

Agronomic Advancement of Rice: A Review

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Abstract: Rice is the second most important food grain in terms of human nutrition and calorie intake, providing more than one-fifth of the total calories consumed worldwide. India, being the center of origin of rice, is the storehouse of a large number of local varieties and landraces. Our state, West Bengal is known as ‘bowl of rice’ as it is the staple food and the major cultivated food crop of the state. From a wild aquatic grass, Indian farmers over the centuries selected and cultivated thousands of varieties of rice; no other cultivated crop has been developed to such an extent to fit thousands of ecological niches all over the country. Local indigenous rice varieties have adjusted over long periods to the ecosystems of their regions including climatic variations, thus ensuring at least minimum levels of output even in bad years. The present review work is carried out to discuss different agronomic features, seed phenotyping as well as the germination physiology along with studying the interrelationship between physiochemical & anatomical characters in rice, all in the light of superior yield potential.

Key Words: *Rice, crop, agronomic features, seed phenotyping, photosynthesis.*

Introduction:

Rice is the world's 2nd most important food crop of human consumption (FAOSTAT, 2014) feeding about 2.5 billion people worldwide. The total annual production of milled rice in the world during 2018-2019 was about 501 million metric tons (USDA FAS, 2019). The Green Revolution technology developed at the International Rice Research Institute (IRRI) in the 1960s increased worldwide rice production. It is imperative to increase rice production in different rice-growing ecosystems to feed the increasing world population (Khush 2005).

Rice belonging to the genus *Oryza*, comprises of four species complexes: *O. sativa*, *O. officinalis*, *O. ridleyi* and *O. granulata* (Ricepedia, 2019). The genus contains 24 recognized species including 22 wild species and 2 cultivated ones: *O. sativa* and *O. glaberrima*. The 23 wild species represent the 10 genome types distributed throughout the tropical and subtropical areas of the world. (Sanni et al. 2013). The 10 different genome types are based on chromosome pairing behavior at meiosis in interspecific hybrids and are designated as AA, BB, CC, EE, FF and GG (diploid genomes) and BBCC, CCDD, HHJJ and HHKK (allotetraploid genomes) (Ge et al 1999, Sengupta et al 2009, Sanchez and Wing 2013).

India is the second-largest producer of rice after China (Patel et al 2019) and inhabitants of Gangetic West Bengal depend on rice as their staple food. West Bengal has diverse local germplasms with special characteristics. Local landraces are facing serious threat of extinction due to hybridization and genetic engineering techniques. Although these techniques are beneficial from the commercial point of view, germplasm preservation of the local varieties is needed for their unique beneficial traits. Thus, such varieties need to be characterized systematically. In the present work characterization of rice genotypes based on

morphological and physiochemical parameters, seed protein profiling, germination efficiency, leaf anatomy and its relation to photosynthetic efficiency and molecular marker-assisted polymorphism detection has been emphasized. In West Bengal, rice is cultivated in three seasons viz., *Aus* (autumn rice), *Aman* (winter rice) and *Boro* (summer rice). Rice cultivation spans diverse agro-climatic regions like irrigated, rain-fed, coastal saline, and flood-prone ecosystems (Rice Knowledge Management Portal). Farmers do not solely rely on yield as the criterion to select a particular rice variety. A variety is also selected based on its ability to fit into a particular cropping system, meet household demand and have practices applicable by the farmers in their land (Samanta and Mallik 2004).

Rice cultivars differ in milling, cooking and textural properties as well as their suitability for different purposes. Genetic traits, environment and cultivation practices including application of fertilizers are responsible for variation in rice quality.

Various strategies to increase the yield potential of rice include conventional hybridization and selection, ideotype breeding, hybrid breeding, exploitation of wild species germplasm, enhancement of photosynthesis, genomic and physiological approaches (Khush 2013). Advances in molecular biology and genomics have opened new avenues to apply innovative approaches to rice breeding.

Agronomic characters

Seed characters:

Seed weight: The rice grain comprises of the hull/husk and the caryopsis. Removal of the hull/husk during initial milling procedures produces brown rice. The rice caryopsis is further composed of pericarp, aleurone layer plus seed coat and nucellus, embryo, and starchy endosperm (Zhou et al 2002). Further abrasive milling removing the outer maternal tissues as byproducts of rice bran and polish, gives the final milled or polished or white rice. Brown rice or the dehusked grain has the lowest protein content and total dietary fibre among the major cereal grains, but the highest content of starch and available carbohydrates (USDA 2016). While the milled rice (white rice) is richest in starch as it is mainly the endosperm portion, the brown rice also contains higher levels of protein content, crude fat, crude ash, phenolics, phytic acids and dietary fibres. Pigments if present, are located in the pericarp (Juliano 2019). Thus the seed weight is the measure of the nutritional components present in the seed/grain, which is further regulated by the grain production factors. The main component of the starch grain being the starch shows differential compositions of the two major forms as the linear chain amylose and the highly branched amylopectin, assembled in a clustered structure formed of granules further being composed of starch molecules laid down in concentric rings. The amylase and amylopectin contents variability in different rice varieties majorly affect their corresponding cooking characteristics, texture, stickiness, water absorption ability & volume expansion, hardness and even the whiteness and gloss of the milled rice (Zhou et al. 2002) further affecting their grain yield and effectiveness in the market from the acceptance and popularity point of view of the market. Among several factors, rice yield depends upon the size and mass of kernels. These factors also determine the commercial value of milled rice based on human perception (Singh et al. 2019).

Seed size: ‘Grain size’ or seed size is an important and most stable component among the seed characters in determining the ‘grain yield’, which in turn is correlated with the grain-filling rate (Fujita et al. 1984). ‘Grain yield’ being the primary economic target or issue is a determining character to choose a particular variety for large scale agricultural crop practice. Thus, apart from the grain-filling time and other environmental conditions including the amount of irrigation water (Guo et al. 2015), which regulate the ‘Grain production’, grain or seed size attains a major point in focus, somewhat indicating larger size pointing towards more yield. Seed shape also plays a role in differential yield study. It is observed that very naturally large grain facilitates more dry matter accumulation over small grain with time in the grain-filling period (Coronel et al. 1983).

Awn: Different varieties of cultivated rice are characterized by mainly awnless seeds or rarely seeds with short awns lacking barbs. It is being speculated that today’s cultivated rice has been domesticated from the wild rice variety, several years ago through different morphological, physiological as well as genetic level changes (Hua et al. 2015), among which, complete loss of awn or if present then in reduced form is a distinct change. Currently, the presence of awn facilitates the process of seed collection, storage and associated human-handled matters.

Aroma: The unique aroma of scented rice grains gets imparted mainly due to the presence of several primary and secondary metabolites which are basically volatile organic compounds (VOCs). In this case, a novel compound named 2-acetyl-1-pyrroline (2AP) has been observed to be the significant factor found as the primary contributor in imparting the unique fragrance in rice. It has been reported that both aromatic and non-aromatic rice varieties possess the characteristic VOC ‘2AP’ but the only difference is the concentration of the potential compound between them (Wani et al. 2016). In scented rice varieties, aroma-causing volatile compounds are synthesized in aerial plant parts and finally get deposited in the mature grains. Also, the availability of primary and secondary metabolites including these VOC’s is highly variable across the different developmental stages of the corresponding rice plant (Hinge et al 2016). This aroma of the rice grain acts as a crucial factor in imposing a premium market value and also gaining consumers’ preference (Wani et al. 2016).

Panicle characters:

The different panicle characters are mainly the ‘yield contributing’ factors that ultimately depend on production efficiency. It has been observed experimentally that lower grain yield occurs due to a lower number of spikelets per panicle, a lower percentage of filled grains (Sun Guo-Xin et al 2015), thus denoting that superior panicle characters correspond to superior yield.

The terminologies related to rice plant morphology are represented in Fig 1.

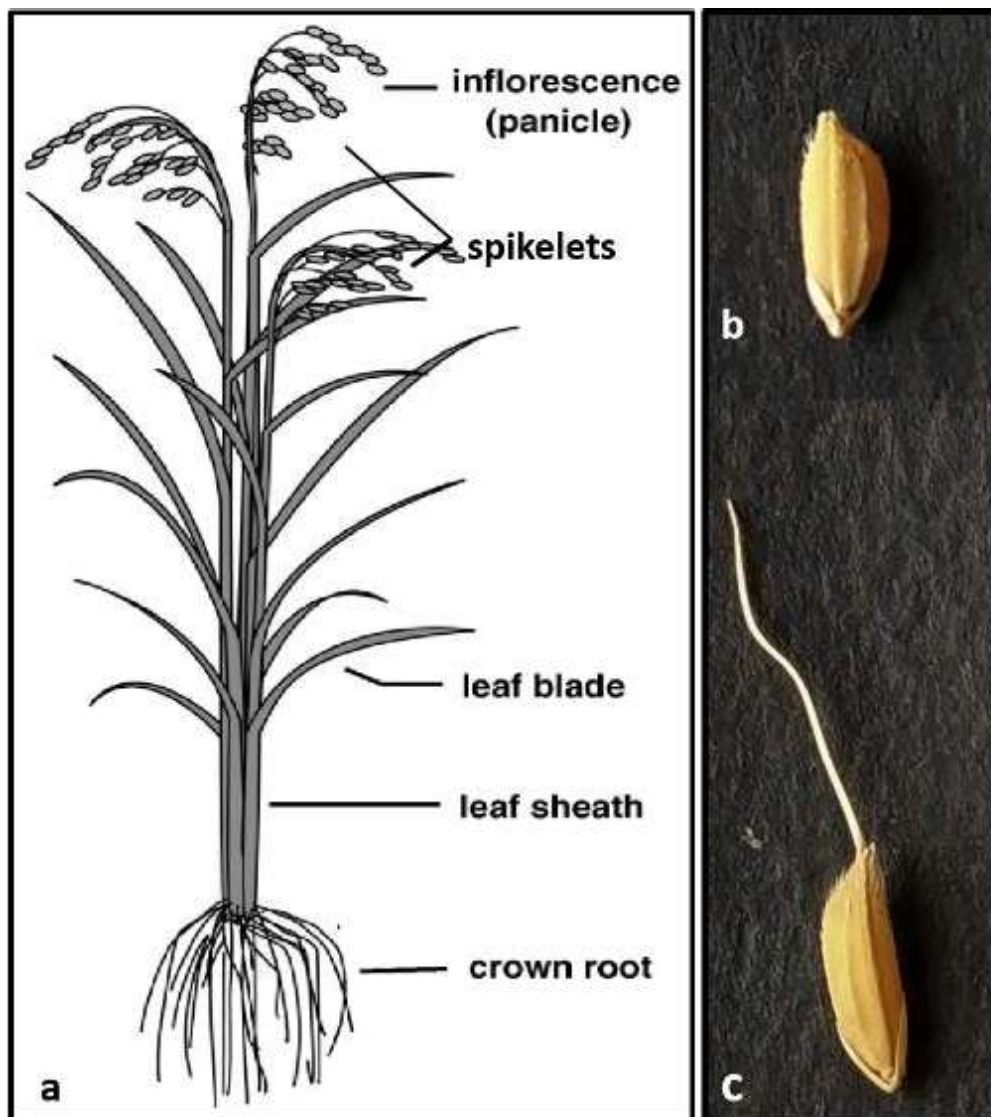


Fig 1. a: A mature rice plant. **b:** A seed without awn. **c:** A seed with awn (adapted from Itoh *et al* 2005)

Study of seed phenotype

Phenomics is the systematic study of phenotypes with the help of automatic modern multifunctional high-throughput phenotyping tools and techniques. One such major technique is the image-based plant phenotyping method involving several image analysis methods to measure and quantify different plant phenotypic traits. Software have been designed to perform specific tasks related to this task managing the analysis of the phenotypic traits of interest. This image-based phenotyping tools provide a vast ease to the huge and time-consuming task of manual image analysis as well as quantification related to the phenotypic plant traits (Zhao *et al* 2019). Man-machine coordination also reduces the chances of errors while measuring the data. The present modern age of plant bioscience is thus progressing towards more and more precision and advancement day by day.

Comparison between wild species and cultivated ones revealed similarity in seed morphology (Kasem *et al* 2010) and endosperm morphology (Shapter *et al* 2008). Chemutai *et al* (2016)

classified African rice genotypes based on alkali digestion (indicating variation in amylopectin chain length) and gel consistency assay. Difference in gel consistency of cooked rice indicated differential expression of waxy (Wx) gene. Screening for better cooking and edible traits such as linear kernel elongation, water absorption and volume expansion as well as fuel consumption can be selected based on the above assays. Four exotic rice varieties of Afghanistan showed wide variations with respect to plant growth (plant length, tiller number, leaf number, days to heading, and maturity); grain yield and panicle number per hill, spikelet number per panicle; physicochemical properties like protein, amylose, and lipid contents; antioxidant activities; and internal structure of endosperm. Such studies help in sustainable selection and cultivation of preferable varieties (Kakar et al 2019). Pre-harvest and post-harvest ageing affect the physical qualities of rice like cooking, pasting and thermal properties. Post cooking, aged rice was found to be harder, fluffier and less sticky than fresh rice, being mainly affected by duration and temperature during storage (Keawpeng et al 2015). Grain traits are highly associated with rice production and serve as key factors for grain yield and its market value (Yao et al 2016). Abiotic and biotic stress resistance and other traits have been successfully introduced from wild species into cultivated rice, resulting in improved cultivated varieties (Vaughan 1994). However, wild species have traits beneficial for use with intrinsically similar starches and functionalities to cultivated rice. Analysis of the morphological and edible properties of the indigenous cultivar seed grain is required for commercial use. Physicochemical tests based on rice chemical composition, cooking quality, gelatinization temperature and physical properties of cooked rice are used to analyze rice germplasm diversity. Rice eating and cooking quality (ECQ) is mainly determined by amylose content, gelatinization temperature and gel consistency (ZhiXi et al 2010).

Germination efficiency

Seed germination is an early and crucial stage in plant life cycle, referring to the complex physiological and biochemical process starting from the uptake of water by the dry seeds and ending with the successful radicle protrusion (Bewly 1997), involving a series of coordinated signal transduction and gene expression regulation, the actual sequence of which is still unknown. A number of exogenous and endogenous factors act in the regulation of the germination procedure and its efficiency including water, as one of the most crucial decisive factors, temperature, light, circadian rhythm, and phytohormones i.e. GA (Gibberellic acid) and ABA (Abscisic acid) being the two main phytohormones that antagonistically regulate seed germination by controlling GA and ABA-responsive functional proteins creating a protein mobilization during the germination process. Thus seed germination efficiency can precisely determine its ultimate seedling growth and even crop yield in the broader prospect (Yang 2013).

Seed vigour or the potential of a seed to germinate rapidly and uniformly under a wide range of field conditions is an essential requirement for agricultural production (Finch-savage et al 2015). Other measures of vigorous varieties include seed filling rate, germination percentage and uniform seedling growth. These features are beneficial from the commercial point of view of the productivity of a variety. High seed filling rate and short seed filling duration

caused a significant decrease in the total starch and amylose contents and an increase in the amylopectin content (Wang et al 2020). The role of physio-morphological, biochemical and molecular marker analysis in rapid germination of seeds and seedling biomass has been reviewed in detail by Mahender et al (2015). Major QTLs for seedling vigour index of direct seeded rice along with abiotic stress tolerance capacity contribute to screening efficiency of rice varieties.

Protein profile

Rice has a relatively low protein (7% to 10% DW) compared with other cereals (Khush 1997). Storage proteins are accumulated during seed development and are coded by multi gene families. Rice storage proteins are of four types: albumins, globulins, prolamin, and glutelin (Fig 2). The nature of bands on SDS page is genotype specific and can serve as reliable marker due to their polymorphic nature and normally being unaffected by environmental conditions during the seed development and maturation (Sadia et al 2009; Mehtre and Dahat 2001). Protein bands detected in specific rice varieties could serve as biochemical markers. Genetic diversity of storage proteins can be thus beneficial in pedigree analysis and nutritional quality improvement. Endosperm is the reservoir of starch and proteins are accumulated during seed development. Several transcription factors are involved in the expression of the genes for storage substances. The rice *flo2* mutation resulted in reduced grain size and starch quality. Map-based cloning identified *FLOURY ENDOSPERM2* (*FLO2*), a member of a novel gene family conserved in plants, as the gene responsible for the rice *flo2* mutation. *FLO2* was abundantly expressed in developing seeds coincident with the production of storage starch and protein, as well as in leaves, while abundant expression of its homologs was observed only in leaves. The *flo2* mutation decreased the expression of genes involved in the production of storage starch and storage proteins in the endosperm. Differences between cultivars in their responsiveness of *FLO2* expression during high-temperature stress indicated that *FLO2* may be involved in heat tolerance during seed development. Overexpression of *FLO2* enlarged the size of grains significantly. These results suggest that *FLO2* plays a pivotal regulatory role in rice grain size and starch quality by affecting storage substance accumulation in the endosperm (She et al 2010).

Studies have been carried out extensively on rice proteome. Overall, 480 reproducible protein spots were detected by two-dimensional electrophoresis on pH 4-7 gels and 302 proteins were identified by MALDI-TOF MS and database searches. Together, these proteins represented 252 gene products and were classified into 12 functional categories, most of which were involved in metabolic pathways. Database searches combined with hydropathy plots and gene ontology analysis showed that most rice seed proteins were hydrophilic and were related to binding, catalytic, cellular or metabolic processes. (Yang et al 2013).

He et al (2013) carried out protein profiling in the germinating rice seeds. In total, 673 proteins were identified and could be sorted into 14 functional groups. The largest group was metabolism related. The metabolic proteins were integrated into different metabolic pathways to show the style of reserves mobilization and precursor preparation during the germination.

Analysis of the regulatory proteins indicated that regulation of redox homeostasis and gene expression also play important roles for rice seed germination.

Interrelationship between the physiochemical & anatomical characters

Genomic DNA isolation and molecular phylogenetic study:

Completion of the rice genome sequence (Yu et al 2002) and advances in transcriptomics research has made it possible to identify and map a number of genes through linkage to DNA markers precisely. Genes for resistance to pathogenic infection and abiotic stress are commonly linked to markers. Molecular marker-aided selection (MAS) combined with conventional breeding approaches help to identify the individual genotypes associated with grain quality, abiotic and biotic stress tolerance features, which can be used to improve the breeding efficiency. ZhiXi et al 2009 developed 51 gene-tagged molecular markers according to sequence variations in 18 starch synthesis-related genes from 16 typical rice cultivars. This genotypic differentiation of germplasm provides the basis for selection and breeding of new elite rice varieties. Artificial selection is normally based on desired phenotypic traits and novel multiple alleles might exist in wild rice species. Correlation in agronomic characteristics, aroma and SSR markers helped in selection of favorable hybrid varieties which can be utilized in breeding programmes (Kibria et al 2008). Depending upon quantification of genetic diversion among aromatic accessions based on SSR markers Alijumaili et al (2017) identified and selected accessions for varietal development in breeding programs. Construction of dendrogram to identify genetic similarities among these genotypes showed that accessions from the same regions cluster mostly together implying a correlation between molecular groupings and geographical source. Combinatorial analysis based on seedling morphology in response to salinity stress and SSR markers linked with salt tolerance quantitative trait loci helped to detect the true salt tolerant genotypes (Ali et al 2014). The authors successfully identified three SSR markers for salt resistance screening. The role of molecular markers and marker-assisted selection for polygenic traits, abiotic and biotic stress resistance, agronomic traits and grain quality has been reviewed in details by Jena et al (2008).

Random Amplified Polymorphic DNA (RAPD), a PCR based marker analysis is performed routinely to assess the genetic diversity and genetic similarity quotient among different cultivars, using random decamer primers. Conservation of genetic variability paves way for germplasm preservation as well as selection of genetically diverse cultivars for crop improvement programs. Dendrogram analysis based on similarity coefficient helps to group cultivars into clusters and is indicative of intraspecific or intraspecific hybridization. Such an approach has been investigated by several authors (Rahman et al 20016, Pervaiz et al 2010, Jena et al 2010, Rajani et al 2013, Abdulrazzak 2014, Rubel et al 2014). Single and multigrain Aman varieties provided a platform to identify improved varieties and grain relatedness at DNA level (Mitra et al 2017). 14 improved varieties and 27 landraces of rice varieties cultivated by Indian farmers subjected to morphological and SSR marker analysis

revealed the possible linkage or pleiotropic effects of the genomic regions associated with certain grain quality traits (Pachauri et al 2013).

Banerjee et al 2010 pointed out that biochemical (isozyme and total soluble protein) and molecular (RAPD) polymorphism profile among 18 traditional and improved rice varieties can substantiate morphological data to establish distinctiveness among the varieties. Zhang et al 2011 correlated population structure and genetic diversity and noted that gene diversity and across the genome of two populations might help to identify candidate genes for the traits under domestication and artificial selection.

Photosynthetic efficiency:

Enhanced photosynthesis by conventional breeding

Leaf is intricately linked to plant yield as it is the site of transpiration and photosynthesis. In rice plant, the flag leaf below the panicle provides photosynthetic product to the panicle (Wang and Li 2005). Crops with an enhanced photosynthetic mechanism would better utilize the solar radiation that can be translated into yield. This subsequently will help in producing more grain yield, reduce water loss and increase nitrogen use efficiency, especially in hot and dry environments.

Analysing rates of individual leaf photosynthesis (P_n) is necessary for yield increase. The P_n values of the two backcrossed inbred lines at an ambient CO_2 concentration of $370 \mu\text{mol mol}^{-1}$ as well as at a saturating concentration of CO_2 were 20–50% higher than those of the parental *indica* varieties. In comparison to the parent, the inbred lines did not show a higher amount or activity of Rubisco under similar leaf nitrogen contents. However higher mesophyll conductance with respect to CO_2 flux was attributed to better development and higher density of mesophyll cells. These lines had higher electron transport and growth rates. Since atmospheric CO_2 is expected to increase in the future; it is possible to obtain significantly higher P_n under enhanced as well as normal atmospheric CO_2 levels (Adachi et al 2014). He et al 2016 reported that photosynthetic rate (in the flag leaf and 13th leaf) of two lines obtained by *indica* x *japonica* backcross was 20% higher than the high yielding *indica* parent. Although there was no consistent difference in stomatal conductance and Rubisco content, increase in mesophyll cell number and conductance was related to the higher photosynthetic efficiency.

Enhanced photosynthesis by conversion of C_3 to C_4 :

A striking approach towards increasing the agricultural productivity of rice is to convert the C_3 photosynthetic mechanism to C_4 . The efficiency of C_4 photosynthesis has generated a great interest and some serious efforts in engineering a functional C_4 photosynthetic pathway into C_3 crop species i.e., rice aiding in higher rates of photosynthesis in the experimental rice plants. As the evolution of C_4 plants took place from C_3 ones over a period of 30 million years, it is expected that key genes and gene regulatory pathways were inherited from the C_3 plants. Hence several techniques including genome-wide deep-sequencing, gene discovery and editing have been applied towards engineering C_4 rice plants.

In C_3 plants, photosynthetic reactions occur primarily within the mesophyll cells where ribulose-1, 5-bisphosphate carboxylase/oxygenase (Rubisco) fixes CO_2 in the Calvin cycle. In hot dry environments, however, this fixation reaction is competitively inhibited by O_2 , leading to the energetically wasteful process of photorespiration. C_4 plants evolved to overcome this inefficiency, through the development of mechanisms that concentrate CO_2 around Rubisco. In the C_4 photosynthesis, β -Carbonic Anhydrase (CA), present in a localized way in the cytosol of the leaf mesophyll cells, is responsible for the formation of HCO_3^- from CO_2 , which in turn acts as the substrate for the O_2 -insensitive phosphoenolpyruvate (PEP) carboxylase in the initial step of C_4 photosynthetic pathway where thus through this CO_2 fixation, a four-carbon first stable compound Oxaloacetic acid (OAA) is formed. CO_2 is thus first fixed into OAA by the (PEP) carboxylase. The four-carbon compound is then shuttled to a separate compartment (either within the same cell or in another cell) where it is decarboxylated to release CO_2 for fixation by Rubisco in the Calvin cycle. Decarboxylation is carried out by one or more of three enzymes — NAD-malic enzyme (NAD- ME), NADP-ME, phosphoenolpyruvate carboxykinase (PEP-CK), depending on the biochemical subtype. The active role of Carbonic Anhydrase (CA) in C_4 photosynthesis, as well as plant growth, paved the path to explore its potentiality to generate a functional C_4 rice plant exhibiting a higher rate of photosynthesis via proper genetic regulation and expression of at least some of the CA in rice mesophyll cell cytosol (Chatterjee et al 2021). Also the studies conducted by Chatterjee et al (2021) showed that a CA gene mutant (*low CO₂ responsive mutant 1, lcr1*) display stunted growth at ambient pCO_2 whereas, their growth restored at elevated pCO_2 .

A typical monocot C_4 plant exhibits the Kranz anatomy with every mesophyll cell is in direct contact with an adjacent bundle sheath cell which in turn is directly in contact with a vein. The current strategy is aimed at generating C_4 photosynthesis with Kranz anatomy, the so-called “proto-Kranz” anatomy. In order understand the underlying mechanism; several researches have been focused on comparative transcriptomic studies that provide genome-wide expression profiles in C_3 versus C_4 plants, at different stages of C_4 development and in bundle sheath versus mesophyll cells (Wang et al 2017).

Rice exhibits higher mesophyll transfer conductance, greater stromal CO_2 content, lower CO_2 compensation points at warm temperature and less oxygen sensitivity of photosynthesis than cool temperate grasses. Rice vein length per leaf, mesophyll thickness and intercellular space volume are intermediate between those of most C_3 and C_4 grasses, indicating that the introduction of Kranz anatomy into rice may not require radical changes in leaf anatomy; however, deep lobe of chlorenchyma cells may constrain efforts to engineer C_4 photosynthesis into rice (Sage et al 2009).

In order to achieve the proto-Kranz anatomy, Wang et al (2017) introduced maize *GOLDEN2-LIKE* genes leading to increased mitochondria and chloroplast development followed by increased accumulation of photosynthetic enzymes and increase in volume of sheath cells surrounding the veins.

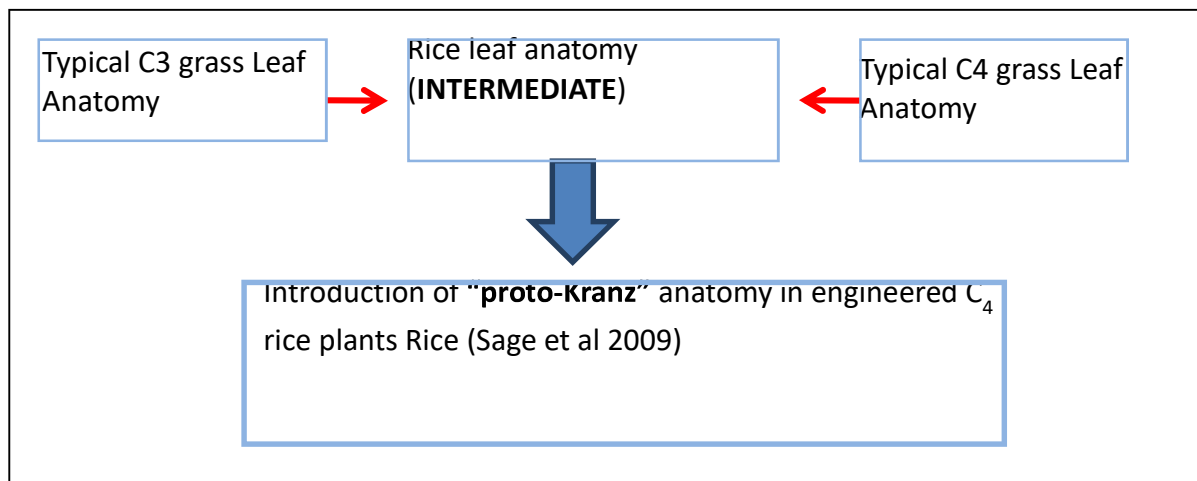


Fig 2: Enhancing photosynthetic efficiency in rice plant

Aiming to determine the photosynthetic light-use efficiency of a leaf, Song et al (2016) developed a 3-D model which pointed out that different chloroplasts can experience drastically different light conditions, even when they are located at the same distance from the leaf surface; bundle sheath extensions, which are strips of parenchyma, collenchyma or sclerenchyma cells connecting the vascular bundles with the epidermis, can influence photosynthetic light-use efficiency of leaves; and chloroplast positioning can also influence the light-use efficiency of leaves (Fig 3).

Leaf hydraulic conductance and mesophyll conductance both represent major constraints to photosynthetic rate. Leaf hydraulic conductance inside xylem, leaf hydraulic conductance outside xylem, stomatal conductance and anatomical and structural leaf traits in 11 *Oryza* genotypes were investigated by Xiong et al (2016) to elucidate the correlation of H₂O and CO₂ diffusion inside leaves. All of the leaf functional and anatomical traits varied significantly among genotypes and it were proved that leaf hydraulic conductance and mesophyll conductance are related to leaf anatomical and structural features.

Conclusion

The present study reviews an overall analysis of seed morphology and agronomic characters to explore the worldwide focus on rice as a major food crop. Additionally from the further review of literature, it was established that distinct physiochemical, as well as molecular techniques, were extensively studied in different rice varieties. Molecular techniques like marker-assisted selection with a combination of conventional breeding in correlation with agronomic characters might become more useful in exploration of the rice indigenous varieties present. Morphological markers are reliable means of superior varietal selection. However, detection of QTL is limited in this case due to the effect of differential environmental response. Biochemical (isozyme) markers on the other hand have been used to

study linkage relationships and for genetic analysis (Agarwal et al 2008) in rice. Although conventional breeders depend on a combination of these techniques; environmental influence, role developmental stage and a low number of biochemical markers hinder unbiased selection. These limitations are largely overcome by the use of DNA markers. Genome Wide Association Studies (GWAS) involving statistics based phenotypic and genotypic data correlation in order to reveal markers located adjacent to the locus controlling trait of interest (Shabir et al 2017).

As growing of local conventional cultivars is highly cost-effective thus more agricultural practices including these local varieties must be encouraged. Thus from the present overall study of seed morphology and agronomic characters of rice basically might establish a small but interesting avenue for future aspects by exploring them at genetic and molecular level.

Future prospects

Rice is a major food crop in the cereal group around the world; so major attention remains essential to improve yield and quality of rice. This task can be achieved by harnessing novel alleles from available germplasm, including wild species and the use of modern molecular techniques helpful in developing high yielding rice varieties. In this situation, it is supposed that molecular marker application in genetic mapping will enable the rice breeders to detect the genes controlling agronomically important traits. The high-throughput techniques result in discovery of molecular markers that will be useful in identifying the rice genotypes carrying desired characters as these have been effectively used to develop linkage maps and mapping genes required for varietal development. In general, the selection of a molecular marker technique is based on reliability, statistical power and level of polymorphisms. When these marker techniques reach a higher degree of automation then it will be suitable to use DNA markers directing to a new “Green Revolution” in the agricultural world. Presently, the enormous development of more efficient DNA markers will go on in future, because they can serve as an important tool for plant breeders and geneticists to develop the cultivars of rice for food security and sustainable productivity.

Seeds comprise a protective covering, a small embryonic plant, and a nutrient-storage organ rich in protein. Seed storage proteins (SSP) have been studied for decades by cell biologists, and many of the complicated aspects of their processing, assembly, and compartmentalization are now well understood. While much of the data from mass spectrometry-based proteomic analysis of seeds is descriptive, it has nevertheless provided a preliminary metabolic picture explaining much of their biology. Contemporary studies are moving more toward analysis of protein interactions and posttranslational modifications, and functions of metabolic networks.

Many aspects of the biology of seeds make them an attractive platform for heterologous protein expression.

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