem : Anthocyanin colouration of internodes
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
1	SR-F7 -1		2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	3	5	9	3	1	1	1	1	1	1	5	7	1	–	1
2	SR-F7 - 2		2	3	3	1	–	9	5	5	9	1	9	1	9	3	1	5	3	1	9	1	1	1	1	3	5	5	7	1	1	–	1
3	SR-F7 - 3		2	3	5	1	–	9	5	7	9	1	9	1	9	3	1	7	3	1	9	3	1	1	1	5	5	1	5	3	1	–	1
4	SR-F7 - 4		2	3	5	1	–	9	3	7	9	1	9	1	9	3	1	5	3	1	9	1	1	1	1	1	5	5	3	1	1	–	1
5	SR-F7 - 5		2	3	5	1	–	9	5	7	9	1	9	1	9	3	1	5	3	1	9	3	1	1	1	1	7	5	5	1	1	–	1
6	SR-F7 - 6		2	3	5	1	–	9	5	5	9	1	9	1	9	3	2	5	3	5	9	1	3	1	1	1	1	1	5	3	1	–	1
7	SR-F7 - 7		2	3	5	1	–	9	5	7	9	1	9	1	9	3	1	7	3	3	9	1	3	1	1	3	7	5	3	5	1	–	1
8	SR-F7 - 8		2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	3	5	9	3	1	1	1	1	1	5	5	5	1	–	1
9	SR-F7 - 9		2	1	7	1	–	1	–	7	9	1	9	1	9	3	1	3	3	5	9	3	1	1	1	1	1	5	1	1	1	–	1
10	SR-F7 - 10		2	3	5	1	–	9	5	7	9	1	9	1	9	3	2	5	3	1	9	3	1	1	1	1	1	5	3	3	1	–	1
11	SR-F7 - 11		2	3	5	1	–	9	5	7	9	1	9	1	9	3	2	7	3	3	9	5	3	1	1	3	7	5	5	7	1	–	1
12	SR-F7 - 12		2	3	5	1	–	9	5	7	9	1	9	1	9	3	1	3	5	5	9	1	1	1	1	5	5	1	3	1	1	–	1
13	SR-F7 - 13		2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	3	3	9	1	1	1	1	1	5	5	5	5	1	–	1
14	SR-F7 - 14		2	3	5	1	–	9	7	5	9	1	9	1	9	3	2	7	3	5	9	1	3	1	1	1	5	5	5	1	1	–	1
15	SR-F7 - 15		2	3	5	1	–	9	5	5	9	1	9	1	9	3	2	5	5	5	9	3	1	1	1	1	5	5	5	1	1	–	1
16	SR-F7 - 16		2	3	5	1	–	9	5	7	9	1	9	1	9	3	1	7	5	5	9	5	1	1	1	1	5	5	7	5	1	–	1
17	SR-F7 - 17		2	3	5	1	–	9	5	5	9	1	9	1	9	3	1	5	5	1	9	3	1	1	1	1	5	5	5	5	1	–	1
18	SR-F7 - 18		2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	3	3	3	9	1	3	1	1	1	1	1	3	1	1	–	1
19	SR-F7 - 19		2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	3	5	9	3	1	1	1	1	1	1	3	1	1	–	1
20	SR-F7 - 20		2	1	7	1	–	1	–	7	9	1	9	1	9	3	1	5	3	5	9	3	1	1	1	1	1	1	5	3	1	–	1
21	SR-F7 - 21		2	3	7	1	–	9	7	5	9	1	9	1	9	3	1	3	3	3	9	5	3	1	1	1	5	1	3	3	1	–	1
22	SR-F7 - 22		2	1	7	1	–	1	–	7	9	1	9	1	9	3	1	3	3	5	9	3	1	1	1	1	1	1	3	1	1	–	1
23	SR-F7 - 23		2	1	7	1	–	1	–	7	9	1	9	1	9	3	1	3	3	5	9	3	1	1	1	1	1	1	5	1	1	–	1

24	SR-F7 - 24	2	1	7	1	–	1	–	7	9	1	9	1	9	3	1	5	5	5	9	3	3	1	1	1	1	1	5	1	1	–	1
25	SR-F7 - 25	2	3	5	1	–	9	5	5	9	1	9	1	9	3	1	5	5	5	9	3	1	1	1	1	5	5	3	3	1	–	1
26	SR-F7 - 26	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	5	5	9	3	3	1	1	1	1	1	5	3	1	–	1
27	SR-F7 - 27	2	3	5	1	–	9	5	5	9	1	9	1	9	3	1	5	5	3	9	1	1	1	1	1	5	5	5	1	1	–	1
28	SR-F7 - 28	2	3	5	1	–	9	5	7	9	1	9	1	9	3	1	5	5	3	9	1	1	1	1	1	5	5	5	1	1	–	1
29	SR-F7 - 29	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	3	3	5	9	1	3	1	1	1	1	1	3	1	1	–	1
30	SR-F7 - 30	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	5	5	3	9	1	1	1	1	3	1	1	5	5	1	–	1
31	SR-F7 - 31	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	7	3	3	9	1	1	1	1	3	1	3	3	1	1	–	1
32	SR-F7 - 32	2	3	5	9	3	9	5	9	9	1	9	1	9	3	2	3	3	5	9	3	3	1	1	3	5	5	5	3	1	–	1
33	SR-F7 - 33	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	3	3	9	1	3	1	1	1	1	1	3	3	1	–	1
34	SR-F7 - 34	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	5	5	9	1	1	1	1	1	1	5	3	1	1	–	1
35	SR-F7 - 35	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	3	3	9	5	7	9	1	1	1	1	7	1	1	–	1
36	SR-F7 - 36	2	2	5	1	–	9	5	7	9	1	9	1	9	3	1	5	3	5	9	3	3	1	1	1	1	1	3	1	1	–	1
37	SR-F7 - 37	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	5	5	9	3	3	1	1	1	1	1	5	1	1	–	1
38	SR-F7 - 38	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	3	5	5	9	1	1	1	1	1	1	1	7	1	1	–	1
39	SR-F7 - 39	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	3	5	5	9	3	3	1	1	1	1	1	3	1	1	–	1
40	SR-F7 - 40	2	1	7	1	–	1	–	9	9	1	9	1	9	3	1	5	5	5	9	1	1	1	1	1	1	1	3	1	1	–	1
41	SR-F7 - 41	2	3	5	1	–	9	5	5	9	1	9	1	9	3	2	7	3	5	9	3	3	1	1	1	7	5	7	5	1	–	1
42	SR-F7 - 42	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	7	5	5	9	3	3	1	1	1	1	1	5	5	1	–	1
43	SR-F7 - 43	2	3	5	1	–	9	5	7	9	1	9	1	9	3	2	3	3	5	9	3	3	1	1	1	1	1	5	5	1	–	1
44	SR-F7 - 44	2	3	5	9	2	9	7	7	9	1	9	1	9	3	2	3	3	3	9	3	3	1	1	1	7	5	7	3	1	–	1
45	SR-F7 - 45	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	3	3	9	1	1	1	1	1	1	1	7	3	1	–	1
46	SR-F7 - 46	2	3	7	1	–	9	5	7	9	1	9	1	9	3	2	3	3	5	9	1	3	1	3	5	7	5	5	1	1	–	1
47	SR-F7 - 47	2	3	5	1	–	9	5	9	9	1	9	1	9	3	1	7	5	5	9	3	1	1	1	3	1	1	7	5	1	–	1
48	SR-F7 - 48	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	7	5	3	9	1	3	1	1	1	5	5	5	7	1	–	1
49	SR-F7 - 49	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	5	5	3	9	1	3	1	1	1	1	1	3	1	1	–	1
50	SR-F7 - 50	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	5	5	9	3	3	1	1	1	1	1	5	5	1	–	1
51	SR-F7 - 51	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	5	5	3	9	3	1	1	1	1	1	1	3	5	1	–	1
52	SR-F7 - 52	2	3	5	1	–	9	5	9	9	1	9	1	9	3	1	5	5	5	9	3	3	1	1	1	9	5	5	7	1	–	1
53	SR-F7 - 53	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	3	3	9	3	3	1	1	3	1	1	3	1	1	–	1
54	SR-F7 - 54	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	5	3	9	5	1	1	1	1	1	1	5	3	1	–	1
55	SR-F7 - 55	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	3	3	9	3	3	1	1	1	1	1	5	3	1	–	1
56	SR-F7 - 56	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	3	5	9	1	3	1	1	1	1	1	5	3	1	–	1
57	SR-F7 - 57	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	3	3	9	3	3	1	1	1	1	1	5	1	1	–	1
58	SR-F7 - 58	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	5	3	9	1	3	1	1	1	1	1	5	5	1	–	1
59	SR-F7 - 59	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	3	3	3	9	3	3	1	1	1	1	1	5	1	1	–	1
60	SR-F7 - 60	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	5	5	3	9	1	3	1	1	1	1	1	5	3	1	–	1
61	SR-F7 - 61	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	3	3	1	9	3	3	1	1	1	1	1	5	1	1	–	1

62	SR-F7 - 62	2	3	5	1	–	9	5	5	9	1	9	1	9	3	2	5	3	3	9	3	3	1	1	1	7	5	5	3	1	–	1
63	SR-F7 - 63	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	5	3	3	9	5	3	1	1	1	1	1	5	5	1	–	1
64	SR-F7 - 64	2	4	5	9	4	9	9	9	9	3	9	1	9	3	3	5	5	3	9	1	3	1	5	5	9	5	5	1	1	–	1
65	SR-F7 - 65	2	3	5	9	3	9	5	9	9	1	9	1	9	3	2	5	3	3	9	5	3	1	1	1	1	1	3	5	1	–	1
66	SR-F7 - 66	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	5	3	3	9	3	3	1	1	1	1	1	3	3	1	–	1
67	SR-F7 - 67	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	3	3	9	3	3	1	1	1	1	1	3	1	1	–	1
68	SR-F7 - 68	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	3	1	9	3	3	1	1	1	1	5	5	1	1	–	1
69	SR-F7 - 69	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	3	1	9	1	1	1	1	3	1	1	3	1	1	–	1
70	SR-F7 - 70	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	3	1	9	3	3	1	1	1	1	1	3	1	1	–	1
71	SR-F7 - 71	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	3	1	9	5	3	1	1	1	1	1	5	3	1	–	1
72	SR-F7 - 72	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	3	5	1	9	3	3	1	1	1	1	1	5	3	1	–	1
73	SR-F7 - 73	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	3	3	3	9	1	3	1	1	1	1	1	3	1	1	–	1
74	SR-F7 - 74	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	5	3	3	9	3	3	1	1	1	1	1	5	1	1	–	1
75	SR-F7 - 75	2	2	5	1	–	1	5	5	9	1	9	1	9	3	1	5	5	5	9	5	3	1	3	3	7	5	5	1	1	–	1
76	SR-F7 - 76	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	5	3	1	9	1	3	1	1	1	1	1	3	1	1	–	1
77	SR-F7 - 77	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	5	3	1	9	3	3	1	3	1	1	1	5	3	1	–	1
78	SR-F7 - 78	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	7	5	1	9	3	3	1	3	1	1	1	5	5	1	–	1
79	SR-F7 - 79	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	3	3	3	9	5	3	1	1	1	1	1	3	1	1	–	1
80	SR-F7 - 80	2	2	5	1	–	9	5	5	9	1	9	1	9	3	2	3	3	5	9	3	3	1	3	1	1	1	3	1	1	–	1
81	SR-F7 - 81	2	1	7	1	–	1	–	5	9	1	9	1	9	3	1	3	3	5	9	3	3	1	1	1	1	1	5	1	1	–	1
82	SR-F7 - 82	2	2	5	1	–	9	5	7	9	1	9	1	9	3	1	5	3	3	9	3	3	1	1	1	1	1	7	1	1	–	1
83	SR-F7 - 83	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	3	3	9	3	3	1	1	1	1	1	5	1	1	–	1
84	SR-F7 - 84	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	3	3	9	3	1	1	3	1	1	1	3	1	1	–	1
85	SR-F7 - 85	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	7	3	1	9	3	3	1	3	1	1	1	5	3	1	–	1
86	SR-F7 - 86	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	5	3	1	9	3	5	1	1	3	1	1	5	5	1	–	1
87	SR-F7 - 87	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	3	3	3	9	3	3	1	3	1	1	1	3	3	1	–	1
88	SR-F7 - 88	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	3	3	1	9	5	3	1	1	1	1	1	5	3	1	–	1
89	SR-F7 - 89	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	5	3	3	9	5	5	1	1	1	1	1	5	5	1	–	1
90	SR-F7 - 90	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	3	3	3	9	1	5	1	1	1	1	1	3	1	1	–	1
91	SR-F7 - 91	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	3	3	1	9	5	3	1	1	1	1	1	3	1	1	–	1
92	SR-F7 - 92	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	7	3	3	9	5	3	1	1	1	1	1	3	5	1	–	1
93	SR-F7 - 93	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	7	3	3	9	1	3	1	1	1	5	5	5	5	1	–	1
94	SR-F7 - 94	2	1	7	1	–	1	–	9	9	1	9	1	9	3	1	5	5	3	9	1	3	1	1	1	1	1	3	1	1	–	1
95	SR-F7 - 95	2	2	5	1	–	9	5	9	9	1	9	1	9	3	1	7	3	3	9	5	3	1	3	1	7	5	5	3	1	–	1
96	SR-F7 - 96	2	2	5	1	–	9	5	9	9	1	9	1	9	3	1	5	3	3	9	5	3	1	1	1	7	5	3	1	1	–	1
97	SR-F7 - 97	2	2	5	1	–	9	5	9	9	1	9	1	9	3	1	7	3	1	9	5	3	1	1	1	5	5	5	3	1	–	1
98	SR-F7 - 98	2	2	5	1	–	9	5	9	9	1	9	1	9	3	2	7	3	3	9	3	3	1	1	1	7	5	3	7	1	–	1
99	SR-F7 - 99	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	7	3	3	9	1	5	1	1	1	1	1	5	1	1	–	1

100	SR-F7 - 100	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	7	3	1	9	1	3	1	3	3	1	3	5	1	1	–	1
101	SR-F7 - 101	2	2	3	1	–	1	–	5	9	1	9	1	9	3	1	3	3	3	9	5	3	1	1	1	1	1	5	1	1	–	1
102	SR-F7 - 102	2	1	3	1	–	9	5	9	9	1	9	1	9	3	1	3	3	5	9	5	3	1	1	1	7	5	5	3	1	–	1
103	SR-F7 - 103	2	1	3	1	–	1	–	5	9	1	9	1	9	3	1	5	3	5	9	1	3	1	1	1	1	5	3	1	1	–	1
104	SR-F7 - 104	2	2	5	1	–	1	–	5	9	1	9	1	9	3	1	5	3	5	9	3	3	1	1	1	1	1	7	3	1	–	1
105	SR-F7 - 105	2	2	5	9	2	9	5	7	9	1	9	1	9	3	1	3	3	3	9	3	3	1	1	1	5	5	5	1	1	–	1
106	SR-F7 - 106	2	2	3	1	–	1	–	9	9	1	9	1	9	3	1	5	3	3	9	5	3	1	1	1	7	5	5	1	1	–	1
107	SR-F7 - 107	2	1	5	1	–	1	–	9	9	1	9	1	9	3	1	5	3	1	9	3	3	1	1	1	7	7	5	5	1	–	1
108	SR-F7 - 108	2	1	3	1	–	1	–	5	9	1	9	1	9	3	1	5	3	3	9	3	1	1	3	3	1	1	5	3	1	–	1
109	SR-F7 - 109	2	1	3	1	–	1	–	9	9	1	9	1	9	3	1	5	3	3	9	3	3	1	3	3	1	1	5	3	1	–	1
110	SR-F7 - 110	2	1	3	1	–	1	–	5	9	1	9	1	9	3	1	5	5	1	9	1	3	1	1	1	1	1	3	3	1	–	1
111	SR-F7 - 111	2	1	3	1	–	1	–	5	9	1	9	1	9	3	1	3	3	5	9	1	3	1	1	1	1	1	3	1	1	–	1
112	SR-F7 - 112	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	3	1	9	1	5	1	1	1	1	1	7	1	1	–	1
113	SR-F7 - 113	2	2	3	1	–	1	–	5	9	1	9	1	9	3	1	3	5	3	9	3	3	1	1	1	1	1	5	1	1	–	1
114	SR-F7 - 114	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	3	1	9	5	3	1	1	1	9	5	5	3	1	–	1
115	SR-F7 - 115	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	3	3	3	9	1	3	1	1	1	1	1	5	1	1	–	1
116	SR-F7 - 116	2	1	3	1	–	1	–	5	9	1	9	1	9	3	1	5	3	3	9	3	3	1	1	1	1	1	5	1	1	–	1
117	SR-F7 - 117	2	2	3	1	–	1	–	7	9	1	9	1	9	3	1	5	3	3	9	3	3	1	1	1	1	1	3	1	1	–	1
118	SR-F7 - 118	2	1	3	1	–	9	5	9	9	1	9	1	9	3	1	3	3	3	9	3	3	1	1	1	1	1	3	3	1	–	1
119	SR-F7 - 119	2	1	3	1	–	1	–	5	9	1	9	1	9	3	1	3	3	3	9	1	3	1	1	1	1	1	3	1	1	–	1
120	SR-F7 - 120	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	5	3	3	9	3	3	1	1	3	7	5	5	5	1	–	1
121	SR-F7 - 121	2	1	3	1	–	1	–	5	9	1	9	1	9	3	1	5	3	7	9	3	3	1	1	1	1	1	3	1	1	–	1
122	SR-F7 - 122	2	3	5	1	–	1	–	7	9	1	9	1	9	3	1	5	5	5	9	3	1	1	1	1	1	1	7	5	1	–	1
123	SR-F7 - 123	2	2	5	1	2	9	7	7	9	1	9	1	9	3	2	5	3	3	9	1	1	1	1	1	7	5	5	1	1	–	1
124	SR-F7 - 124	2	2	5	1	–	9	5	3	9	1	9	1	9	3	1	5	3	3	9	1	1	1	1	1	7	5	5	1	1	–	1
125	SR-F7 - 125	2	1	5	1	–	9	3	5	9	1	9	1	9	3	1	5	3	3	9	5	3	1	1	1	1	1	5	3	1	–	1
126	SR-F7 - 126	2	1	3	1	–	1	–	5	9	1	9	1	9	3	1	5	3	3	9	1	3	1	1	1	1	1	5	3	1	–	1
127	SR-F7 - 127	2	4	3	1	–	1	–	7	9	1	9	1	9	3	1	3	3	5	9	1	3	1	1	1	1	1	5	1	1	–	1
128	SR-F7 - 128	2	1	5	9	3	9	9	5	9	1	9	1	9	3	2	3	3	3	9	3	3	1	1	1	5	5	3	3	1	–	1
129	SR-F7 - 129	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	3	3	9	3	3	1	1	1	1	1	3	1	1	–	1
130	SR-F7 - 130	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	3	3	5	9	1	3	1	1	1	1	1	5	1	1	–	1
131	SR-F7 - 131	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	3	3	3	9	1	3	1	1	1	1	1	3	1	1	–	1
132	SR-F7 - 132	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	3	3	3	9	3	3	1	1	1	1	1	3	1	1	–	1
133	SR-F7 - 133	2	1	3	1	–	1	–	5	9	1	9	1	9	3	1	5	3	5	9	3	3	1	1	1	1	1	7	3	1	–	1
134	SR-F7 - 134	2	1	3	1	–	1	–	5	9	1	9	1	9	3	1	3	3	3	9	3	3	1	1	1	1	1	5	1	1	–	1
135	SR-F7 - 135	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	3	5	9	5	3	1	1	1	1	1	7	3	1	–	1
136	SR-F7 - 136	2	1	3	1	–	1	–	5	9	1	9	1	9	3	1	3	3	1	9	1	3	1	1	1	1	1	5	1	1	–	1
137	SR-F7 - 137	2	1	3	1	–	1	–	5	9	1	9	1	9	3	1	3	3	1	9	1	3	1	1	1	1	1	5	1	1	–	1

138	SR-F7 - 138	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	3	3	3	9	3	3	1	1	1	1	1	3	1	1	–	1
139	SR-F7 - 139	2	1	3	1	–	1	–	5	9	1	9	1	9	3	1	3	3	3	9	5	3	1	1	1	5	5	3	1	1	–	1
140	SR-F7 - 140	2	1	3	1	–	1	–	7	9	1	9	1	9	3	1	3	3	5	9	5	3	1	1	1	1	1	5	1	1	–	1
141	SR-F7 - 141	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	5	3	5	9	3	3	1	1	1	1	1	3	1	1	–	1
142	SR-F7 - 142	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	5	5	9	1	1	1	1	1	7	5	3	1	1	–	1
143	SR-F7 - 143	2	3	5	9	2	9	7	9	9	1	9	1	9	3	1	5	3	3	9	3	1	1	1	1	7	5	5	3	1	–	1
144	SR-F7 - 144	2	3	3	1	–	1	–	5	9	1	9	1	9	3	2	3	3	1	9	5	3	1	1	3	1	5	5	5	1	–	1
145	SR-F7 - 145	2	2	3	1	–	1	–	5	9	1	9	1	9	3	1	3	3	3	9	5	3	1	1	3	1	1	5	3	1	–	1
146	SR-F7 - 146	2	2	3	1	–	1	–	5	9	1	9	1	9	3	1	3	3	3	9	5	3	1	1	3	1	1	5	1	1	–	1
147	SR-F7 - 147	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	3	3	9	1	3	1	1	3	1	1	3	1	1	–	1
148	SR-F7 - 148	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	5	5	3	9	3	3	1	1	1	1	1	5	3	1	–	1
149	SR-F7 - 149	2	3	5	9	2	9	5	5	9	1	9	1	9	3	1	5	3	1	9	1	3	1	1	1	1	1	5	1	1	–	1
150	SR-F7 - 150	2	1	3	1	–	1	–	7	9	1	9	1	9	3	1	3	3	3	9	3	3	1	1	1	1	1	3	1	1	–	1
151	SR-F7 - 151	2	3	5	1	–	1	–	5	9	1	9	1	9	3	1	5	3	3	9	5	3	1	1	1	1	5	7	5	1	–	1
152	SR-F7 - 152	2	3	5	9	2	9	5	5	9	1	9	1	9	3	2	3	3	3	9	5	3	1	1	1	5	5	5	1	1	–	1
153	SR-F7 - 153	2	3	3	1	–	1	–	7	9	1	9	1	9	3	1	5	5	1	9	3	3	1	1	1	1	1	5	5	1	–	1
154	SR-F7 - 154	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	5	1	9	3	3	1	1	1	1	1	5	5	1	–	1
155	SR-F7 - 155	2	1	5	9	2	9	5	5	9	1	9	1	9	3	1	5	3	1	9	3	3	1	1	1	1	5	5	3	1	–	1
156	SR-F7 - 156	2	1	5	9	2	9	5	9	9	1	9	1	9	3	1	7	3	7	9	5	3	1	1	1	5	5	5	5	1	–	1
157	SR-F7 - 157	2	2	5	9	2	9	5	7	9	1	9	1	9	3	2	7	3	3	9	3	3	1	1	1	1	5	5	5	1	–	1
158	SR-F7 - 158	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	5	5	3	9	3	3	1	1	1	1	1	5	3	1	–	1
159	SR-F7 - 159	2	1	5	1	–	1	–	7	9	1	9	1	9	3	1	5	5	5	9	3	3	1	1	1	1	1	5	3	1	–	1
160	SR-F7 - 160	2	1	5	1	–	1	–	5	9	1	9	1	9	3	1	5	5	5	9	3	3	1	1	1	1	1	7	1	1	–	1

SR-F7: F_7 population derived from the cross Swarna x Ranbir basmati

160 lines. Based on the study done by Mehla and Kumar (2008) on various morphological characters responsible for identification of rice cultivars, they concluded that existstance of wide variation among the rice cultivars in respect to morphological characters viz. awn length, panicle length, leaf blade colour and leaf sheath colour, node base colour, awning, distribution of awns, stigma colour, anthocyanin colouration of stem nodes and internodes, hence, these characters can be used for identification of rice cultivars. Nethra *et al* (2005) observed polymorphism for traits of panicle awns, apiculus and node anthocyanin pigmentation, and stigma colour. Yan *et al.,* (2007) also observed polymorphism for the traits days to 50% flowering, plant height, awn type, plant type, colour of lemma and palea, pubescence of lemma based on 1,790 entries sampled from 114 countries.Thimmanna *et al.,* (2000) observed the characters such as leaf length and width, pubescence of leaf, colour, leaf angle, ligule shape and colour, auricle colour, internode colour, panicle type, secondary branching, exertion, awning, seed length and width, 1000 grain weight and suggested the usefulness in differentiating the parental lines of rice hybrids.

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ORIGINAL RESEARCH ARTICLE OPEN ACCESS

Allelic Variation of Sheath Blight QTLs among Genotypes Promising for Sheath Blight Tolerance

Jyothi Badri*, Susmita Dey, Prakasam V, Sneha Nymagoud, Priyanka C, Hajira Shaik, Sundaram RM, Sheshu Madhav M, Eswari KB, Bhadana VP, Ram T and Subba Rao LV

ICAR-Indian Institute of Rice Research, Rajendrangar, Hyderabad 500030, India
*Corresponding author: jyothirishik@gmail.com

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Abstract

The fungus, *Rhizoctonia solani* causing sheath blight disease in rice is omnipresent and no durable resistance source is available in the rice germplasm for this pathogen. However, moderate resistance has been reported in some of the rice genotypes and more than fifty QTLs for sheath blight tolerance have been identified in the past. The present investigation validates seven QTLs initially from two moderately resistant genotypes 'Tetep' and 'Teqing' in a set of rice lines, *viz*., Gumdhan, Ngonolasha, Wazuhophek, Phougak, RP 2068-18-3-5 and 10-3, which have been recently reported to be novel sources of moderate resistance to sheath blight. Allelic variation for a QTL marker was not observed between the source genotype and the selected susceptible genotypes and both the source genotype and susceptible genotypes showed similar allelic position at the QTL loci.

Keywords: Rice, Sheath blight, QTLs, Allelic variation

Introduction

Rice sheath blight (ShB), caused by the soil-borne fungal pathogen *Rhizoctonia solani* Ku¨hn, is one of the three major diseases of rice that greatly reduces yield and grain quality worldwide (Savary *et al* 2006). The pathogen *R. solani* is a semi-saprophytic fungus with wide host range. Even though research has been focused on identification of sources of resistance, till date, no major source of resistance has been identified (Susmita Dey *et al* 2016). Thus the major problem in the development of ShB-resistant rice varieties is the lack of donors having high degree of resistance to the pathogen.

A few rice varieties, *viz*., Teqing, Tetep, Tadukan, Jasmine 85 and WSS5 were frequently used in the genetic analysis of ShB resistance (Pan *et al* 1999a, 1999b; Zuo *et al* 2000; Pinson *et al* 2005; Liu *et al* 2006; Channamallikarjuna *et al* 2010; Shiobara *et al* 2013, Zeng *et al* 2014; Yadav *et al* 2015). In these studies, over 50 QTLs associated with resistance have been report and also these studies have concluded that resistance to ShB is a complex, quantitative trait, governed by polygenes and in some rice varieties it is controlled by few major genes and several minor genes. However, neither the identified QTLs have been utilized in development of sheath blight resistant cultivars nor their breeding value has been assessed so far. Moreover, Jasmine 85 which was earlier reported as tolerant and even though QTLs have been dentified from the variety, showed high level of susceptibility in one of our recent studies (Susmita Dey *et al* 2016). QTL analysis can provide genetic information about individual components of a complex trait. As earlier reports indicate that sheath blight resistance in rice is governed by several minor genes or QTLs each with small effect, pyramiding of such QTLs is expected to result in considerably increased resistance to ShB in the pyramided cultivars. In our earlier work, we have identified four land races (Phougak, Gumdhan, Wazuhophek, Ngonolasha) and two elite breeding lines (RP 2068-18-3-5 and 10-3) with moderate resistance to sheath blight. These results were based on four years (2012-2015) of stringent screening both under field and glasshouse conditions coupled with characterization of agro-morphological traits (Dey *et al* 2016). The present investigation is undertaken to assess the allelic variation of reported ShB QTLs in these moderately resistant genotypes.

Material and Methods

A total of 11 genotypes including two moderately resistant checks (Tetep and Teqing), six tolerant to ShB as identified by Dey *et al.*, 2016 (RP-2068-18-3-5, 10-3, Wazuhophek, Ngonolasha, Gumdhan and Phougak) and three susceptible checks (IR 50, Swarna and BPT 5204) were screened for the eight reported QTLs of which six were from Tetep and two from Teqing (Table 1).

Table 1. Details about QTL used in the present investigation

Sl. No.	QTL	Chr	Marker interval	PV (%)	Reference
1	*qSBR 1-1*	1	RM1232 - RM 306	15.01	Channamallikarjuna *et al.*, 2010
2	*qSBR 3-1*	3	RM 251- RM 338	9.96	
3	*qSBR 7-1*	7	RM 3691-RM 336	10.02	
4	*qSBR 7-1*	7	RM 5481- RM 3691	26.05	
5	*qSBR 11-2*	11	RM 3428 – RM 209	7.81	
6	*qSBR 11-3*	11	RM 536 - RM 202	21.59	
7	*Qsbr 2a*	2	RM 29-RM 341	7.81	Loan *et al.*, 2004
8	*Qsbr3*	3	RM 156-RM16	9.30	

Results

Out of 15 SSRs reported to be linked to the eight QTLs analyzed in this study, six were monomorphic, while nine were polymorphic with PIC values ranging from 0.3696 to 0.6044 (Table 2).

Table 2. Allelic variation and PIC Values for 15 SSR loci identified among 15 genotypes

Sl. No.	Chr	SSR	No. of alleles	PIC
1	1	RM 1232	3	0.3696
2	1	RM 306	3	0.5644
3	2	RM 29	1	-
4	2	RM 341	3	0.5333
5	3	RM 338	1	-
6	3	RM 156	1	-
7	3	RM 251	3	0.4756
8	3	RM16	3	0.4178
9	7	RM 5481	1	-
10	7	RM 336	3	0.44
11	7	RM 3691	3	0.5244
12	11	RM 209	1	-
13	11	RM 536	1	-
14	11	RM 3428	3	0.6
15	11	RM 202	3	0.6044

qSBR1-1

The left flanking marker RM 1232 was polymorphic with three alleles. Tetep type allele was shown by all the tolerant genotypes except RP 2068-18-3-5. The right flanking marker RM 306 had shown polymorphism with three alleles ranging from147-182 bp, while the Tetep specific type allele was a 175 bp allele. The allele similar to that of Tetep was shown by another moderately resistance check- Teqing and five genotypes *viz*., 10-3, Ngonolasha, Gumdhan, RP-2068-18-3-5 and Phougak. One genotype, Wazuhophek had allele size of 182 bp similar to that of susceptible check IR50 and BPT 5204. There was no amplification for this marker in one susceptible check Swarna. Both the flanking markers showed amplification of the Tetep specific allele among one or two susceptible checks.

qSBR3-1

The left flanking marker RM 251 was polymorphic, amplifying three alleles ranging from 127-179 bp with PIC value of 0.4756. Tetep type type allele was 165 bp and it was present in four genotypes *viz*., 10-3, Ngonolasha, Gumdhan, RP-2068-18-3-5, and Phougak. However, the same type of allele was also present in the susceptible check Swarna. The other moderately resistance check Teqing and one susceptible check BPT 5204 had second type of allele at 179 bp. Third type allele (127 bp) was shown by one susceptible check, IR 50. Tolerant genotype Wazuho phek was found to have heterozygous alleles of which one was similar to Teqing type and other similar to IR 50 type. Though RM 251 was polymorphic with three alleles, the alleles could not be differentiated in terms of resistance and susceptibility as the same type of allele was present in both moderately resistant genotypes and susceptible genotypes. On the other hand, the right flanking marker RM 338 was found to be monomorphic in all the genotypes.

qSBR7-1

The left flanking marker RM 3691 displayed polymorphism, amplifying three alleles ranging from 135-180 bp, of which, the 165 bp is the Tetep specific allele. A similar allele was also amplified by the tolerance genotyped RP-2068-18-3-5 and the susceptible check BPT. The other moderately resistant check Teqing, two susceptible checks (IR50 and Swarna) and four moderately resistant genotypes *viz.*, 10-3, Wazuho phek, Gumdhan and Phougak amplified an allele of size 180 bp. Only, Ngonolasha, another moderately suscceptible variety, amplified a different allele (135 bp) as compared to genotypes. The right flanking marker RM 336 was also found to be polymorphic, amplifying three alleles ranging from173-225 bp, of which 218 bp was

amplified in Tetep. Similar allele was amplified by the susceptible check BPT 5204 and the moderately resistant genotype, Ngonolasha. The other moderately resistance check Teqing, two susceptible checks (IR50 and Swarna) and four genotypes *viz.*, 10-3, Gumdhan, RP-2068-18-3-5 and Phougak amplified an alleles of size 173 bp. Wazuho phek amplified an allele of size 225 bp with repect to RM 336. Though the flanking markers of the QTL *qSBR7-1* showed polymorphism with three alleles, the alleles cannot be differentiated in terms of resistance and susceptibility as the same type of allele was observed present in both moderately resistant genotypes and susceptible genotypes.

SBR7-1

The left flanking marker for the QTL was monomorphic among the rice lines analyzed amplifying a 166 bp fragment. The right flanking marker RM 3691 displayed polymorphism with three alleles ranging from135-180 bp. Among them, the 165 bp is Tetep specific. The same allele was also present in the moderate resistant genotype RP-2068-18-3-5 and also in the susceptible check BPT 5204. The other moderately resistance check Teqing, two susceptible checks (IR50 and Swarna) and four moderately resistant genotypes *viz.*, 10-3, Wazuhophek, Gumdhan and Phougak amplified an allele if size 180 bp. Ngonolasha, another moderately resistant genotype was found to amplify a different allele (135 bp.

qSBR11-2

The left flanking marker RM 3428 showed polymorphism, amplifying three alleles ranging from 230-305 bp, of which 255 bp is specific for Tetep. A similar allele was amplified by two susceptible checks (IR 50 and BPT 5204) and two moderately tolerant rice lines, *viz.*, 10-3 and RP-2068-18-3-5. The other moderately resistance checks- Jasmine 85 amplified an alleles of size 230 bp. The susceptible check Swarna and seven promising moderately tolerant genotypes *viz.*, SM-801, Ngonolasha, Wazuho phek, Gumdhan, BG-380-2, Phougak and Thangmoi amplified an allele of size 305 bp. Though the left flanking marker, RM 3428 was polymorphic with three alleles, the alleles cannot be differentiated in terms of resistance and susceptibility as the same type of allele was present in both moderately resistant genotypes and susceptible genotypes. On the other hand, the right flanking marker, RM209 was observed to be monomorphic amplifying a 133 bp fragment.

qSBR11-3

The left flanking marker RM536 was observed to be monomorphic amplifying a 110 bp fragment. The right flanking marker RM 202 was polymorphic with three allelic positions ranging from 194-252 bp, of which the 194 bp was Tetep specific allele. Similar allele was amplified by moderately resistance check Teqing and two moderately resistant genotypes viz., Wazuhophek and Phougak. All the three susceptible checks along with 10-3 amplified an allele of size 243bp. Only one land race Ngonolasha displayed allelic variation at this locus amplifying a 252 bp fragment, while Gumdhan was found to have heterozygous alleles of which one was similar to the Tetep type and other similar to Ngonolasha type allele.

QSbr2a

The left flanking marker RM 29 was monomorphic amplifying a fragement of size 196 bp. The right flanking marker RM 341 displayed polymorphism, amplifying three alleles ranging from 139-212 bp. Among them, a 187 bp was specific for Teqing. A similar allele was amplified by the two suseptible checks (Swarna and BPT 5204), the moderately resistant genotype RP-2068-18-3-5 and Tetep. Two promosing genotypes *viz*., 10-3 and Wazuhophek amplified the second type allele at 139 bp. Susceptible check IR50 and two genotypes *viz.*, Ngonolasha and Phougak amplified the third type of allele of size 212 bp. Only Gumdhan was found to be heterozygous with three alleles at139 bp, 187 bp and 212 bp.

QSbr3

The left flanking marker for the QTL, RM156, displayed monomorphism. The right flanking RM16 was polymorphic with three alleles ranging 181-266 bp, of which 187 bp is of Teqing type. A similar allele was amplified in the moderately resistance check Tetep and six promising genotypes *viz*., 10-3, Ngonolasha, Wazuho phek, Gumdhan, RP-2068-18-3-5 and Phougak. Three susceptible checks (IR50, Swarna and BPT5204) amplified the third type allele of 266 bp. Allelic variation with respect to the marker, RM16 was observed to clearly distinguish moderately resistant genotypes and susceptible genotypes.

Discussion

The present investigation validated few of the reported QTLs from Tetep and Teqing for their association with tolerance to sheath blight. None of the QTLs except *QSbr 3* from Teqing showed allelic difference among tolerant genotype (from which it was reported) and susceptible genotype. For all the QTLs except *QSbr 3* (QTL from Teqing), either or both the flanking markers were amplified similar type of alleles both in Tetep/Teqing and one or two susceptible checks. Thus, the allele responsible for tolerance to sheath blight in novel sources *viz*., Gumdhan, Wazuhophek, Ngonolasha, Phougak, RP 2068-18-3-5 and 10-3 may or may not be a different one from that of the Tetep or Teqing.

Mostly, the ShB resistance phenotyping methods are based only on relative lesion height (SES scale 2002) that do not take into account a comprehensive phenotyping of the component traits based on agro-morphological traits (Susmita Dey *et al* 2016). Hence, it is often reported

that there is no consistency in disease reaction among genotypes and genotype reported as resistant in one season shows susceptible reaction in the next season. Furthermore, Zheng *et al* (2015) after surveying the phenotypes of different lines/individuals in mapping populations stated that majority of the reported QTLs are co-localized with plant height associated QTLs and are irrelevant for physiological/genetic ShB resistance. As there is no consistency in disease reaction and no evidence on practical utility of reported Shb-QTLs, it can be inferred that traits used so far to evaluate ShB resistance are quite inadequate. To gain deeper insights and to come out with substantial knowledge on ShB resistance/tolerance, comprehensive phenotyping for several associated traits can be considered imperative.

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ORIGINAL RESEARCH ARTICLE OPEN ACCESS

Genetic Diversity Analysis for Yield Traits in Upland Rice (*Oryza sativa* L.)

S. Muthuramu* and S. Sakthivel

Agricultural Research Station, Tamil Nadu Agricultural University, Paramakudi - 623 707.
*Corresponding author:smuthuramu@gmail.com

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Abstract

The present experiment comprised with thirty seven advanced rice cultures and conducted during *Rabi* 2016-17 under upland rice ecosystem. They were evaluated for nine yield and yield related traits *viz.*, days to 50% flowering, plant height, number of productive tillers per plant, number of panicles per square metre plot area, panicle length, number of filled grains per panicle, grain yield, straw yield and harvest index using D^2 analysis. Based on the analysis, the genotypes were grouped into eight clusters. Maximum number of genotypes (21 genotypes) was grouped in cluster I. Cluster II consists of ten genotypes and others were represented by a single genotype each. Maximum inter cluster distance was observed between cluster III and VIII (7.75) followed by between cluster III and VI (7.11) indicating wider genetic diversity between genotypes. Hence the genotype PM 16003 had wider diversity with IET 25134 and PM 14041 and these lines may be utilized in further breeding programme for the exploitation of hybrid vigour. The intra cluster distance was maximum in cluster I (4.07) followed by cluster II (3.88) indicates hybridization involving genotypes within the same clusters may result in good cross combinations. Among the nine traits studied, number of panicles per square metre area contributed maximum divergence (22.22%) followed by panicle length (17.12%), plant height (14.41), filled grains per panicle (11.26) and days to fifty per cent flowering (10.96%). Hence these altogether contribute more than seventy five per cent towards total divergence. Therefore these characters may be given importance during hybridization programme in upland rice ecosystem.

Keywords: Genetic diversity, yield traits, upland rice.

Introduction

Rice is one of the principle food crops and one third of the world population and two thirds of the Indian population is utilizing rice as staple food. It contributes 43 per cent of caloric requirement and 20-25% of agricultural income. In India, rice is grown in an area of 43.5 million ha (23% of gross cropped area) with an annual production of 90 million tons. Most of the Asian countries have been able to keep pace between rice production growth rate and that of population during the last four decades. This has been mainly possible due to the contributions made by the green revolution technologies. However, it is of great concern to note that the rate of growth in rice production has started declining during 90's and there has been a plateauing effect. The population growth in most of the Asian countries, except China, continues to be around 2% per year. Hence it is very pertinent to critically consider whether the rice production can be further increased to keep pace with population growth. With the current green revolution technologies it is estimated that by 2020 at least 115-120 million tons of milled rice is to be produced in India to maintain the present level of self-sufficiency. In order to meet the food requirement of growing population, development of high yielding varieties is essential.

The success of any breeding programme depends on the selection of parents for hybridization. The parents involved in the development of varieties should be divergent. The germplasm provides immense scope for wide variability. Genetic divergence is an efficient tool for an effective choice of parents for hybridization programme. Such study also selects the genetically divergent parents to obtain desirable combinations in the segregating generations. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme (Vivekanandan and Subramanian, 1993). An attempt was made in the present investigation to assess the genetic diversity of thirty seven advanced rice cultures for yield traits in upland rice ecosystem.

Materials and methods

The experimental material comprised with thirty seven advanced rice cultures collected from various research institutes which were evaluated in a randomized block design with three replications at Agricultural Research Station, Tamil Nadu Agricultural University, Paramakudi during *Rabi* 2016-17. The experimental site is located at 9" 21' N latitude, 78" 22' E longitudes and an altitude of 242 m above mean sea level with average annual rainfall of 840 mm. This site has clay loam soil texture with pH of 8.0. Each genotype was raised in 5x2 m plot keeping

15 x 10 cm spacing. The recommended agronomic practices followed to raise good crop stand. The data were recorded on ten randomly selected plants from each replication for various quantitative traits studied were *viz,* days to 50% flowering, plant height (cm), number of productive tillers per plant, number of panicles per square metre plot area, panicle length, number of filled grains per panicle and grain yield (kg), straw yield (kg) and harvest index. The genetic distance between the genotypes was worked out using Mahalanobis D^2 analysis (1936) and grouping of varieties into clusters was done following the Tochers method as detailed by Rao, 1952.

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating existence of variability among the genotypes. Based on the relative magnitude of D^2 values, thirty seven genotypes were grouped into eight clusters (Table 1). Maximum number of genotypes (21 genotypes) was grouped in cluster I. Cluster II consists of ten genotypes and others were represented by a single genotype each. The overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were distributed in different clusters. Similar findings of non- correspondence of geographic origin with genetic diversity were also reported by Shanmugasundaram *et al.,* (2000) and Nayak *et al.,* (2004). The intra and inter cluster distance are presented in Table 2. Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes. The maximum inter cluster distance was observed between cluster III and VIII (7.75) followed by between cluster III and VI (7.11) indicating wider genetic diversity among the genotypes between these groups. The hybrids developed from the selected members of these clusters would produce highly variable population in the segregating generations. Surprisingly the clusters identified with maximum inter cluster distance were possessed a single genotype in each cluster. Hence selection of parents for hybridization is already over. The minimum inter cluster distance was found between cluster III and V (3.44) followed by between cluster II and VI (4.55). These genotypes in these clusters are genetically very close and hence, hybridization among the varieties will not give fruitful result.

Table 2. Intra (diagonal) and inter cluster average distance of yield traits in 37 genotypes

	I	II	III	IV	V	VI	VII	VIII
I	4.07	5.85	6.31	5.05	5.81	5.78	6.61	6.65
II		3.88	5.75	5.75	6.05	6.65	5.80	6.54
III			0.00	6.83	3.44	7.11	4.55	7.75
IV				0.00	6.64	4.65	6.42	6.46
V					0.00	6.96	5.97	6.55
VI						0.00	5.17	6.28
VII							0.00	6.09
VIII								0.00

The maximum intra cluster distance was observed in cluster I (4.07) followed by cluster II (3.88). Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would

Table 1. Clustering pattern of 37 genotypes

Cluster	No. of genotypes	Name of genotypes
I	21	IR12-L369 (G3), IR13-L382 (G6), IR13-L391 (G7), IR12-L356 (G2), IR13-L114 (G4), IR13-L137 (G5), IR12-L353 (G1), IR14-L235 (G12), IR13-L406 (G9), IR13-L400 (G8), IR13-L413 (G10), IET 25106 (G18), PM 14048 (G34), IET 25114 (G21), IET 24690 (G16), PM 14032 (G27), PM 14046 (G33), IR14-L177 (G11), PM 14049 (G35), PM 16002 (G14) and PM 16001 (G13).
II	10	PM 14030 (G26), PM 14044 (G32), PM 14018 (G25), PM 14038 (G28), Anna(R)4 (G37), PM 14050 (G36), IET 25107 (G19), PM 13017 (G24), PM 14042 (G30) and PM 14043 (G31).
III	1	PM 16003 (G15)
IV	1	IET 25118 (G22)
V	1	IET 25105 (G17)
VI	1	PM 14041 (G29)
VII	1	IET 25111 (G20)
VIII	1	IET 25134 (G23)

Table 3. Cluster mean of different yield characters in 37 rice genotypes

Cluster	Days to 50% flowering	Plant Height (cm)	Productive tillers per plant	No. of panicles per sq. metre	Panicle length (cm)	Filled grains / panicle	Grain yield (kg/ha)	Straw yield (kg/ha)	Harvest Index
I	53.92	78.32	6.84	121.71	21.41	84.49	1420.32	4247.62	0.27
II	58.20	67.80	6.27	185.87	19.58	77.53	1931.33	4966.67	0.28
III	63.67	71.73	7.00	137.33	20.63	130.33	1533.33	3933.33	0.30
IV	52.00	77.27	7.67	104.33	17.17	57.67	666.67	2333.33	0.22
V	58.00	72.47	6.67	102.33	21.27	142.33	1943.33	3600.00	0.41
VI	46.67	73.87	8.33	118.67	16.83	64.00	1233.33	6800.00	0.15
VII	59.67	59.60	8.00	125.33	18.33	71.00	983.33	4733.33	0.24
VIII	57.00	60.47	4.33	77.33	18.90	57.67	733.33	700.00	0.54

be made use of in improvement through inter-varietal hybridization (Joshi *et al.,* 2008). A perusal of results of cluster means (Table 3) revealed that cluster I with twenty one genotypes exhibited highest mean value for panicle length (21.41) and plant height (78.32). Cluster II had genotypes with maximum number of panicles per square metre area (185.87) and the genotype in Cluster III (PM 16003) had taken more days for fifty per cent flowering (63.67). Cluster IV was characterized by lowest grain yield (666.67), while the cluster V had maximum number of filled grains per panicle (142.33) and grain yield (1943.33). The genotype PM 14041 with more straw yield (6800.00) and highest productive tillers per plant (8.33) was grouped in cluster VI. The Genotype IET 25111 (Cluster VII) had shown short stature (59.60). The genotype IET 25134 possessing lowest mean values for productive tillers per plant (4.33), number of panicles per square metre area (77.33), filled grains per panicle (57.67) and straw yield (700.00) but highest harvest index (0.54) was grouped in cluster VIII. None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. However the cluster II recorded desirable mean value for maximum number of productive traits *viz.*, productive tillers per plant, number of panicles per square metre area, panicle length, filled grains per panicle and grain yield. Similar results were also reported by Banumathy *et al.,* (2010) and *Rai et al.,* (2014), thereby underlining the fact that the hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. Based on the *per se* performance of the best genotypes within the clusters, they may be directly selected or may be used as potential parents in hybridization programme.

The contribution of each trait to total divergence is presented in table 4. Among the traits studied, number of panicles per square metre area contributed maximum divergence (22.22%) followed by panicle length (17.12%), plant height (14.41), filled grains per panicle (11.26) and days to fifty per cent flowering (10.96%). The minimum percentage of contribution was observed in harvest index (3.75%) followed by productive tillers (5.41%), grain yield (6.76%) and straw yield (8.11%). The traits *viz.*, number of panicles per square metre area, panicle length, plant height, filled grains per panicle and days to fifty per cent flowering contributed more than seventy five per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population.

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

Character	No. of Times Ranked First	Contribution (%)
Plant Height (cm)	73	10.96
Days to 50% flowering	96	14.41
Productive tillers per plant	36	5.41
No. of panicles per sq. metre	148	22.22
Panicle length (cm)	114	17.12
Filled grains / panicle	75	11.26
Grain yield (kg/ha)	45	6.76
Straw yield (kg/ha)	54	8.11
Harvest Index	25	3.75
Total	**666**	**100**

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ORIGINAL RESEARCH ARTICLE OPEN ACCESS

Genetic Diversity Studies using SSR and EST-SSR Markers in Maintainer Lines of Rice Hybrids

Nihar S, Ramesha MS, Sundaram RM, Neeraja CN and Kemparaju KB*

ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad 500030, India
* Author for correspondence:kbkemparaju@gmail.com

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Abstract

The performance and heterosis of hybrids are associated with genetic divergence between their parental lines. The present study has been conducted at ICAR-Indian Institute of Rice Research to assess the genetic diversity of 29 rice genotypes including rice hybrid maintainer lines using selected nine EST (Expressed Sequence Tag) based and thirteen reported SSR (Simple Sequence Repeats) markers to identify distinguishable alleles. All nine EST derived microsatellite markers were found to be polymorphic and generated total of 29 alleles in the 29 genotypes. The number of alleles per SSR marker ranged from 2-4 with an average value of 3.2. The polymorphic information content (PIC) for these SSR markers ranged from 0.68 (RMES 9-2) to 0.89 (RMES 5-2) and marker RMES 3-2, RMES 5-2, RMES 6-1, RMES 9-2 generated maximum four alleles. For reported SSR markers, the number of alleles per marker ranged from 1-3 with an average value of 1.9. The PIC value ranged from 0.59 (RM25645) to 0.89 (RM10290) and markers RM25640, RM25645, RM25672, RM10300, RM25641 generated maximum three alleles. This study highlights that EST derived SSR markers are efficient and suitable for assessing the genetic relatedness of the genotypes and studied maintainer lines exhibited high level of genetic diversity.

Keywords: Diversity, Simple sequence repeats (SSR), Expressed Sequence Tag (EST), Hybrid rice, Maintainer lines

Introduction

Rice is the staple food for most of the South Asian countries and it feeds two-third of the world's population. To meet the needs of the growing population of our country, the forecast demand of rice production for the year 2025 is 140 million tonnes. Due to ever increasing limitations in resources, the enhancement of rice production must come from higher absolute yields, which can be met by the hybrid rice technology. Quantitative genetic theory suggests that high heterosis can be expected in a hybrid if the source populations have (i) a high frequency of genes with partial or complete dominance and/or (ii) maximum differences in gene frequencies of over-dominant loci (Hallauer *et al.,* 1988). Consequently, for an optimum exploitation of heterosis, parents should be derived from genetically divergent germplasm pools, commonly referred to as heterotic groups (Melchinger and Gumber, 1998).

Genetic diversity can be measured by different methods such as pedigree analysis, morphological data and molecular markers. Molecular markers have proven useful for assessment of genetic variation in germplasm collections (Mohammadi and Prasanna, 2003) in order to identify the most diverse ones for the development of hybrids.

At present, genomic SSRs are popularly used in rice due to the availability of more than 20,000 markers. But with the current trend towards the use of functional markers, there is enormous scope for the utilization of EST-SSR markers, these are mined from simple sequence repeats (SSRs). Characterization of tall landraces of rice (*Oryza sativa* L.) using gene-derived simple sequence repeats was reported by Neeraja *et al.,* (2005). Analysis of genetic variability based on these functional targets, provides opportunities to study functional diversity and to identify corresponding genes controlling traits of complex inheritance.

The objective of present study is to assess the genetic diversity of maintainer lines with EST derived SSRs and reported SSR markers.

Materials and Methods

Twenty nine genotypes *viz.*, 26 Back Cross Progeny (BCP) lines and three known maintainer lines (Table 1) were used in this study.

Table 1. Rice genotypes selected for the study

Sl. No.	Genotype	Sl. No.	Genotype
1	BCP 48.2	16	BPC 148
2	BCP 85	17	BPC 23
3	BCP 30.2	18	BCP 12.1
4	BCP 35	19	BCP 64
5	BCP 136	20	BCP 139.1
6	BCP 53	21	BCP 154
7	BCP 36.1	22	BCP 3.1
8	BCP 4	23	BCP 138

9	BCP 58	24	1BCP 150
10	BCP 105	25	BCP 14.2
11	BCP 107	26	BCP 5.1
12	BCP 13.2	27	97B
13	BPC 132.2	28	25B
14	BCP 87.1	29	APMS 6B
15	BCP 147		

Molecular analysis

The leaf samples from selected plant material were collected in to labeled 1.5 ml eppendorf tubes in morning hours from field and stored in -20C refrigerator. DNA Isolation was done according to the Zhang *et al.,* (1995) method. The isolated genomic DNA was quantified at 280nm using Nano drop UV Spectrophotometer. The cereal EST-SSR database at http://www.graingenes.org/cgi-bin/ace/query/graingenes was used to select rice EST-SSRs that are hyper polymorphic (with repeat length of 60 bp or more) which are uniformly distributed across the rice genome. Total of nine EST-SSRs (from seven chromosomes) and 13 SSR markers were selected and list given in Table 2 & 3. PCR primer pairs for the selected EST-SSR markers were synthesized by M/s Integrated DNA technologies, USA. The genomic DNA of 29 rice genotypes isolated as described earlier were subjected to PCR amplification as per the procedure described by Panaud *et al.,* (1996). PCR amplified products were resolved in 4% super fine resolution (SFR) agarose gels for EST primers and 3% gels for SSR markers in 0.5X TBE buffer at 200V for 3.5 hrs using Submarine Horizontal Electrophoresis Unit (CBS Scientific, USA). Before loading, PCR amplified products

Table 2. EST-SSR markers selected for the study

Marker Name	Repeat Motif	Forward Primer (5' TO 3')	Reverse Primer (5' TO 3')
Chromosome 2			
RMES 2-1	AG	ACCAAGGCAACCCATGAAT	ACCTGCGGCTTCTTCTTCTT
RMES 2-2	AG	CACCTCCCAATCTTAACCCA	GGGAAGGTGTTGGAGGTGTA
Chromosome 3			
RMES 3-2	AT	ACGGATTCACTGGGTTCTGT	CACCAGAAAGCATCACCTCA
Chromosome 5			
RMES 5-1	AG	TATGATAGCGCCTTCGGAGT	GAGATTAACGTGCGCTCCTC
RMES 5-2	AG	CTCTTACCCCACCAAGGACA	AAAGCGCGCAAAAGAAAAT
Chromosome 6			
RMES 6-1	AT	CTGCCACCGGTGTAGCTAGT	TGGCCCCATCGTATATGAAC
Chromosome 7			
RMES 7-2	AG	TGGCCCTCATGAGACATACA	TTAAGCAATCAAAGGGGGTG
Chromosome 8			
RMES 8-1	AAG	GGAGGAGGAGGAGGATCTTG	CTTCTCCGACGACGAGTTCT
Chromosome 9			
RMES 9-2	AG	CCACGTTGATAAGCTCATTGC	TGGGCACCGAAAATAAAATC

Table 3. SSR markers selected for the study

Marker Name	Chromosome #	Repeat Motif	Forward Primer (5' to 3')	Reverse Primer (5'to 3')
RM 25626	10	GAA	ATGCTCTCAAGTGTGTCAAGG	AACCTCTGGAGTATGTGTAGTGC
RM 25640	10	-	-	-
RM 25645	10	-	-	-
RM 25636	10	AGA	AGCAACACGGGATGGCTAAATCC	AGGTATCGTCTCGGCGTCTCTCC
RM 25669	10	CA	GCAAGGATCACAAACAAAGAGTGC	GGCACCAATTCTAGGAAGGTATGC
RM 25672	10	-	-	-
RM 10290	1	CT	CATCTCGATCAGTCCACCATGC	AGGATTACCATGGCCTCAAGAGC
RM 10296	1	CGC	AAGAGGACCTGCGCCATGAACG	CATCCCTTTCGCCTTCGACTTCC
RM 10303	1	TGGA	TCACTACTACACCCAGCTCGTTCC	TCTCCCTCCTTCACCTGTCTCC
RM 10287	1	-	-	-
RM 10300	1	AGCT	AAAGACAGAATGCCCAGCGATCC	CCTCCACCCATTGGATGACACC
RM 25641	10	-	-	-
RM 25654	10	CGA	TCCTCTACCAGTACCGCACC	GCTGGATCACAGATCATTGC

Plate legends:

1	BCP 48.2	7	BCP 36.1	13	BPC 132.2	19	BCP 64	25	BCP 14.2
2	BCP 85	8	BCP 4	14	BCP 87.1	20	BCP 139.1	26	BCP 5.1
3	BCP 30.2	9	BCP 58	15	BCP 147	21	BCP 154	27	97B
4	BCP 35	10	BCP 105	16	BPC 148	22	BCP 3.1	28	25B
5	BCP 136	11	BCP 107	17	BPC 23	23	BCP 138	29	APMS 6B
6	BCP 53	12	BCP 13.2	18	BCP 12.1	24	1BCP 150	30	100 bp ladder

were mixed with 1/6th volume of gel loading dye (40% sucrose; 0.25% bromophenol blue). The sizes of amplified fragments were determined by comparing with 100 bp ladder (MBI Fermentas, Lithuania). The gels were stained in Ethidium Bromide (10mg/ml) for 3 min, destained in distilled water for another 2 min, placed over the UV-transilluminator and documented at 300 nm using ALPHA IMAGER gel documentation system (M/s Alpha innotech, USA).

Markers were scored for the presence '1' and absence '0' of the corresponding band among the genotypes. A data matrix comprising of '1' and '0' were subjected to cluster analysis. Dendrogram was constructed based on Squared euclidean distance similarity matrix using Jaccard's coefficient. Data analysis was done using the software NTSYSpc version 2.02 (Rohlf, 1994).

The polymorphism information content (PIC) for each SSR marker was calculated according to the formula:

$$PIC=1-\Sigma Pi^2- \Sigma\Sigma Pi^2Pj^2$$

where 'i' is the total number of alleles detected for SSR marker and 'Pi' is the frequency of the allele and j=i+1. The PIC value was calculated using the online software- 'Polymorphism Information Content Calculator' available at *www.agri.huji.ac.*

Result and Discussion

This study was carried out to find genetic diversity of maintainer lines using selected EST derived SSR and reported SSR markers. The extent of genetic diversity in the germplasm can be estimated by adopting various methods like morphological, biochemical and/or molecular analyses. Though number of methods is employed in assessing the genetic diversity of a species, but accuracy of assessment is questionable. The recent developments in molecular biology has resulted in development of simple, easily assayable PCR based DNA markers. Multilocus markers like RAPD, ISSR, AFLP *etc.*, are the most popularly used markers for genetic diversity analysis (Phillips and Vasil, 2001). Among them, SSR markers are useful for a variety of applications in genetics and plant breeding because of their reproducibility, multiallelic nature, co dominant inheritance, relative abundance and good genome coverage.

With the establishment of expressed sequence tag (EST) sequencing projects for gene discovery programs in several plant species, SSR can be identified from these clones and thus generation of EST-SSR markers is relatively easy and inexpensive because they are a byproduct of the sequence data from genes. These are useful as molecular markers because their development is represent transcribed genes, their frequency is abundantly high (Morgante *et al.*, 2002), assumed to reflect more accurately and putative function can often be deduced by a homology search.

In this study, genetic diversity of 29 genotypes was assessed using nine EST-SSR markers and 13 reported SSR markers. EST-SSR markers found polymorphic and generated 29 alleles (Plate 1). The number of alleles per SSR marker ranged from 2-4 with an average value of 3.2. The polymorphic information content (PIC) for these markers ranged from 0.68 (RMES 9-2) to 0.89 (RMES 5-2) and markers RMES 3-2, RMES 5-2, RMES 6-1 and RMES 9-2 generated maximum alleles *i.e.*, four (Table 4). The reported primers were also found polymorphic and generated total of 19 alleles (Plate 2). The number of alleles per SSR marker ranged from 1-3 with an average value of 1.9. The polymorphic information content (PIC) for these 13 SSR markers ranged from 0.59 (RM25645) to 0.89 (RM10290) and markers RM25640, RM25645, RM25672, RM10300 RM25641 generated maximum alleles of three (Table 5). Panaud *et al.*, (1996) and Olufowote *et al.*, (1997) obtained similar number of alleles but higher PIC value (0.89) compared to our study. The PIC values are dependent on the genetic diversity of the accessions chosen. In present investigation, high proportion of closely related cultivars that might be the reason for lower PIC compared to earlier published reports along with EST-SSR primers. It showed less polymorphic compared with genomic SSRs in crop plants because of greater DNA sequence conservation in transcribed regions (Cho *et al.*, 2000).

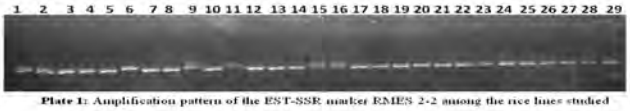

Plate 1: Amplification pattern of the EST-SSR marker RMES 2-2 among the rice lines studied

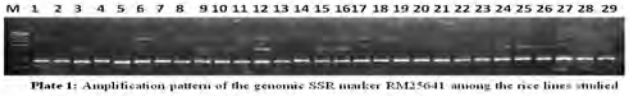

Plate 1: Amplification pattern of the genomic SSR marker RM25641 among the rice lines studied

Plate legends:

1	BCP48.2	7	BCP36.1	13	BPC132.2	19	BCP64	25	BCP14.2
2	BCP 85	8	BCP4	14	BCP87.1	20	BCP139.1	26	BCP5.1
3	BCP30.2	9	BCP58	15	BCP147	21	BCP154	27	97B
4	BCP35	10	BCP105	16	BPC148	22	BCP3.1	28	25B
5	BCP136	11	BCP107	17	BPC23	23	BCP139	29	APMS 6B
6	BCP53	12	BCP13.2	18	BCP12.1	24	1BCP150	M	100 bp ladder

Figures:

Table 4. Polymorphism Information of EST-SSR markers

EST marker	Total alleles	Polymorphic Information content (PIC)
RMES 2-1	3	0.876
RMES 2-2	2	0.747
RMES 3-2	4	0.708
RMES 5-1	3	0.817
RMES 5-2	4	0.889
RMES 6-1	4	0.700
RMES 8-1	2	0.840
RMES 7-2	3	0.801
RMES 9-2	4	0.679

Table 5. Polymorphism Information of SSR markers

SSR markers	Total alleles	Polymorphic Information content (PIC)
RM25626	1	0
RM25640	2	0.845422
RM25645	2	0.592747
RM25672	2	0.618906
RM10290	3	0.899326
RM10296	1	0
RM10303	1	0
RM10287	3	0.876338
RM10300	2	0.642687
RM25641	2	0.737218

Cluster analysis was performed using Jaccard's similarity coefficient of 48 alleles and generated dendrogram (Figure 1) with mean genetic similarity of 0.56 (range 0.20 to 1.0) indicating a high diversity. These observations are similar to studies of Garland *et al.*, (1999) who obtained mean genetic similarity of 0.5 (range 0.0 to 1.0) in analysis of genetic diversity of 43 rice cultivars with 10 SSR primer pairs. The dendrogram generated using SSR marker data grouped all the 29 genotypes into two major clusters with 28 percent similarity among them.

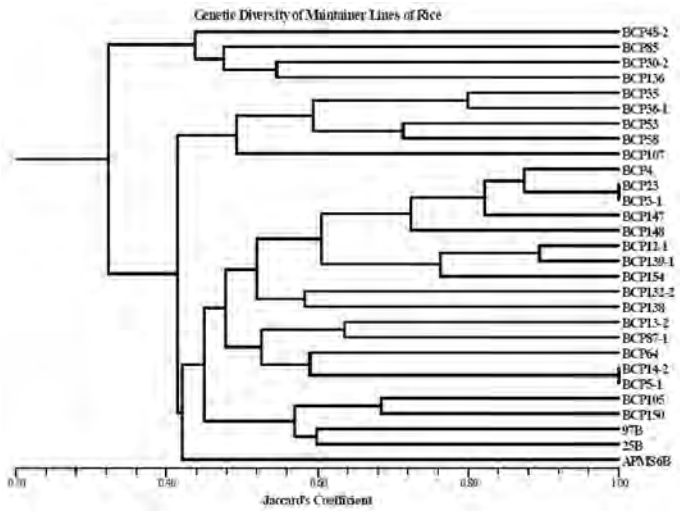

Figure 1. Cluster analysis based on Jacord similarity co-efficient

The use of EST-SSR markers in genetic diversity studies helped in grouping the genotypes according to their genetic relatedness. When more clusters are obtained with few genotypes in each cluster, the significance in clustering is high because of the presence of higher genetic differences between the genotypes in a cluster. Hence, augmented use of EST-SSRs from genes with known functions should be very powerful in unraveling the functional diversity of the genotypes under study.

The present study highlights two important issues *i.e.*, EST-SSR markers are efficient and suitable for assessing the genetic relatedness of the genotypes. Secondly, maintainer lines under study exhibited high level of genetic diversity.

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ORIGINAL RESEARCH ARTICLE OPEN ACCESS

Qualitative Characteristics of Red Rice and White Rice Procured from Local Market of Uttarakhand: A Comparative Study

Rita singh Raghuvanshi, Anuradha Dutta*, Gunjan Tewari and Shweta Suri

Department of Foods and Nutrition, College of Home Science, G.B. Pant University of Agriculture and Technology, Pantnagar- 263145 (U.S. Nagar), Uttarakhand, India
*Corresponding author - adutta.gbpuat@gmail.com

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Abstract

The present study was undertaken with the objective to evaluate and compare the physical characteristics, nutritional quality, antioxidant properties and glycemic index of indigenously grown raw red rice grown in Udham Singh Nagar district of Uttarakhand and white rice (Sarbati) procured from local market of Uttarakhand, India. Of the thirteen physical quality parameters evaluated, red rice proved to be superior to white rice in all parameters barring seed length. Red rice was found to have a higher iron, magnesium, calcium, and zinc content than white rice. Regarding other nutrients the study revealed that red rice has a higher crude protein (10.49%) and crude fiber (2.71%) content as compared to white rice. The nutritional quality of red rice was found to be comparable to many millets, fruits and vegetables. It showed excellent antioxidant properties too such as total phenolic content (143.38 mg GAE/100g of phenol), total flavonoid content (120.0 mg R.E. /100 gm of flavonoid) and DPPH scavenging activity (25 per cent). Red rice was found to have a lower glycemic index (63.15 ± 2.63mg/dl) than white rice due to which it can be a part of the diets of diabetics as well as persons suffering from other non-communicable diseases. Red rice is a storehouse of nutritional excellence and is a healthier alternative to white or polished rice.

Keywords: Red rice, Antioxidants, Glycemic index, Nutritional composition, Physico-chemical characteristics.

Abbreviations: DPPH:2, 2 Diphenyl 2 picryl hydrazyl hydrate;TFC:Total flavonoid content; TPC:Total phenol content; R.E:Retinol equivalent; GAE:Gallic acid equivalent

Introduction

Rice (*Oryza Sativa L.*) is one of the most popular and important cereal crops. It is the staple food of more than three billion people (Bhattacharjee *et al*.**,** 2002) in 39 countries,that comprises of nearly half of the world's population. Commercially more than two thousand varieties of rice are grown throughout the world. Over 2 billion people in Asia derive 80% of their energy needs from rice, which contains 80% carbohydrates, 7–8% crude protein, 3% crude fat, and 3% crude fiber (Juliano, 1985). Champagne *et al.,* (2006) stated that rice is mainly composed of starch. Vandeputte *et al.,* (2004) mentioned rice starch as the major constituent of rice grain**.** Moldenhauer *et al*.**,** (2006) added that the same level of starch is the base of determining the quality that the cooked rice would depict.

Rice is widely consumed as white rice in milled and parboiled form. There are many special cultivars of rice that contain colour pigments, such as black rice, red rice and brown rice. Their name refer to the kernel colour (black, red or purple) which is formed by deposition of anthocyanin in different layers of the pericarp, seed coat and aleurone (Chaudhary *et al*,. 2001). The origin of coloured rice is as old as rice itself. Rice with a red bran layer is called red rice. Though, the colour is confined to the bran layer, a tinge of red remains even after a high degree of milling. Unmilled rice has a higher nutrient content than milled or polished white rice. Red rice contains 7g/100g protein, 5.5mg/100g iron, 3.3mg/100g zinc, and 2g/100g fibre respectively. Red rice has a nutritional value more than that of milled and or polished rice FAO (2004).

Rice was known to the civilization 5000 BC. However the Chinese, Southern and East Asians are believed to have learnt the practice of growing rice around 2000 BC (Chaudhary *et al*., 2001).

De candolle (1886) and Watt (1892) believed that rice was originally cultivated in South India. India is one of the rice producing country with larger area involved in the cultivation of rice. Historians believe that the well-known variety of rice was first domesticated in the area covering the foothills of the Eastern Himalayas. Rice seems to have appeared around 1400 BC in southern India after its domestication in the northern plains. Some say that the word rice is derived from the Tamil word "*Arisi"* (Hiziroglu *et al.,* 2007). The rice crop forms the basic economic activity directly or indirectly for about 150 million rural households in India (Krishnaiah *et al*., 2000).

Ancient Indian literature Charaka Samhita, authored by great Charaka mentioned rice with red husk and grain as the best which is efficacious and subdues the diseases (Kumar, 1988; Krishnamurthy, 1991). Eaten as a whole grain, Red rice is commonly consumed in Himachal Pradesh, Uttar Pradesh and South India, especially Karnataka and Tamil Nadu and is predominantly known for its aroma and taste. But rice consumers often prefer to have polished white rice despite the valuable food content of coloured rice which is lost when bran is removed while polishing**.**

The choice of carbohydrate-rich foods in the habitual diet should take into account not only their chemical composition but also their ability to influence postprandial glycemia (glycemic index) (Riccardi *et al*., 2008). Polyphenol and flavonoid which have antioxidant capacity present in many foods and vegetables are regarded as the functional materials. Regular intake of these phytochemicals can reduce many chronic diseases such as cardiovascular diseases, heart diseases, diabetes, obesity and certain cancers, and improve endothelial function and reduce blood pressure (Liu, 2007; Yawadio *et al.,* 2007; Jonathan *et al.,* 2006).

Little or no information is available on nutritive value of red rice grown in tarai region of Uttarakhand. Therefore, the study is aimed to estimate and analyse the physical characteristics, nutritional quality, antioxidant properties and glycemic index of white rice and red rice.

Materials and Methods:

Procurement of sample: Samples of two types of rice (*Oryza Sativa L.*) *viz.* indigenously grown raw red rice from Udham Singh Nagar district of Uttarakhand, and white rice (Sarbati) were procured from Uttarakhand Agricultural Production Board and the local market respectively.

Estimation of nutritional quality: Dehusked red rice and milled, polished white rice samples were analysed in triplicate for proximate composition such as percent moisture, crude protein, total ash, crude fat and crude fibre. Proximate composition was determined by the method given by AOAC (2000). The carbohydrate percentage was determined by the difference method as reported by **(**Onyeike *et al.,* 1995). The calorific value (Kcal/100g) of sample was calculated by summing up the product of multiplication of per cent crude protein, crude fat and carbohydrate present in the sample by 4, 9 and 4 respectively.

Minerals: Calcium, iron, zinc, and magnesium in the sample were estimated using atomic absorption spectrophotometer. Ash solutions were prepared using wet-ashing procedure as described by Raghuramulu (2003).

Physical properties: The physical properties of white rice and red rice such as Seed volume, seed weight, seed density, hydration capacity, swelling capacity, length of grains, bulk density, and kernel elongation were estimated by the procedure reported by (Williams *et al.,* 1983). Alkali spread value was calculated by method described by (Little *et al.,* 1958) and the kernel elongation was calculated as described by (Azeez *et al.,* 1966).

The hydration capacity of the grain is an important attribute which affects the cooking quality and in turn organoleptic qualities of product Potty (1996). The author also reported that large sized particles have low bulk density; progressive size reduction increases the bulk density significantly.

Cooking quality: Different grain samples take different time for cooking therefore the rice samples were soaked for a constant period of 60 minutes and cooked for 3 different timing *viz.* 20, 30 and 40minutes. The number of cooked grains were counted and put in 500ml of boiling water and timed from the time the water started boiling again. After specified period remaining water was drained off and the softness of the grain was gauged manually by pressing them between the thumb and index finger. The cooked grains were counted and recorded in percentage.

Antioxidant properties: Total flavonoid content (TFC), total phenol content (TPC) and DPPH scavenging activity were determined.

Total flavonoid content - Total flavanoid content was determined according to the method given by Zhishen *et al.,* (1999).

Total Phenol content: The Total Phenol content was determined according to the method given by Singleton *et al.,* (1999) using Folin- ciocalteu reagent.

DPPH scavenging activity: The total antioxidant activity was determined according to the method given by Brand *et al.,* (1995) using 1,1- diphenyl-2-picryl hydrazyl (DPPH)**.**

Glycemic Index: The glycemic index of white rice and red rice was determined using the procedure described by (Brouns *et al.,* 2005).

Statistical Analysis: The data obtained on the proximate composition, mineral content, physical properties and antioxidant content of white and red rice were further analysed statistically. Mean ± S.D. was calculated for chemical composition of white and red rice.

Results and discussion

Nutritional composition of white rice and red rice: The results of proximate composition and minerals are presented in Table 1. White rice was found to have 12.7% moisture, 7.6% crude protein, 0.46% ash, 0.62% fat, 0.23% fibre, and 78.34% carbohydrate. On the other hand, red rice was found to have 12.75% moisture, 10.49% crude protein, 1.53% ash, 1.815 fat, 2.7% fibre and 70.19% carbohydrate content. The protein content of red rice is comparable to other cereals and millets such as Whole wheat (11.8%),

Barley (11.5%), Bajra (11.6%) and Jowar(10.4%). The ash content of Red Rice was higher than that of White Rice. Red rice is a rich source of fibre as compared to whole wheat (1.2%), Bajra (1.2%) and many vegetables such as amaranth, spinach, cucumber and carrot (Gopalan *et al.,* 2007). The total physiological energy was recorded as 349.34 kcal in white rice and 341.29 kcal in red rice.

Red rice was found to be a rich mineral source. It had 13.45mg iron, 192.27 mg magnesium, 8.71 mg calcium, and 1.91 mg zinc while white rice was found to have 7.65 mg iron, 46.45 mg magnesium, 7.94 mg calcium and 1.49 mg zinc. Red rice has an iron content more than whole wheat (5.3mg) (Gopalan *et al.,* 2007). Thus, it can be recommended for the people suffering with iron deficiency as rice forms a major part of the diet. A high magnesium content in red rice seeks its importance in the diet of individuals suffering with various heart disorders, especially those related to elevated cholesterol level and hypertension.

Physical properties of white rice and red rice: The Physical properties of red rice are presented in table 1 compared to white rice sample. Red rice was found to have a higher 1000 kernel weight (18.3g), seed weight (1.827g), seed density (1.59 g/ml), seed volume (1.1 ml), hydration capacity(0.347 g/100 seeds), hydration index (0.19), swelling capacity (1.6 ml/100 seeds), swelling index (1.41), kernel elongation (1.32 cm) and bulk density (0.82 gm/l). Also it has a high gelatinization temperature and cooking time. However, the length of the red rice grain is less than white rice. The physical properties of red rice suggest that it has more density than the white rice.

Table 1. Proximate composition and physical properties of white rice and red rice

Nutritional parameters	White rice	Red rice
Moisture Content (g/100 gram)	12.75±0.15	12.7±0.13
Crude Fat Content (g/100 gram)	0.62±0.015	1.81±0.011
Crude Fiber Content (g/100 gram)	0.23±0.02	2.71±0.1
Crude Protein Content (g/100 gram)	7.6±0.23	10.49±0.43
Total Ash Content (g/100 gram)	0.46±0.04	1.53±0.01
Carbohydrate Content (g/100 gram)	78.34±1.5	70.19±1.0
Energy Content (kcal/100 gram)	349.34±2.5	341±1.2
Thousand kernel weight (g)	14.2±0.51	18.3±0.83
Seed weight (g)	1.42±0.02	1.827±0.02
Seed volume (ml)	1.16±0.05	1.1±0.05
Seed density (g/ml)	1.22±0.072	1.59±0.083
Hydration capacity (g/100 seeds)	0.179±0.03	0.347±0.02
Hydration index	0.125±0.02	0.19±0.009
Swelling capacity (ml/100seeds)	0.85±0.35	1.6±0.1
Swelling index	0.72±0.34	1.41±0.11
Length of grain(cm)	0.7±0.1	0.56±0.057
Bulk density of 1g of sample(g/l)	0.703± 0.005	0.82±0.017
Kernel elongation	1.28 cm± 0.127	1.32cm± 0.096
Gelatinization Temp (Alkali spread value)	1-5scale point	High (1-2 scale point)
Cooking quality	30- 40 min	more than 60 min

Antioxidant property of white rice and red rice: The results of antioxidant properties are presented in Table 2. The total phenolic content and total flavonoids content of red rice was found to be 143.38 mg GAE/100 gm and 120 mg R.E./100 gm respectively. The DPPH scavenging activity was found to be 25%. Sompong *et al.,* (2011) found the total phenolic content of ten red rice varieties ranging between 79.2 and 691.4 mg FA equivalent/ 100 gm. Shen *et al.,* (2009) recorded 147.2 mg RE/100 gm as the mean flavonoid content of red rice varieties. On the other hand, the total phenol and flavonoids content of white rice was found to be 24.26 mg GAE/100 gm and 166.23 mg R.E./100 gm. The DPPH scavenging activity was found to be 20%. Yafang *et al.,* (2011) found the phenolic content of white rice to be ranging between 42.57 mg GAE/100 g to 100.7 mg GAE/100 g and flavonoid content ranged between 62.1 mg RE/100 g to 182.6 mg RE/100 g.

Table 2. Mineral and Antioxidant properties of white rice and red rice

II. Minerals and Antioxidant properties	White rice	Red rice
Calcium Content (mg/100g)	7.94±0.17	8.71±0.65
Iron Content(mg/100g)	7.65±0.22	13.45±0.60
Magnesium Content (mg/100g)	46.45±0.649	192.27±5.98
Zinc content(mg/100g)	1.49±0.039	1.91±0.036
Total flavonoid content (mg R.E./100 gm of flavonoid)	166.23±0.25	120.0 ±0.38

Total phenolic content (mg GAE/100g of phenol)	24.26±1.05	143.38 ±1.5
DPPH scavenging activity%	20%	25%

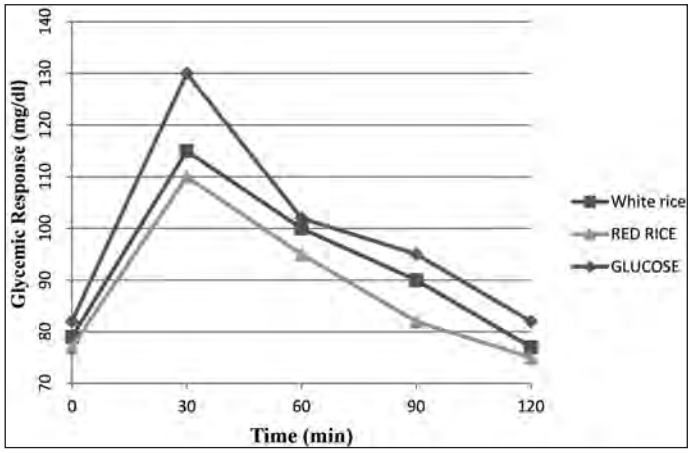

Figure 1. Blood glucose response curve for White and Red rice

Glycemic Index: The glycemic index of white rice and red rice was recorded as 71.7±0.91 and 63.15±2.63 respectively. White rice has 8 per cent more carbohydrate and 2.5 per cent less crude fibre relatively**.** Fiber rich foods like red rice generally have a low glycemic index (GI) (Radulian *et al.,* 2009). As red rice is relatively rich in crude fibre, it may be eaten in small quantities by the diabetic individuals and incorporated in daily diet by the healthy people too.

Conclusion

In the present study it was found that red rice has a higher content of crude fiber, crude protein, minerals and antioxidants than white rice. It has a higher nutrient density and lower glycemic index which makes it comparatively superior than white rice. Red rice has multifaceted nutritional values which make it a highly beneficial superfood. However, red rice has been relegated from plates and fields due to the emergence of white rice as a predominant staple food since the advent of green revolution. Although the scientific community is totally aware of its wonders as a source of minerals, protein and antioxidants, y*et al*one they cannot make a significant mark without an immense market demand. The red rice must evolve onto its journey as a gift of nature rather than ending as weedy and wild rice. Looking onto its health properties, it will be desirable to have processed food items such as puffed and flaked rice, coloured noodles and snack items prepared from red rice adding to its popularisation and commercialisation as an important food grain.

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REVIEW ARTICLE OPEN ACCESS

Soil Health Improving Strategies for Resilient Rice Based Cropping Systems of India

Ch. Srinivasarao, K. Srinivas, K.L. Sharma, Sumanta Kundu

Central Research Institute for Dryland Agriculture, Saidabad, Santoshnagar, Hyderabad- 500059
Email Id: cherukumalli2011@gmail.com

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Abstract

Rice and rice based cropping systems contribute largely to the total food production, sustainability of this system is vital for food and nutritional security. Because of its wide adaptability to diverse soil types and conditions including problem soils (for its beneficial effects during soil amelioration), the crop encounters a variety of field problems which are further aggravated by improper and inefficient management of resources and inputs. Sustainable rice production through soil health management can be achieved by adopting integrated nutrient management, site specific nutrient management and also conservation agriculture practices. Research reports of long term studies reveal that organic manures in addition to fertilizers sustain high crop yields over long periods compared to application of only fertilizers. The results also indicate the scope for substituting more than 25% of recommended dose of NPK with organic sources in intensive cropping systems. Under ideal conditions, green manures and grain legumes when integrated into the cropping system have the potential to meet more than 50% of N requirement of the immediate rice crop. Similarly, site specific soil nutrient management (SSNM) approach was utilized in rice-wheat system at several locations to evaluate its application for achieving total system productivity of 15-17 tons/ha and also in rice-rice cropping systems. Conservation agriculture based resource conserving technologies (RCT's) such as zero tillage and bed planting were also being promoted in rice-wheat system for maintenance of soil fertility. This paper deals with some of the important strategies of soil health and nutrient management for Resilient Rice Based Cropping Systems of India.

Keywords: Soil Health, Rice based cropping systems

Introduction

Rice is the most important food crop of the country contributing nearly 45% to the total food grain production. The crop ranks first in the use of land (> 44 M. ha) and water resources (> 50% irrigation water), and inputs (38-40% of fertilizers and 17-18% of pesticides) but the efficiency of these inputs is considerably low (RKMP, http://www.rkmp.co.in/fertimeter).

Rice farming is practiced in diverse agro-ecological zones, but most of the rice farming occurs in warm/ cool humid subtropics, warm humid tropics and in warm sub-humid tropics. Rice farming is practiced in several agro ecological zones in India. No other country in the world has such diversity in rice ecosystems than India. Because the rice cultivation is so widespread in India, the following four distinct rice ecosystems have been recognized (DRD, 2014).

- Irrigated Rice Eco System
- Upland Rice Eco System
- Rainfed Lowland Rice Eco System
- Flood Prone Rice Eco System

In irrigated rice ecosystems, the rice fields have assured water supply for one or more crops a year. This is the major rice ecosystem. The rainfed lowland ecosystem is characterized by low soil moisture and the soils are often hungry and thirsty for major part of the year. The upland rice ecosystem exists in several forms such as shifting or Jhum rice and permanent settled rice cultivation. This is cultivated on level to sloppy fields/plots. These fields are rarely flooded and mostly aerobic. Rice is directly seeded on plowed dry soil or dibbled in soil. In flooded rice ecosystem, the fields are level to slightly sloping or depressed fields. Fields are flooded to 50 cm or more for more than ten consecutive days during crop growth. Rice is transplanted in puddled soil.

Some of the rice based cropping patterns being followed in India are: Rice-Rice-Rice, Rice-Rice-Cereals (other than rice) Rice-Rice-Pulses, Rice-Groundnut, Rice-Wheat, Rice-Wheat-Pulses, Rice-Toria-Wheat, and Rice-Fish farming system (DRD, 2014). Among the above mentioned cropping patterns followed in the country, Rice-wheat cropping pattern is the largest one and is being practiced in the Indo-Gangetic plains of India for a long time.

With no scope for further increase in net cultivated area (~142 M. ha), much of the desired increase in food grain production in India has to be attained through productivity enhancement of major crops like rice, wheat, maize (which

contribute > 80% to total food grain production) by 3.0 to 7.5% annually (NAAS, 2006). While fertilizers, together with improved varieties and irrigation have contributed significantly to the overall growth in productivity of rice, declining use of organic manures, imbalanced and blanket application of fertilizers without proper rationale are causing deterioration of soil health in soils under rice production. While there is further need to increase cropping intensity, efficient management of inputs and resources including organics and inorganics to enhance input use efficiency is essential to economize on input costs and to improve factor productivity.

Rice growing soils in India

More than 15 major soil groups of diverse characteristics are cropped to rice under different ecosystems (rain fed upland to deep water and irrigated), and agro climatic conditions. The crop is grown in 11 out of 15 agro climatic zones (west and eastern Himalayas, IGP, major portion of southern and eastern plateau region, eastern and western coastal region and the islands of Indian Ocean). Major soil types that are cropped to rice and rice based cropping systems listed in the Table 1 suggest that predominantly alluvial soils, red and yellow loams, shallow to deep black soils and lateritic soils are cultivated to rice. More than 50% of land area in the country is affected by various soil problems that influence the agricultural productivity. Rice having the largest area (~ 45.0 M.ha) in the country and the world is grown in a variety of soil types with wide range of characteristics. In brief, the soil characteristics vary widely from sandy loam to clay in texture; soil pH from 3.0-10.5; organic carbon from 0.2 to > 2.0%; cation exchange capacity (me/100g soil) from < 10.0 – 50.0; and very low to high available nutrient status (Rao *et al.*, 2013).

Table 1. Major rice soils in India

Soil	Classification
Riverine and coastal alluvium	Inceptisols, Entisols
Red and yellow loams	Alfisols
Hill, submontane and terai soils	Inceptisols, Alfisols, Mollisols
Laterites	Ultisols, Oxisols
Peaty soils (acidic)	Inceptisols
Shallow black soils	Inceptisols
Medium and deep black soils	Vertisols

Rao et al., (2013)

Flooding and puddling of a soil brings about a series of physico-chemical changes, the intensity and extent of this change depend, however, on the initial soil characteristics before flooding.. Flooding soil is a great pH neutralizer. In problem soils, this neutralizes acidity and alkalinity thereby influencing favorably to an extent in the release and availability of plant nutrients. As rice and rice based cropping systems contribute largely to the total food production, sustainability of this system is vital for food and nutritional security. Further, water shortage being experienced in the country is threatening the conventional rice cultivation system warranting a re-look into the current practices and design strategies for enhancing resource quality and water productivity.

Because of its wide adaptability to diverse soil types and conditions including problem soils (for its beneficial effects during soil amelioration) the crop encounters a variety of field problems which is further aggravated by improper and inefficient management of resources and inputs. Important soil and management related constraints / problems encountered in rice production in India are listed as follows:

Soil and management related constraints in rice production in India

- Increasing area under soil salinization (8-10 M ha) (salt affected) - major portion is cropped to rice
- About 15 M.ha of rice soils are acidic associated with toxicity of Fe, Al, Mn and As
- Deficiency of K, Ca, Mg, B, Si, and problem of P fixation
- About 8.0 M.ha of rice area is deficient in zinc (Zn)
- Nearly 50 and 80% of Indian soils are responsive (low to medium) to potassium and phosphorous, respectively
- Blanket fertilizer management/recommendation over large domains
- Nutrient depletion (N, K, S) and loss of soil organic matter in intensive cropping systems
- About 3.0 M ha area in northwestern states under rice-wheat cropping system is affected by Mn deficiency
- Nutrient problems related to deficiency of N, P, K, Zn, Fe, S, Ca, B, and toxicity of Fe, Al, H_2S, As and Se
- Overall stagnation or deceleration of growth in productivity of crops and cropping systems
- Wet season rice followed by dry season fallow causes considerable buildup of nitrate in soil profiles. This NO_3 gets lost from the soil when fields are reflooded and puddled for planting rice in the following wet season
- Data indicate that iron (Fe) content of ground water in all the districts is high due to high content of Fe-bearing minerals in soils, and such ground water is not suitable for irrigation unless properly managed. Continuous

use of such irrigation water causes Fe- toxicity and other nutrient imbalances in crop plants. It also greatly reduces P availability in the soil. Precipitation of iron in surface and subsurface layers may clog the pores of the soils. As a result, drainage is impeded and crop plants suffer from inadequate O_2 supply in the root zone.

Sustainable rice production through soil health management can be achieved by following integrated nutrient management, site specific nutrient management and by following conservation agriculture practices.

Nutrient requirements of rice based cropping systems

Production of each ton of rice grains removes 20.1 kg N, 4.9 kg P, and 25.0 kg K, while one ton of wheat grains removes 24.5, 3.8, and 27.3 kg N, P, and K, respectively (Tandon and Sekhon, 1988). Information on nutrient removal by intensive cropping systems is required for developing future nutrient management strategies which vary substantially.

Integrated Nutrient Management

The basic concept underlying INM is the maintenance of soil fertility, sustainable agricultural productivity and improving profitability through judicious and efficient use of fertilizers, organic manures, crop residues, bio fertilizers, suitable agrochemical practices, conservation agricultural practices and nutrient efficient genotypes. The system also involves monitoring all the pathways of nutrient flows in the cropping system from all the sources to maximize the profits.

Organic sources of plant nutrients include growing of legumes in the cropping system, green manures, crop residues, organic manures (FYM, compost, vermicompost, biogas slurry, phosphocompost, biocompost, pressmud, oil cakes etc) and bio fertilizers. Available information show that organic manures in addition to fertilizers sustain high crop yields over long periods as compared to application of only fertilizers as observed in many long term studies. The results indicate scope for substituting more than 25% of recommended dose of NPK with organic sources in intensive cropping systems. Under ideal conditions, green manures and grain legumes when integrated into the cropping system have the potential to meet more than 50% of N requirement of the immediate rice crop. Further, addition of organic manures as part substitutes or supplementary (add on) improved soil physic-chemical and biological properties and ultimately its quality. Biofertilizers (N fixing, P solubilising, cellulolytic microorganisms) facilitate economizing fertilizer nutrient use through utilizing BNF systems, solubilising less mobile nutrients from fixed components and recycling of nutrients from crop residues. Integration of such systems makes the production system more stable and sustainable.

Legumes and green manures

Legumes are considered as soil builders and rice-legume is more ideal in terms of nutrient addition, especially N and also helps regenerate destroyed rice soil structure (on account of puddling) through their favourable rhizosphere effects. Similarly, in upland rice-chick pea system, chick pea system improves P availability by acidifying its rhizosphere due to its acidic root exudates like citric acid. This supplies P in addition to N to the succeeding upland rice which lacks advantage of flooding. Inclusion of legumes in the cropping sequence gives a lot of scope to economise on certain nutrients. The experimental results from rice-wheat and berseem-rice indicated that there is considerable opportunity to save on P application for rice, if the preceding crops of wheat and berseem receive recommended dose of P. In cereal-legume or oil seed-legume, legumes need small amounts of P fertilizer and virtually no N and the fertilizer inputs can go to the non-legume component.

Grain and fodder legumes and green manures can fix atmospheric N to the extent of 50-500 kg/ha. The residues of legumes after harvest contain 25-100 kg/ha N which is available to the next crop upon decomposition. Green manures under many situations can meet N demand of crops more efficiently than fertilizer urea (Rao *et al.,* 1991). The rate of N release from the green manures depends on the characteristics such as N content, lignin content, etc The practice of growing green manures is on the decline due to increased cropping intensity and availability of fertilizers at subsidized rates, and non availability of green manure seed. Inclusion of grain or fodder legumes in the cropping system is a viable alternative to green manure crops.

Crop residues

Crop residues are good sources of plant nutrients and are important components for the stability of agricultural ecosystems. About 500 million tons of crop residues are produced in India alone (MNRE, 2009). In areas, where mechanical harvesting is practiced, a large quantity of crop residues are left in the field, which can be recycled for nutrient supply. About 25% of nitrogen (N) and phosphorus (P), 50% of sulfur (S), and 75% of potassium (K) uptake by cereal crops are retained in crop residues, making them valuable nutrient sources. Both rice and wheat are exhaustive feeders, and the double cropping system is heavily depleting the soil of its nutrient content. A rice-wheat sequence that yields 7 tons per ha of rice and 4 tons per ha of wheat removes more than 300 kg N, 30 kg P, and 300 kg K per ha from the soil. If crop residues could be better managed, this would directly improve crop yields by increasing soil nutrient availability, decreasing erosion,

improving soil structure and increasing soil water holding capacity as a consequence of improving soil organic matter content (Yadvinder Singh *et al.,* 2005).

Rice residue management options

There are several options for managing crop residues. These include being removed from the field, left on the soil surface, incorporated into the soil, burned *in situ*, composted or used as mulch for succeeding crops. Throughout the tropics, there is little recycling of crop residues in the field – these are either harvested for fuel, animal feed or bedding or are burned in the field. Crop residues removed from the field can also be used as bedding for animals, a substrate for composting, biogas generation or mushroom culture or as a raw material for industry. In many parts of the tropics, crop residues are burned in the field due to the ignorance of farmers about their value and lack of proper technology for in situ incorporation of residues. For example, in the intensive rice-wheat cropping system in the Indo-Gangetic plains of South Asia, crop residues, particularly rice straw are not used as animal feed and are disposed of by burning. Complete burning of rice straw at 470°C in muffle furnace resulted in 100, 20, 20 and 80% losses of N, P, K and S, respectively (Sharma and Mishra, 2001).

Decomposition of rice residues

Decaying of crop residues starts as soon as the residues come into contact with the soil. The process of decomposition is controlled by the interaction of three components:the soil organisms or biological processes, the quality of crop residues, and the physical and chemical environment. Burying of rice straw in soil has been reported to accelerate the decomposition in comparison with placing the straw on the soil surface (Kumar and Goh, 2000). Residues rich in lignin and polyphenol contents experience the lowest decay. A large number of organic compounds, particularly phenolic acid and acetic acid are released during the decomposition of crop residues under anaerobic conditions. The accumulation of these organic compounds can adversely affect the seedling growth.

Residue management effects on soil properties

Crop residue management is known to affect either directly or indirectly most of the soil quality indicators-chemical, physical and biological. It is perceived that soil quality is improved by the adoption of sound crop residue management practices (Karlen *et al.,* 1994). Long-term application of crop residues increased the organic matter, total N content and availability of several nutrients (though to a small extent) in soils. The rate of increase in soil organic matter is low due to high turnover rates of C under tropical conditions. Mineralization and immobilization of N occur simultaneously in the soil. The residue quality and availability of soil N are important determinants of N mineralization-immobilization occurring during residue decomposition. The application of crop residues can cause short-term immobilization of both P and S, particularly in aerobic soils. Only a small fraction (5%) of the residue P is available to the plants in the first year, and a major fraction is immobilized as microbial biomass (Stevenson, 1986). Crop residues contain large amounts of K, which upon incorporation increased K availability in soil and helped to reduce K depletion from non-exchangeable K fraction of soil (Chatterjee and Mondal, 1996). Microbial biomass, a small (1-5% by weight) but active fraction of soil organic matter, is of particular concern in soil fertility considerations because it is more susceptible to management practices than the bulk organic matter (Janzen, 1987).

In South Asia, rice crop occupies a major share of total arable land. The recycling of its residues has the great potential to return a considerable amount of plant nutrients

Table 2. Effect of long-term crop residue management on grain yields (t ha^{-1}) of rice and wheat

Crop Residue	N applied (kg ha^{-1})			Mean
	60	120	180	
	Rice (Mean of 10 years)			
Burned	4.65	5.65	6.42	5.57
Removed	4.46	5.50	6.04	5.53
Incorporated	3.62	4.63	5.26	4.51
Mean	4.24	5.26	5.91	
LSD (P=0.05)	Residue 0.55	N 0.16	Residue × N NS	
	Wheat (Mean of 11 years)			
Burned	3.46	4.26	4.64	4.12
Removed	3.48	4.14	4.42	4.02
Incorporated	2.94	3.87	4.34	3.72
Mean	3.29	4.10	4.47	
NS LSD (P=0.05)	Residue 0.25	N 0.22	Residue × N NS	

(Mandal et al., 2004)

to the soil in the rice based crop production systems. Particularly the rice-wheat cropping system is the most intensive production system in the country (Table 2). The yield stagnation consequent upon the declining soil organic carbon is a major threat to this system. Therefore, it is a great challenge to the agriculturists to manage rice residues effectively and efficiently for enhancing sequestration of carbon and maintaining the sustainability of production.

Organic manures

Organic manures vary in their nutrient content, quality and utility as sources of nutrients. When properly managed, they have potential as nutrient sources to supplement 25-35% of nutrient requirements of crops. In rice-wheat system, FYM @ 15.3 t/ha applied to rice was up to 90% as efficient as 150:60:60 kg NPK, while in wheat, FYM applied @ 20-40 t/ha was only 35-45% efficient because of slow nutrient release due to low temperatures. While FYM alone was not so efficient, combined application of FYM and NPK was found to be highly efficient (DRR, 2007; 2008). Long term studies by DRR (DRR, 2007) indicated significant improvement in soil organic carbon with FYM. The increase ranged from 4-49% (Swarup, 2002). FYM influenced soil nutrient status positively and brought about many changes in the physical and biological properties of the soil (Hegde, 1998).

Vermicomposts

Vermicomposts contain higher concentrations of NPK compared to FYM and are usually more effective in promoting crop growth than FYM, presumable due to higher nutrient concentration and better manure characteristics (Barik *et al.,* 2006). The impacts of vermicompost on soil quality were found to be superior to FYM in many cropping systems.

Poultry manure (PM)

Poultry manure has much higher concentrations of NPK, especially P, which makes it a good nutrient source. A laboratory study showed that 45% of PM-N mineralized in 4 weeks as against 12% from FYM (Yadvinder Singh *et al.,* 1988). As nutrient source for rice, 4 t PM + 60 kg N/ha was equivalent to 120 kg N/ha as urea (Yadvinder Singh and Meelu, 1995).

Biogas slurry (BGS)

Biogas slurry contains about 1.4, 1.2 and 1.0% NPK and was as effective as urea for rice and wheat in light textured soils at IARI. It is more efficient source of nutrients than urea alone when more than 50% N requirement is substituted with BGS.

Biocompost (BC)

Biocompost is prepared by mixing press mud cake (PMC) with spent wash from distilleries and contains 1.9, 1.85 and 1.5% NPK besides many micronutrients. It was reported to be a more efficient source than fertilizers when applied @ 5 t/ha BC + 50% RDF for wheat. The material also influenced soil quality (nutrient supply, OC) and recorded 22% more wheat yield (Tripathi *et al.,* 2007).

Press mud cake (PMC)

Press mud cake is a waste product of sugar industry, and about 9.0 m.t. is produced annually. It contains about 1.6, 1.0 and 0.8% NPK. Applied @ 5.0 t/ha along with 40-60 kg N/ha to rice, PMC was equally effective as 120 kg N/ha as urea with significant residual effects on wheat to the extent of 40 kg N and 13 kg P/ha (Yadvinder singh *et al*., 2003). The material also improved soil OC by 50%, total N by 60% and the biological properties by 91% (SMBN).

Phosphocompost (PC or PEC)

Phosphocompost **e**nriched with P (SSP or RP) can be a good organic source of nutrients particularly of P in phosphorous fixing soils. Following NADEP method of composting Increase in P content from 0.69 to 0.92 and 0.98% when enriched with RP and SSP, the latter also improving N content by preventing loss of N through ammonia volatilization during composting has been reported. Combining PSB inoculation with phospocomposting (RP) improved the citrate soluble P (Mishra *et al.,* 1984) which makes it useful even in calcareous soils.

Biofertilizers

Biofertilizers are cultures of micro organisms that are capable of fixing atmosphere N, solubilise less soluble P, mobilise native soil P and K and for accelerating decomposition of organic material while composting or in the fields that of crop residues. N fixers are symbiotic (Rhizobium sp.,) and non symbiotic (Azotobacter; Azospirillum; blue green algae, Azolla *etc.*). Rhizobium cultures are used for the legumes, the residues of which can be recycled into the cereal crop system while Azospirillum BGA and Azolla are directly used in the rice fields. Estimates of N fixation in rice fields ranged from 25-30 kg N/ha by BGA and was reported to increase rice yield by 14%. These were found complimentary to GM and use of neemcake coated urea (NCU) (Singh *et al.,* 1990). BGA inoculation with 50% N as NCU was reported to be equivalent to 120 kg N/ha as urea.

Azolla (fern) has been used as N fixer in rice in China since 6th century. Under field conditions, it can fix 30-40 kg N/ha but requires 15-20 kg P205/ha to fix N. Azolla is grown simultaneously with rice as a dual crop but it is more useful as a source of N when used as a green manure. Phosphate solubilizing organisms (PSB, PSO, PSF) play an important role in solubilizing insoluble P compounds in soil..The organic acids (gluconic, lactic, citric, tantaric acids) released by PSO decompose rockphosphates and release P.

Application of RP with PSO is reported to increase yields of rice. Comparable efficiency of RP + PSO and DAP which improved further with the supplementation of crop residues has been reported. PSOs along with RP are more effective for pulses with different levels of yield improvement but more in the presence of soluble P inoculated with PSO.

Nutrient efficient genotypes

Genotypes differ in their response to applied nutrients, utilization efficiency and nutrient requirement. Exploiting this variability to identify and utilize in specific environments would economize costs on nutrient use and conserve resources. Some of the rice varieties like Rasi, Vikas, RP 5929, some of rice hybrids, etc are reported to be efficient utilizers of nutrients.

Site Specific Nutrient Management (SSNM)

Major factors contributing to the low and declining crop responses to fertilizer nutrients are continuous nutrient mining from the soil due to imbalanced nutrient use (7:2.8:1 NPK) leading to depletion of some of the major, secondary and micro nutrients like N, K, S, Zn, Mn, Fe, B *etc.*, decreasing use of organic nutrient sources such as FYM, compost and green manures / grain legumes in the cropping systems and mismanagement of irrigation systems leading to serious soil degradation.

Sustainable crop production management involves replenishing of nutrients that are removed by crops while taking into consideration other net influxes of nutrients. Indian agriculture is operating at an estimated negative nutrient balance of 10 M. tons. Trends in nutrient use of 23 M tons in 2007-08 is expected to increase to 29.0 M tons (20.7 N, 6.8 P_2O_5 and 2.1 K_2O M. tons) by 2025. However, at the estimated nutrient removal of 37.5 M. tons of NPK (11.9 N + 5.3 P_2O_5 + 20.3 K_2O M. tons), the balance indicates an excess use of N and P_2O_5 and deficit use of nearly 18 M tons of K_2O nutrients which would be alarming. Potassium accounts for 55% of NPK removal, while N and P accounts for 31 and 14% of crop uptake. To achieve the projected food grain demand of 300 M. tons by 2025, about 30 M. tons of NPK from various sources are required in addition to 15 M. t. for the commercial crops totaling nearly 45 M. t (Tiwari, 2001).

Rice – Wheat - Cowpea fodder system removes about 270 kg N/ha, 150 kg P_2O_5/ha and 390 kg K20/ha (total > 800 kg/ha). Annual removals of NPK could range from 440 - 815 kg/ha under high intensity cropping systems. Production of about 8-12 tons of grain/ha is associated with nutrient uptake of 140-330 kg N, 70-120 kg P_2O_5/ha and 200-390 kg K_2O/ha which provides guidelines for framing nutrient management strategies.

Nutrient Management and recommendation process in India is still based on response data arranged over large domains. The SSNM provides an approach for need based feeding of crops with nutrients while recognizing the inherent spatial variability. It aims at nutrient supply at optimal rates and times to achieve high yield and efficiency of nutrient use by the crop. SSNM approach involves three steps – establishing attainable yield targets, effectively use existing nutrient sources and application of fertilizers to fill the deficit between demand and supply of nutrients. Soil nutrient supply potential and its spatial variability, productivity potential and targets for crops and cropping systems, estimation of nutrient requirements, and fertilizer use efficiency besides assessment of resource quality and socioeconomic background of the farmers are essential for developing site specific IPNS.

The SSNM approach followed in India aims at maximizing farmers' profits by achieving maximum economic yield (MEY). The SSNM approach was introduced in priority areas facing one or more of the problems like imbalanced nutrient use with low yields, crops showing nutrient deficiencies in large scale, endemic to pests and diseases linked to nutrient management, evidences of P and K mining and in areas of multi-nutrient deficiencies particularly of secondary and micronutrients. The available knowledge on SSNM was utilized in rice-wheat system at several locations to evaluate its application for achieving total system productivity of 15-17 tons/ha (Tiwari *et al.*, 2006) and also in rice-rice cropping systems. The results were encouraging with highest annual grain yields of > 16t/ha at Modipuram, Ludhiana; 14-16 t/ha at Kanpur; 12-14 t/ha at Faizabad, Varanasi, Pantnagar, Sabour, R.S.Pura; 10-12 t/ha at Ranchi and 8-10 t/ha at Palampur. Averaged over all locations, SSNM showed yield advantage of 3.4 t/ha or 34% over farmers' fertilizer practices with benefit cost ratio of 4.9 (additional income > Rs 15000). In many locations yields of rice were more than 10 t/ha because of hybrids.

Real time N management using LCC

Leaf colour chart approach is very important in managing N in rice crop. Some of the steps include

- Leaf color chart (LCC) is used only for top dressing of N
- Read the color of top few leaves at 7-10 days interval from early tillering to booting stage
- Apply fertilizer N @ 50, 75, 100 or 125 kg urea / ha as top dressing, respectively for low, medium, high, or very high response environments each time at tillering and 3-5 days before panicle initiation stage

Management of nutrients other than Nitrogen:

Phosphorous (P) management:

The second most important plant nutrient, P is required for better root and shoot growth, starch mobilization and as source of energy. P is mobile within the plant and promotes tillering, root development, early flowering, and ripening. It is particularly important in early growth stages. Hence all recommended P should be applied as basal dose. Rice requires 5-9 kg P_2O_5 / ton of grain and recovers about 15-25% of applied P with substantial residual effects. Depending on site characteristics, for a 6.0 t target yield/ ha, about 50 kg P_2O_5 /ha fertilizer is required at native soil productivity of 4.0 t/ha, 6 kg P_2O_5 /ton requirement and 25% recovery efficiency.

Potassium (K):

Indian soils though show medium to high K fertility, the outflow of K by crops and cropping systems is very high (at 20-25 kg K_20/ton grain). At the current levels, overall balance of K in the system is negative in majority of the cropping systems needing K application in quantities sufficient to prevent depletion of the nutrient to acute levels.

- Recommended sources of K are MOP (50%) and paddy straw (50%)
- Half of the recommended K should be applied as basal and remaining half at panicle initiation stage especially for hybrid rice.
- Recycling of crop residues rich in K, split application in high productivity systems (eg. Hybrids), additional dose of K in acid soil environments prone to iron, Al, sulfide toxicity etc all benefit the crop system and support high crop production.
- The strategy involves diagnosis and application of deficient nutrients. More important in the management of these nutrients is whether to apply, if so how to apply and the timing rather than how much to apply.

Zinc (Zn): The zinc is widely deficient in Indian rice soils (>8.0 million ha) and is required in initial stages of rice growth for developing aerenchyma tissue, biosynthesis of auxins, protein synthesis and gene expression. Soil application in acutely deficient in high pH soils (@ 30-50 kg/ha) and/or mid season correction by spraying $ZnSO_4$ or chelated zinc (0.50%) are recommended.

Sulphur (S): Being a constituent of important amino acids such as cysteine, cystine, methionine and proteins, and generally required in larger quantum for oil seed crops, the outflow of S even by cereal crops like rice is also high (3-5 kg/ton grain). This suggests for efficient S management considering the total S removal by a cropping system particularly in high rainfall rain fed lowland rice systems where reports of S depletion and response to S application have been reported. Non-use of S fertilizers and increasing cropping intensity are also contributing to the emerging problems of S nutrition. S sources like gypsum, phosphogypsum, ammonium sulphate, elemental S, and organic manures / crop residues as a part of INM are recommended to supply about 30kg S/ha per crop as efficiency of S is relatively low.

The rice yields under different soil fertility management practices are given in Table 3.

Table 3. Rice yields (t/ha) with long term soil fertility management (1989 to 2012) in RBCS

Treatment	Titabar	Mandya	Maruteru	Faizabad
Control 1	2.14	2.39	2.89	1.89
100% PK	3.01	2.91	3.36	1.92
100% N	3.37	3.65	4.05	2.83
100% NP	3.58	4.15	4.48	2.97
100% NPK + Zn + S	4.22	4.84	4.97	3.34
100% NPKZnS + FYM/PM @ 5t/ha	4.71	5.46	4.97	4.36
100% NPK –Zn	3.98	4.70	4.68	3.16
100% NPK – S	4.11	4.65	4.73	3.14
100% N+50% PK	3.67	4.29	4.44	2.97
50% NPK	3.27	3.90	4.28	2.69
50% NPK+ 50% GM-N	3.61	4.84	4.43	2.98
50% NPK+ 50% FYM-N	3.72	4.91	4.69	2.98
50% NPK+25% GM-N+25% FYM-N	3.75	5.47	4.52	3.06
FYM @ 10 t/ha	3.80	4.12	4.40	2.72

DRR (2012)

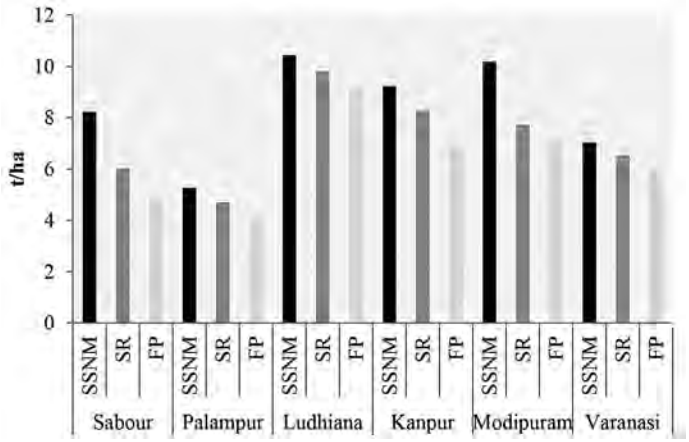

Figure 1. Grain yield of rice with site specific nutrient management (SSNM), state recommendation (SR) and farmers' practice (FP) at selected research centres under PDFSR, Modipuram *(NAAS, 2012)*

Conservation Agriculture Practices

The rice-wheat production system has played an important role in the food security and has remained its cornerstone for rural development and natural resource conservation in Indo-Gangetic plains of not only in India but also across South Asia. But recently second generation problems have started appearing such as

- declining productivity,
- plateauing of crop productivity,
- declining soil organic matter,
- receding ground water table,
- wide spread resource degradation,
- diminishing farm profitability, *etc*.,

These are mainly attributed to intensive conventional production. At present, the challenge is to produce more food from the same land and water resources by alternative systems, while sustaining soil health, environment and improving sustainable farm profitability. A holistic approach is needed to tackle these problems and to improve the sustainability of this cropping system. This necessitates that more attention be given to issues threatening sustainability by adopting various strategies including conservation agriculture.

- Genetic improvement is one of the most efficient approaches to develop rice cultivars suited to conservation agriculture based technologies.
- Conventional crop establishment practice in rice involves manual transplanting of rice in puddled soil which involves excessive tillage, high energy consumption.
- The anaerobic condition of flooded soils in rice crop after transplanted, the imparted soil structure of the puddled layer and compacted layer that strengthens to form a hard pan of increased strength on drying are major impediments to the establishment and growth of ensuing crops.
- Due to these factors, many farmers are shifting from transplanting to direct sowing.
- The varieties developed for conventional tillage system do not necessarily have the same performance and specific genotypes are recommended for no-till system.
- Vigorous modern rice cultivars are increasingly required, which would not only facilitate rapid seedling establishment under a wide range of field conditions but also have increased competitive ability against weeds.
- CA based resource conserving technologies (RCT's) such as zero tillage and bed planting are being promoted in rice-wheat system.
- Direct seeded rice suffers from one or the other stresses such as high pH, micronutrient deficiency, high or low moisture, undulating land, *etc.* For such direct seeded rice (DSR), we need cultivars that do not suffer from iron chlorosis, Zn and P deficiency, and beside these, they should be able to germinate when seeds are placed deeper in moist zones.
- Development of varieties, which can resist moisture stress, is necessary for increasing overall water productivity.
- Rice is the world's most important staple food crop. Conventional flooded rice cultivation in Asia provides more than 75% of the world's rice supply for half the earth's main staple food (Cabangon *et al.*, 2002). However, rice production consumes about 30% of all freshwater used worldwide.
- In Asia, flood-irrigated rice consumes more than 45% of total freshwater available (Barker *et al.*, 1999).
- The global water scarcity analysis has revealed that up to two-third of world population will be affected by water scarcity over the next several decades

(Wallace and Gregory, 2002). By 2025, 15 out of 75 million hectare of Asia's flood-irrigated rice crop will experience water shortage (Tuong and Bouman 2003).

- Decreasing water availability for agriculture threatens the productivity of irrigated rice ecosystem. Therefore, there should be more emphasis on water conservation and improved efficiency of use and reallocation of water from one use to another, presumably shifting to a higher value use.
- Alternatives to the conventional flooded rice cultivation need to be developed world wide to reduce water consumption and produce more rice with less water.
- Rice transplanting is a labour intensive and arduous operation which is about 25 per cent of the total labour requirement for the crop production. Besides, it is time consuming and backbreaking operation.
- Direct sowing of rice by suitable drills is another alternative so as to cater the needs and requirements of farmers. Moreover, increasing energy prices, limited water and labour availability for transplanting, warrant farmers as well as researchers to develop alternate production systems for rice.
- "Conservation agriculture (CA) is a concept for resource saving agricultural crop production that strives to achieve acceptable profits together with high and sustained production levels while concurrently conserving the environment (FAO, 2007)."
- Laser land levelling is an important component of resource conservation technology that can improve water productivity at field level. Lantican *et al.,* (1999) studied the effect of precise land levelling on yield of direct seeded rice in Philippines and found that yield for direct seeded rice was significantly improved with precise land levelling. Yield advantage in both direct seeded as well as puddled transplanted rice with laser land levelling was observed. In India also, it has been experienced in many farmers' participatory trials that a saving of 20-25 per cent of irrigation water can be achieved by laser land levelling (Ravi Gopal *et al.,* 2010). Precise land levelling ensures better crop establishment, improved fertilizer use efficiency as well as easy farm operations.

Conclusion

Sustainable rice production through soil health management in rice based cropping systems in India can be achieved through a proper understanding of the nutrient needs and meeting them through site specific integrated nutrient management and use of conservation agriculture technologies.

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ORIGINAL RESEARCH ARTICLE OPEN ACCESS

Effect of Humic and Fulvic Acid with Different Levels of NPK on Rice Yield

G. Venkateshprasath[1], M. Meyyappan[1*], M. Ganapathy[2] and A. Angayarkanni[3]

[1] Department of Agronomy, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamilnadu - 608 002
[2] Department of Soil Science and Agricultural chemistry, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamilnadu - 608 002

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Abstract

Field experiment was conducted at Annamalai University Experimental Farm, Annamalai Nagar during Sornavari season (March to June, 2016) to study the effect of NPK at different levels along with soil and foliar application of organic substitutes on the growth and yield of rice. Among the treatments, application of 100 per cent NPK + FYM @ 12.5 t/ha + Isabion foliar application @1250 ml/ha on 20 and 50 DAT ranked first regarding number of productive tillers/m^2, filled grains/panicle, grain and straw yield.

Keywords: FYM,Humic acid, Fulvic acid, Yield parameters and yield

Abbreviations used

USDA ; United States Department of Agriculture
ml ; millilitre
t ; Tonnes Kg ; Kilogram
ha ; Hectare DAT ; Days After Sowing
% ; Per cent @ ; at the rate of
FYM ; Farm Yard Manure Co_2 ; Carbon dioxide
ADT(R) ; Aduthura Rice
NPK ; Nitrogen, Phosphorus and Potassium

Introduction

According to USDA 2016-17 statistics, rice is grown in 114 countries across the world in an area of 161.35 million hectares with a production of 480.13 million metric tons and the productivity is 4.44 t/ha. In India, during 2016-17 rice is grown in an area of 433.88 lakh hectares with a production of 104.32 million tonnes and the productivity is 2.4 t/ha (Annual Report, 2016-17). Continuous use of inorganic fertilizers leads to deterioration of soil physical, chemical properties and biological activities in soil (Mahajan *et al.,* 2008). The only way out to this gloomy scenario is to develop sustainable and nutrient balance technological packages, which would increase the rice production without harming the precious environment. Improving soil fertility is severely constrained due to the decline of FYM from the livestock system. Hence, it is necessary to find out an alternative source for FYM. Humic acids are water soluble organic acids naturally present in soil organic matter, comprising a large family of organic compounds with similar characteristics that are products of organic matter transformations by soil micro-organisms. Humic acid improves soil aggregation, aeration, permeability, water holding capacity, hormonal activity, microbial growth, organic matter mineralization, solubilisation, availability of microelements and some macro elements. Fulvic acid provides a multitude of benefits like a powerful organic electrolyte, enhances cell division, elongation and root growth. Further, it increases the plant's oxygen uptake capacity with an associated increase in chlorophyll production, as a foliar spray and increase the permeability of plant membranes and uptake of nutrients. Application of amino acids led to decreased nitrate content and increased the total nitrogen content in plants.

Materials and Methods

A field experiment was conducted at Annamalai University Experimental Farm, Annamalai Nagar during Sornavari season (March to June, 2016) to study the effect of NPK at different levels along with soil and foliar application of organic substitutes on the growth and yield of rice variety, ADT(R)-45. The farm is situated at 110 24' North latitude, 79^0 44' East longitude and at an altitude of 5.79 m above mean sea level. The texture is clayey loam with low in nitrogen, medium in phosphorus and high in potassium. The experiment was laid out in Randomized Block Design with three replications. There were twelve treatments *viz.*, T_1- 100% NPK + FYM @ 12.5 t/ha, T_2- 100% NPK + eM power (Humic acid and Fulvic acid) @ 12.5kg/ha on 7 and 35 DAT, T_3- 75**%** NPK + eM power @ 12.5kg/ha on 7 and 35 DAT, T_4- 50**%** NPK + eM power @ 12.5kg/ha on 7 and 35 DAT, T_5- 100% NPK + FYM @ 12.5 t/ha + Humic plus P foliar spray @ 625g/ha on 20 and 50 DAT, T_6- 100% NPK + eM power @ 12.5kg/ha on 7 and 35 DAT + Humic plus P foliar spray @ 625g/ha on 20 and 50 DAT, T_{7-} 75% NPK + eM power @ 12.5kg/ha on

7 and 35 DAT + Humic plus P foliar spray @ 625g/ha on 20 and 50 DAT, T_8- 50% NPK + eM power @ 12.5kg/ha on 7 and 35 DAT + Humic plus P foliar spray @ 625g/ha on 20 and 50 DAT, T_9- 100% NPK + FYM @ 12.5 t/ha + Isabion foliar spray @1250ml/ha on 20 and 50 DAT, T_{10}- 100% NPK + eM power @ 12.5kg/ha on 7 and 35 DAT + Isabion foliar spray @1250ml/ha on 20 and 50 DAT, T_{11}- 75% NPK + eM power @ 12.5kg/ha on 7 and 35 DAT + Isabion foliar spray @1250ml/ha on 20 and 50 DAT, T_{12}- 50% NPK + eM power @ 12.5kg/ha on 7 and 35 DAT + Isabion foliar spray @1250ml/ha on 20 and 50 DAT were tried. Based on the treatment schedule 100, 75 and 50 per cent of recommended dose of N, P and K were applied to the respective plots. Well decomposed farm yard manure @ 12.5 t /ha was applied to the respective plots as per treatment schedule. The organic granule, eM power is recommended @ 12.5 kg/ha and applied in two equal splits on 7 and 35 DAT to the respective plots as per treatment schedule. Humic plus P is an organic water soluble organic product containing 75 per cent potassium Humate, 15 per cent Fulvic acid and plant growth promoters. It is recommended @ 625 g/ha and sprayed on 20 and 50 DAT. Isabion contains organic fraction derived from amino acids, peptide mixture @ 62.5 per cent w/w as major compound. It is recommended @ 1250 ml/ha and sprayed on 20 and 50 DAT.

Results and Discussion

Among the treatments, the highest number of(511) productive tillers/m^2 and number of (106) filled grains/ panicle were observed in T_9- 100% NPK + FYM @ 12.5 t/ha + Isabion foliar spray application @1250 ml/ha on 20 and 50 DAT (Table -1). The increase in grain yield was recorded up to 450 and 180 kg/ha respectively due to foliar application of isabion or Humic plus P when compared to conventional method of 100 per cent NPK and FYM applications. Within the treatments, the highest grain yield of 5.88 t/ha was recorded in T_9- 100% NPK + FYM @ 12.5 t/ha + Isabion foliar spray application @1250 ml/ha on 20 and 50 DAT. The next in order was T_5-100% NPK + FYM @ 12.5 t/ha + Humic plus P foliar spray application @ 625g/ha on 20 and 50 DAT and T_1- 100% NPK + FYM application @ 12.5 t/ha. The reduction in grain yield due to reduced NPK application was improved further by Isabion or Humic plus P foliar spray @ 1250 ml/ha or 625ml/ha on 20 and 50 DAT. The same trend was noticed in terms of straw yield.

The combined beneficial effect of NPK and FYM in terms of improving the soil physical, chemical and biological properties, presence of hormones in FYM and availability of optimum quantity of nutrients at critical stages favourably influenced the growth parameters of the rice directly and yield parameters indirectly. Further, Humic acid foliar spray might have improved the chlorophyll content, increased the CO_2 assimilation in plants and increased the uptake of nutrients by plants. Among the two foliar sprays along with 100 per cent NPK plus 12.5 t FYM/ha, Isabion @ 1250 ml/ha was found to be better with more number of filled grains/panicle (20) when compared to conventional method of 100 per cent

Table 1. Yield and yield related attributes recorded in the different treatments

Treatments	Number of productive tillers/m^2	Number of filled grains/ panicle	Grain yield (t/ha)	Straw yield (t/ha)
	At harvest	At harvest		
T_1	460	86	5.43	8.26
T_2	410	73	4.78	7.22
T_3	380	65	4.49	6.75
T_4	246	43	3.25	4.95
T_5	480	94	5.61	8.46
T_6	419	81	5.18	7.82
T_7	382	73	4.86	7.34
T_8	251	48	3.46	5.23
T_9	511	106	5.88	8.89
T_{10}	421	92	5.24	7.92
T_{11}	384	82	5.01	7.62
T_{12}	262	52	3.62	5.48
SE_d	23.70	3.78	0.301	0.5529
CD(P=0.05)	49.91	7.82	0.623	1.1467

NPK and 12.5 t FYM application. This might be due to the increased uptake of more amount of nutrients and effective translocation of photosynthates from source to sink. This result is in line with the result of Vanitha and Mohandass (2014).

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ORIGINAL RESEARCH ARTICLE OPEN ACCESS

A Rapid Field Screening Method for Evaluation of Resistance to Leaffolder, *Cnaphalocrocis Medinalis* Guenee in rice

Padmavathi Chintalapati*, Sumalatha Javvaji, Katti Gururaj

ICAR- Indian Institute of Rice Research
Rajendranagar, Hyderabad – 500030, India
*Corresponding author:chintalapatipadmavathi68@gmail.com

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Abstract

Rice leaffolder, *Cnaphalocrocis medinalis* (Guenee) is one of the major foliage feeding insects found in Asia and all the important rice growing regions in India. Identification of resistant sources plays a major role in the eco-friendly management of leaffolders, for which continuous screening of various germplasm lines and breeding material is essential. In the present study, a rapid field screening method was developed for evaluating large number of rice germplasm lines. It involves release of third instar larva on to the rice plants at 30-45 days after transplanting, allowing it to feed for 48 hrs and assessment of damaged leaf area by ImageJ program. It helps in reliable and faster identification of resistant sources. The method is also useful in precise phenotyping of mapping populations in breeding programs for the development of leaffolder resistant varieties.

Keywords: Leaffolder, screening, resistance, damaged leaf area, damaged leaves

Introduction

Rice is the most important staple food crop grown in India in an area of about 41 million hectares with a production of 104.32 million tonnes (Directorate of Economics & Statistics, Government of India, 2016). Rice production is limited by a number of biotic constraints, of which insect pests play a major role causing 25 -30% yield losses. Among the foliage feeders, leaf folder, *Cnaphalocrocis medinalis* (Guenee) has become a major threat to rice production in many Asian Countries including China, Sri Lanka, Vietnam Pakistan, Japan, Korea, Malaysia and India. Larvae fold the leaves by stitching with silken threads and feed on the green mesophyll tissue resulting in white membranous patches that are visible from a distance in the rice field. Rice plants have ability to compensate for the leaf folder damage during tillering stage. However, larval densities at more than three larvae per hill at the maximum tillering stage resulted in 20% unfilled grains. At flowering stage, flag leaf damage of more than 25% resulted in 50% unfilled grains (Padmavathi *et al*, 2013). During the outbreak period, yield reduction of 30–80% was reported from severely damaged fields (Kushwaha, 1988). So far, chemical control is the only practical method available for the farmer for its management and as the damage caused by leaf folder is highly visible to farmers, it triggers them to go for toxic insecticide application.

Growing resistant variety plays a major role in the management of insects especially in low input farming situations of India. It is also highly compatible with other methods of pest management. Screening for insect resistance under natural field conditions is a long term process. At the same time, it is difficult to identify reliable and stable sources of resistance due to variation in insect populations in space and time. To overcome these problems, it is essential to develop and standardize multi or no-choice screening techniques through artificial releases of the pest populations. Keeping this in view, the present study was undertaken to develop a modified feeding test that helps in screening large number of genotypes for resistance to leaffolder in the field.

Materials and Methods

Field experiments were conducted during *Kharif* 2014 at the research farm, Indian Institute of Rice Research, Hyderabad, India. The climate in this region is predominantly semi-arid, with mean temperatures in the range of 22–42° C, and an average annual rainfall of 896 mm.

In the first method, field screening was done as per the standard evaluation system (SES) for rice (IRRI, 2014). Forty eight genotypes were grown in the nursery and after 25 days, transplanted in the main field in rows at spacing of 20 x 10 cm. Taichung Native 1 (TN 1) was grown as susceptible check and W 1263 as resistant check after every 10 rows. The susceptible TN 1 variety was also grown as border and higher doses of nitrogen were given to increase leaffolder populations. All the other recommended agronomic practices were followed in raising the crop. At 25 days after transplanting (DAT), the genotypes were covered with nylon net and leaf folder adults were released

inside the net from greenhouse reared population or by collecting from the neighbouring fields (Plate.1). Adults were released two times, once at 30 DAT and second at 40 DAT @ 100 adults per release. Cotton dipped in 20% honey solution was placed inside the net as food for adults. Adults were allowed to remain in the net for a week and then the net was removed. Observations were then recorded after 30 days on ten randomly selected plants in each genotype. At each observation, total number of leaves and leaf folder damaged leaves were recorded to calculate per cent damage in each genotype. Leaf was considered to be damaged by the leaffolder only when one-third or more of its area showed symptoms. The per cent damaged leaves were converted to adjusted damaged leaves rating (ADLR) using the following formula, which was then converted to 0 to 9 scale. A test was considered valid when damaged leaves in the susceptible check averaged at least 50%.

$$\text{\% damaged leaves in each entry} = \frac{\text{Number of damaged leaves in a hill/plant x 100}}{\text{Total number of leaves in a hill/ plant}}$$

$$\text{Adjusted damaged leaves rating (ADLR)} = \frac{\text{\% damaged leaves in test entry x 100}}{\text{\% damaged leaves in susceptible check}}$$

Based on the adjusted values, entries were rated as follows:

Scale	ADLR
0	No damage
1	1-20%
3	21-40%
5	41-60%
7	61-80%
9	81-100%

In the present study, forty eight rice genotypes were grown in the nursery and after 25 days, transplanted in the main field in rows of 45 hills each at spacing of 20 x 10 cm. Taichung Native 1 (TN 1) was grown as susceptible check and W 1263 as resistant check after every 10 rows, similar to the SES method. In each genotype, three plants/ hills were selected at random and screened, each plant representing one replication. Leaves of each plant in a genotype were covered with a nylon mesh bag and tied at the bottom. A single third instar larva was released on to the leaves from the top of the bag and allowed to feed for 48 hours on the most susceptible stage of the crop, *i.e.*, 30 – 45 DAT (Plate.2). Larvae from the leaf folder culture maintained at IIRR greenhouse as per the standard procedure were used for releases (Padmavathi *et al*, 2013). After 48 hours of feeding, larva was collected and the number of damaged leaves were counted, collected and preserved to estimate the damaged leaf area. Damaged leaves were scanned with Cannon MF 4320-4350 scanner at colour mode with 300dpi image quality. Leaf area fed was measured by using imagej software (Rasband 1997-2016; http://imagej.nih.gov/ij/). The damaged area recorded was converted to adjusted damaged area rating (ADAR) using the following formula:

$$\text{Adjusted damaged area rating (ADAR)} = \frac{\text{Damaged area (mm}^2\text{) in test entry}}{\text{Damaged area (mm}^2\text{) in susceptible check}} \times 100$$

These percentages were converted to 0 to 9 scales as follows:

Scale	ADAR
0	no damage
1	1 to 10%
3	11 to 30%
5	31-50%
7	51-75%
9	more than 75%

In both the methods, genotypes with mean scale score of 0 to 3 were considered resistant, 5 as moderately resistant and 7 to 9 as susceptible.

Results & Discussion

In the first method, the damaged leaves varied from 10.13 to 64.52% with maximum damage in MTU 1160 and minimum damage in W 1263. Adjusted damaged leaves rating ranged from 22.14 to 146.47% in different genotypes with eight entries having damage more than the susceptible check TN1. Based on the scores, six genotypes were found resistant with 3 score including resistant check W1263 and ten were moderately resistant with 5 score. Remaining 32 genotypes were susceptible with 7 and 9 scores (Table 1).

In the special screening method, damaged area varied from 68.41 to 428.81 mm^2 with minimum damaged area in IET 22449 and W 1263 and maximum damaged area in RP Bio 4918-50-13. In the susceptible check TN1, mean damaged area was 268.24 mm^2. Adjusted damaged area rating ranged between 27.06 and 158.08% in various genotypes with four genotypes recording more than 100% damage, higher than the susceptible check, TN1. Based on the scores, six genotypes were found resistant with ≤ 3 score and 19 were moderately resistant with ≤ 5 score. Rest of the 23 genotypes were susceptible showing score range of 7 - 9 (Table 1).

Development of a resistant variety involves continuous effort of screening large number of plant populations and germplasm lines for resistance to rice leaffolder. Leaffolder was considered as a minor and sporadic pest before 1990's and hence, much attention was not given for screening and identification of resistant cultivars. Later during 1985 onwards, Heinrichs *et al* (1985) emphasised the need of identification and breeding of resistant cultivars to combat this pest menace in Asia. Initially, identification of resistant sources was done based on field screening with natural pest populations (Velusamy and Chellaiah,

Table 1. Screening of rice genotypes for resistance to leaffolder, *Cnaphalocrocis medinalis*

Genotype	Method 1		Method 2			Genotype	Method 1		Method 2	
	% ADLR	DS	% ADAR	DS			% ADLR	DS	% ADAR	DS
IET 21850	65.54	7	85.79	9		JGL 21126	81.66	9	101.05	9
IET 22222	75.26	7	95.91	9		JGL 21133	69.21	7	94.27	9
IET 22568	48.41	5	41.27	5		JGL 21794	83.39	9	66.51	7
IET 22552	41.80	5	36.54	5		JGL 21820	90.32	9	38.03	5
IET 22155	22.14	3	29.96	3		JGL 21828	99.77	9	88.35	9
IET 22199	88.53	9	35.50	5		JGL 21851	54.10	5	48.14	5
IET 22223	69.06	7	31.61	5		JGL 21868	65.70	7	57.40	7
IET 22439	67.89	7	137.61	9		JGL 21883	45.52	5	50.88	5
IET 22449	33.48	3	27.06	3		JGL 23634	52.95	5	50.68	5
IET 22486	103.22	9	33.34	5		JGL 23640	49.97	5	59.90	7
IET 22489	33.70	3	50.22	5		JGL 23666	78.29	7	84.78	9
JGL 19621	110.25	9	51.77	7		MTU 1140	43.26	5	50.60	5
JGL 20122	95.81	9	56.07	7		MTU 1153	48.97	5	50.89	5
JGL 20171	110.45	9	59.29	7		MTU 1155	42.24	5	46.43	5
JGL 20624	75.69	7	32.34	5		MTU 1159	68.56	7	158.08	9
JGL 20769	82.56	9	61.64	7		MTU 1160	146.47	9	64.38	7
JGL 20776	47.97	5	72.17	7		MTU 1162	27.68	9	97.55	9
JGL 20777	86.40	9	40.95	5		MTU 1163	36.02	3	27.55	3
JGL 20779	103.39	9	46.53	5		RP 4918-228(S)	62.61	7	62.04	7
JGL 21002	144.37	9	58.01	7		RP Bio 4918-236	129.66	9	100.09	9
JGL 21041	78.62	7	91.68	9		RP Bio 4918-24K	35.68	3	29.20	3
JGL 21066	64.78	7	39.89	5		RP Bio 4918-142	111.76	9	29.10	3
JGL 21075	81.88	9	67.11	7		RP Bio 4918-50-13	72.14	7	49.86	5
JGL 21078	99.41	9	49.55	5		TN 1	100.00	9	100.00	9
JGL 21099	64.43	7	55.01	7		W 1263	23.92	3	27.32	3

ADLR = Adjusted damaged leaves rating; ADAR = Adjusted damaged area rating
Method 1 = SES for rice IRRI method based on damaged leaves
Method 2 = Rapid screening method based on damaged area

1985, Heinrichs *et al*, 1985). However, non- uniform pest pressure and unpredictability of field populations restricted the reliability of the field evaluation. To overcome these limitations, a greenhouse screening method was developed (Waldbauer and Marciano, 1979; Heinrichs *et al.*, 1985). This method involves growing potted plants in the greenhouse and allowing larvae to feed for a prolonged time. Later, Bentur and Kalode (1990) proposed a feeding test to rapidly identify varieties resistant to rice leaffolder in the greenhouse. However, this test has few drawbacks including pupation of the fifth instar larva in case of unsuitable host plant as well as difficulty in accurately assessing the damaged area.

Subsequently, many rice researchers screened germplasm lines in the field under natural populations through SES and identified few cultivars with resistance to rice leaffolder (Heinrichs *et al*, 1985; Velusamy and Chellaiah, 1985; Uthamasamy, 1985; Khan *et al*, 1988; Rekha *et al*, 2001; Anil Verma *et al*, 2015).

However, SES method evaluation of resistance is based on the number of damaged leaves wherein even a slight feeding by the leaffolder larva is considered without taking into account the severity of damage, leading to overestimation of damage. Whereas in the present study, the severity of damage was considered by taking into account only those leaves showing one-third area or more of damage. This gives more accurate estimation of damage due to feeding by leaf folder. Hence, in the present study, more genotypes were found moderately resistant while some of these were graded as highly resistant by SES method. Also, the SES method does not account for insufficient pest pressure as during times of pest escapes whereas the present method offers a reliable alternative in ensuring confirmed pest damage effect through feeding by most damaging third instar larva, through artificial release.

Conclusions

Growing resistant variety is an important tactic accepted by the farmers for the effective management of insect pests. In the present study, an accurate and precise method for rapid field assessment of resistance to rice leaffolder was developed as a reliable alternative to the standard SES method for the identification of resistant sources

and for phenotyping studies in breeding programs for the development of resistant rice varieties.

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Plate 1. Field screening of germplasm lines for resistance to rice leaffolder- SES method

Plate 2. Rapid field screening method for evaluation of resistance to rice leaffolder; A) Field view of screening method B) Covering the leaves of each genotype with a net bag; C) Release of 3rd instar larva inside the net bag; D) Larva and leaf damage after 48 hrs; E) Damaged area measurement with ImageJ

ORIGINAL RESEARCH ARTICLE OPEN ACCESS

Forecasting of Common Paddy Prices in India

Ashwini Darekar and A Amarender Reddy*

National Institute of Agricultural Extension Management (MANAGE), Rajendranagar, Hyderabad 5000030, India
*Corresponding author: anugu.amarender.reddy@gmail.com

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Abstract

Paddy is an important food crop in India and second most in the world. About 35% of net cropped area under paddy and about 50% of the farmers cultivate paddy every year. Farmer's decision making on acreage under paddy depends on the future prices to be realized during harvest period. Hence this paper presents a methodology to forecast prices during harvest period and applied the method to forecast for the *kharif* 2017-18. The time series data on monthly average prices of paddy from January, 2006 to December, 2016 collected from AGMARK was used. ARIMA (Box-Jenkins) model was employed to predict the future prices of paddy. Model parameters were estimated using the R programming software. The performance of fitted model was examined by computing various measures of goodness of fit *viz.*, AIC, BIC and MAPE. The ARIMA model was the most representative model for the price forecast of paddy in overall India. In *kharif* season the paddy is harvested during September – November. The forecast shows that market prices of paddy, would be ruling in the range of Rs. 1,600 – 2,200 per quintal in *kharif* harvesting season, 2017-18.

Keywords: ACF, ARIMA, Box and Jenkins, Forecasting, Moving Average and PACF *etc.*

Introduction

Paddy is one of the most important food crops of India and is second in importance throughout the world. It feeds more than 50 per cent of the world's population. It is the staple food of most of the people in South-East Asia. Asia accounts for about 90 per cent of the world's paddy cultivation and production (Rani *et al.*, 2014). Among the paddy growing countries, India has the largest area under cultivation, though in terms of volume of output, it is second to China. Productivity in India is much lower than in Egypt, Japan, China, Vietnam, USA and Indonesia and even below the world's average (Reddy, 2007; Reddy, 2015). It makes up 42 per cent of India's total food grain production and 45 per cent of the total cereal produced in the country. Each part of the plant has various uses. It is also used in medicine. Paddy bran oil is used for its medicinal properties and is also used as cooking oil. Paddy becomes rice after the removal of husk by threshing. Therefore, rice is a part of paddy.

In India, rice is the most preferred staple food for about 65 per cent of the population. It continues to play a vital role in the country's exports constituting nearly 25 per cent of the total agricultural exports from the country. One-third of the world's paddy cultivation area, is in India. It is grown in almost all the states of India but is mostly concentrated in the river valleys, deltas and low-lying coastal areas of north eastern and southern India. The paddy producing states are Assam, West Bengal, Punjab, Bihar, Madhya Pradesh, Orissa, Andhra Pradesh, Tamil Nadu, Kerala, Karnataka, Maharashtra, Gujarat, Uttar Pradesh and Jammu and Kashmir, which together contribute over 95 per cent of the country's crop. As a result of very good rainfall during monsoon 2016 and various policy initiatives taken by the government, the country has witnessed record food grain production in the current year. As per the forth advance estimates for 2016-17, the total production of Rice is estimated at record 110.15 million tonnes which is also a new record. Production of rice has increased significantly by 4.74 million tonnes (4.54%) than the production of 104.41 million tonnes during 2015-16.

Being a major paddy producing country in world, present study is aimed to forecast the prices of paddy of major producing states of India. As the prices of paddy keep changing from time to time, it creates risks to producers, traders and consumers involved in production, marketing and consumption of paddy. Thus, it is important to forecast the paddy prices. Paddy is grown in both summer and winter seasons. But much of the paddy output comes from the *kharif* crop, sowing of which normally begins with the onset of the Southwest Monsoon. The government fixed the minimum support price (MSP) of paddy at Rs. 1,550 for 2017-18.

This paper applies Autoregressive Integrated Moving Average (ARIMA) forecasting model, the most popular and widely used forecasting model for time series data. Applying ARIMA model Hossain *et al.*, (2006) forecasted three different varieties of pulse prices namely motor, mash

and mung in Bangladesh with monthly data from Jan 1998 to Dec 2000; Wankhede *et al*., (2010) forecasted pigeon pea production in India with annual data from 1950-1951 to 2007-2008; Mandal (2005) forecasted sugarcane production in India; Iqbal *et al.,* (2005) forecasted area and production of wheat in Pakistan; Khin *et al*., (2008) forecasted natural rubber price in world market; Shukla and Jharkharia (2011) forecasted wholesale vegetable market in Ahmedabad; Darekar *et al*., (2015) forecasted onion prices in Lasalgaon and Pimpalgaon market; Assis *et al*., (2010) forecasted cocoa bean prices in Malaysia along with other competing models; Nochai and Nochai (2006) forecasted palm oil prices in Thailand; Masuda and Goldsmith (2009) forecasted world Soybean productions; Cooray (2006) forecasted Sri Lanka's monthly total production of tea and paddy beyond Sept 1988 using monthly data from January 1988 to September 2004. Burark and Sharma (2012) confirmed the suitability of Box-Jenkins univariate ARIMA models in agricultural price forecasting. Paul and as (2010) have attempted forecasting of inland fish production in India by using ARIMA approach.

Methodology and Data:

Data collection

The monthly average price data of paddy for 11 years (from January, 2006 to December, 2016) for Punjab, West Bengal, Uttar Pradesh, Andhra Pradesh and Tamil Nadu has been used for forecasting the prices. As per availability the time series data related to monthly average prices of paddy was collected from AGMARKNET website. Using the data paddy prices were forecasted for harvesting months.

The ARIMA model analyzes and forecasts equally spaced univariate time series data. An ARIMA model predicts a value in a response time series as a linear combination of its own past values. The ARIMA approach was first popularized by Box and Jenkins (1976), and ARIMA models are often referred to as Box-Jenkins models. In this study, the analysis performed by ARIMA is divided into four stages.

Identification Stage: The stationary check of time series data was performed, which revealed that the paddy prices were nonstationary. The nonstationary time series data were made stationary by first order differencing and best fit ARIMA models were developed using the data from January 2006 to December 2016 and used to forecast the prices during harvesting season. Candidate ARIMA models were identified by finding the initial values for the orders of non-seasonal parameters "p"and "q." They were obtained by looking for significant spikes in autocorrelation and partial autocorrelation functions. At the identification stage, one or more models were tentatively chosen which seem to provide statistically adequate representations of the available data. Then precise estimates of parameters of the model were obtained by least squares.

Estimation Stage:ARIMA models are fitted and accuracy of the model was tested on the basis of diagnostics statistics.

Diagnostic Checking: The best model was selected based on the following diagnostics.

(i) Low Akaike Information Criteria (AIC): AIC is estimated by AIC = $(-2\log L + 2m)$, where$m = p+ q$ and L is the likelihood function.

(i) Low Bayesian Information Criteria (BIC): Sometimes, Bayesian Information Criteria (BIC) is also used and estimated by BIC = $\log \sigma 2 + (m\log n)/n$.

(ii) The Mean Absolute Percent Error (MAPE) was used as a measure of accuracy of the models

Forecasting Stage: Future values of the time series are forecasted. R programming software was used for time series analysis and developing ARIMA models and forecasting paddy prices. These methods have also been useful in many types of situations which involve the building of models for discrete time series and dynamic systems. (Granger and Newbold 1970). Originally ARIMA models have been studied extensively by George Box and Gwilym Jenkins during 1968 and their names have frequently been used synonymously with general ARIMA process applied to time series analysis, forecasting and control.

Ansari and Ahamed (2001) applied ARIMA modeling for time series analysis of world tea prices and industrialized countries export prices. Prawin Arya *et.al* (2005) applied Box-Jenkins Approach for Forecasting Copra Wholesale Price Series. Nochai and Titida (2006) used ARIMA model for forecasting oil palm prices. Punitha (2007) used ARIMA model to forecast the arrivals and prices of maize and ground nut in Hubli and Devangere markets in Karnataka state. Moghaddsi and Bita (2008) applied econometric model for wheat price forecasting in Iran. Rabbani *et.al.* (2009) forecasted wheat prices in Bangladesh. Shankar & Prabhakaran (2012) used the ARIMA model for forecasting the milk production in Tamil Nadu. Chaudhari & Tingre (2013) found that ARIMA (1,1,0) was the best fitted model for forecasting of milk production in India.

Results and Discussion

1. Identification

Identification of the model was concerned with deciding the appropriate values of (p,d,q) (P,D,Q). It was done by observing Auto Correlation Function (ACF) and Partial Auto Correlation Function (PACF) values. The Auto Correlation Function helps in choosing the appropriate values for ordering of moving average terms (MA) and Partial Auto-Correlation Function for those autoregressive terms (AR). The ACF and PACF suggest that there is no significant correlation to be captured by an ARMA model (Figure 1).

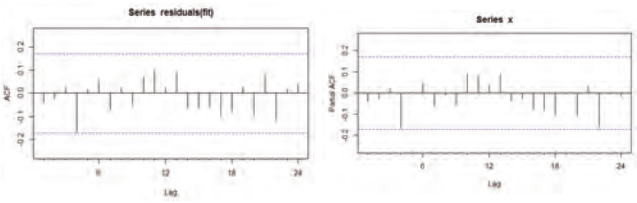

Figure 1:Autocorrelation function (ACF) and Partial autocorrelation function (PACF) of residuals of fitted ARIMA

2. Estimating the parameters

The number of non-zero coefficients in ACF determines order of MA terms and the number of non-zero coefficients in PACF plots determines order of AR terms. Based on the Akaike Information Coefficient (AIC) and Bayesian Information Criteria (BIC), the model ARIMA (1,1,1)(0,0,2), ARIMA (0,1,0), ARIMA (1,1,1)(0,0,1), ARIMA (2,1,1) ARIMA (0,1,0)(0,0,2) ARIMA (0, 1, 0) (0, 0, 2) model was the best fitted model for Punjab, West Bengal, Uttar Pradesh, Andhra Pradesh, Tamil Nadu and India respectively. The results of these coefficients are given in Table 1. ARIMA model was estimated after transforming the variables under study into stationary series through computation of either seasonal or non-seasonal or both, order of differencing. A careful examination of ACF and PACF up to 24 lags revealed the presence of seasonality in the data. However, the series was found to be stationary, since the coefficient dropped to zero after the second lag.

Table 1. Residual analysis of monthly prices of paddy in selected states

Sr. No.	State	ARIMA Model	MAPE	AIC	BIC
1	Punjab	(1,1,1) (0,0,2)	2.12	2019.72	2034.09
2	West Bengal	(0,1,0)	2.77	1365.60	1371.35
3	Uttar Pradesh	(1,1,1) (0,0,1)	5.99	1619.54	1631.04
4	Andhra Pradesh	(2,1,1)	3.86	1471.40	1485.78
5	Tamil Nadu	(0,1,0) (0,0,2)	6.14	1578.90	1587.53
6	India	(0,1,0) (0,0,2)	4.17	1489.66	1498.29

3. Diagnostic checking

Preceding 11 years (2006 - 2016) monthly prices data used for this model. Various methods and literature are studied to judge the appropriate model, the best model has been selected based on the MAPE, minimum AIC and BIC. It has been found that ARIMA (1,1,1)(0,0,2), (0,1,0), (1,1,1) (0,0,1), (2,1,1), (0,1,0)(0,0,2) and (0, 1, 0) (0, 0, 2) model is the best fit for the paddy price data of Punjab, West Bengal, Uttar Pradesh, Andhra Pradesh, Tamil Nadu and India respectively (Table:1).

4. Forecasting

The results of forecast of prices of paddy are shown in the Table 2. The forecasts indicate that there are narrow variations in between the actual and forecasted values of prices of paddy in the selected states and the forecasted values of prices showed an increasing trend in the future months. In *Kharif* season the paddy crop is harvested during September – November. Forecast shows that market prices of paddy, would be ruling in the range of Rs. 1,600 – 2,200 per quintal in *kharif* harvesting season, 2017-18. This forecast is based on past data and model and that actual market price may not turn out to be the same as forecasted. The prices of paddy in the market during harvesting period would be high in Punjab, Uttar Pradesh and Tamil Nadu *i.e.* Rs. 2,000, 1,700 and 1,700 per q respectively. The prices would be low *i.e.* Rs. 1,600 per q in West Bengal and Andhra Pradesh respectively (Table:2). Forecast for the seasonally adjusted paddy prices by using best fit ARIMA model in R programing software shown in Figure 2.

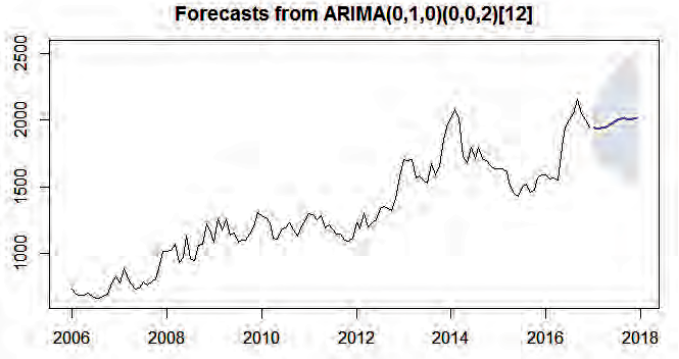

Figure 2: Forecast for the seasonally adjusted paddy prices in India

Table 2. Projected prices for paddy in major producing states during *kharif* harvesting season 2017-18 (Rs./q)

Sr. No.	State	Lower Limit	Mid-point	Upper Limit
1	Punjab	1,200	2,000	2,400
2	West Bengal	1,200	1,600	1,800
3	Uttar Pradesh	1,500	1,700	1,900
4	Andhra Pradesh	1,200	1,600	1,800
5	Tamil Nadu	1,200	1,700	2,000
6	India	**1,600**	**1,800**	**2,200**

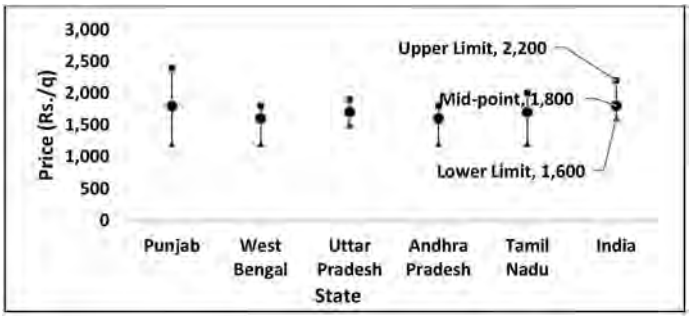

Figure 3. Forecasted paddy prices in India

Forecasted prices of paddy by using ARIMA (0,1,0) (0,0,2) model in India is shown in Figure 3. Thus, from foregoing discussion, it is clearly noted that, such forecasting of future paddy prices can help the farmers to decide the area allocation for paddy in next season and marketing. Besides this, the farmers can also take the decision of marketing of stored paddy immediately or after some months.

Conclusion

The paper forecasted paddy prices for the *kharif* 2017-18 by using historical monthly prices. The paper used ARIMA model to forecast prices. Just like any other method, this technique also does not guarantee perfect forecasts. Nevertheless the model is handy have been successfully used for forecasting in the future. Similar model was used by Almemaychu Amera (2002), Punitha (2007), Darekar *et al.,* (2016) and Jalikatti & Patil (2015) to forecast the prices and arrivals of agricultural commodities and drawn conclusions. ARIMA model is an extrapolation method that requires only the historical time series data on the variable under study. The ARIMA model forecasted prices revealed an increase in the prices of paddy in the future years and also demand for the crop. Hence, increase in the area of production of paddy and their sale in the suitable markets can be planned suitably. This forecast is based on past data and model and that actual market price may not turn out to be the same as forecasted.

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Journal of Rice Research - Authors 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 occasional 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 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 letter 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 and not in arrears of subscription. Authors of invited articles are exempted from this.

Submission of manuscript:

Manuscripts should be sent online to the Journal office to rms_28@rediffmail.com; rmsundaram34@gmail.com as an attachment. All the enclosed figures (as ppt 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 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, and abbreviations used in the paper. 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 and byline should give a clear idea what the articles is about. It should be brief and informative (12-15 words).

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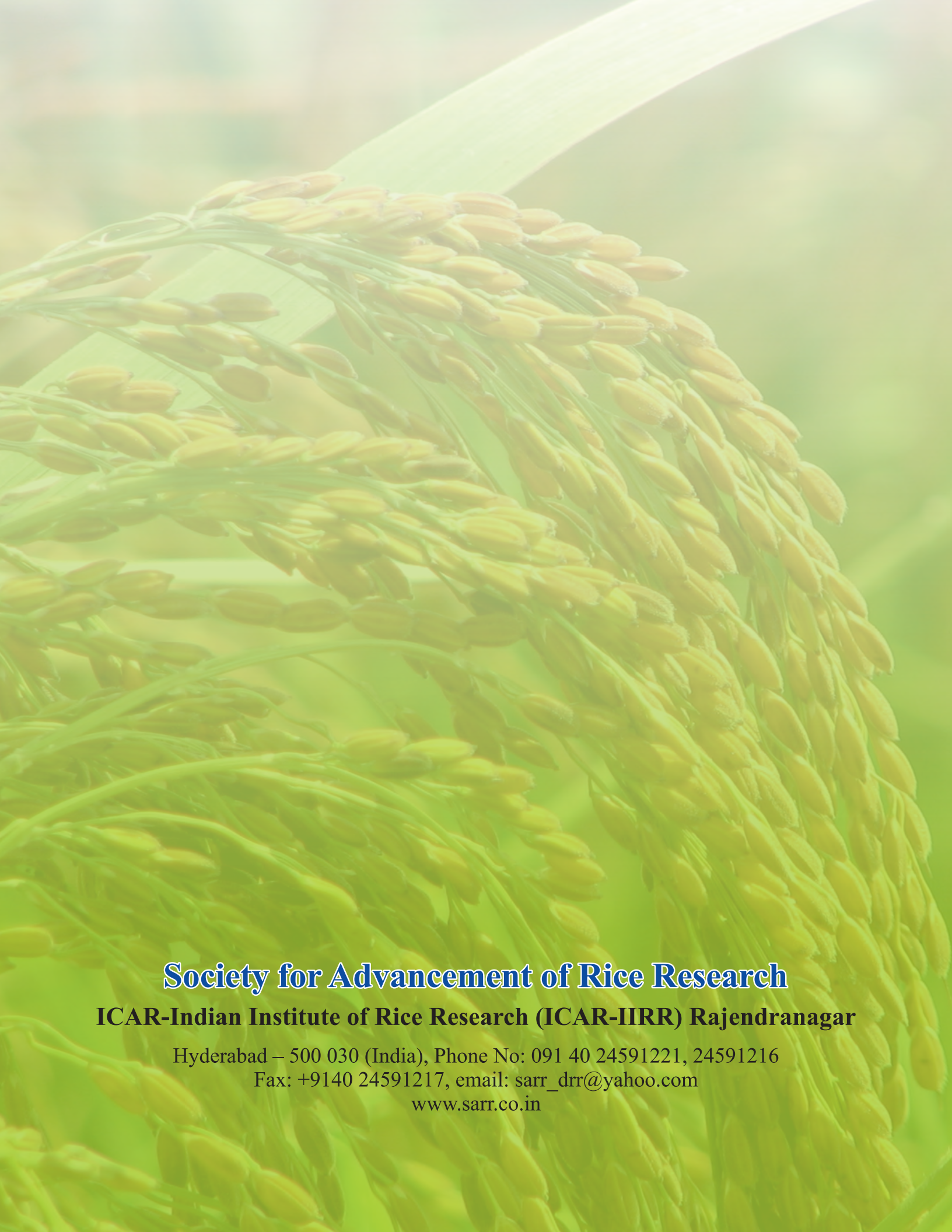
Subba Rao LV, Shobha Rani N, Chiranjeevi M, Chaitanya U, Sudharshan I, Suneetha K, Jyothi Badri and Dipal R Choudhary 2013 DUS Characterization of Rice Varieties. Directorate of Rice Research, Rajendranagar, Hyderabad-500 030, AP, India. 524 pp.

Figures: Photographs and drawings for graphs and charts should be prepared with good contract of dark and light. Figure caption should be brief specifying the crop or soil, major variables presented and lace 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 spellout all the abbreviations. An exponenetial expression (eg. x 103) in the units 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. Follow the articles published in recent journal for table format.



Society for Advancement of Rice Research

ICAR-Indian Institute of Rice Research (ICAR-IIRR) Rajendranagar

Hyderabad – 500 030 (India), Phone No: 091 40 24591221, 24591216
Fax: +9140 24591217, email: sarr_drr@yahoo.com
www.sarr.co.in