IDENTIFICATION AND INVESTIGATING OF GLYCEMIC POTENTIALITY IN GENOTYPE VARIATIONS IN RICE

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Abstract:

The world is confronting a worldwide ascent in passings connected with non-transferable infections (NCDs, for example, diabetes mellitus, heftiness and cardiovascular infirmities. An expected 630 million individuals in creating and created nations are projected to contract diabetes continuously 20301. Moreover, the worldwide frequency of weight has expanded two-overlap, influencing even the more youthful population2. In 2015, 31% of all worldwide passings were expected to cardiovascular disease3. It is right now the main source of death on the planet. These disturbing wellbeing insights require an attention on diet-based healthful intercession across the whole financial shopper range. Along these lines, crop reproducing programs must be surveyed fully intent on expanding the edibility of boring items. For example, staple cereals with gradually absorbable grains can be created by lifting the extent of amylose and safe starch (RS) divisions. This is normally achieved by expanding the extent of amylose or long chain amylopectin to decrease glycemic reaction.

Introduction

Working on the healthful nature of rice grains through balance of bioactive mixtures and micronutrients addresses a proficient method for tending to nourishing security in social orders which rely intensely upon rice as a staple food. White rice makes a significant commitment to the calorific admission of Asian and African populaces, yet its healthful quality is poor contrasted with that of pigmented (dark, purple, red orange, or brown) variations. The mixtures answerable for these shading varieties are the flavonoids anthocyanin and proanthocyanidin, which are known to have dietary benefit. The fast headway made in the advancements hidden genome sequencing, the examination of quality articulation and the securing of worldwide 'omics information, hereditary qualities of grain pigmentation has set out original open doors for applying atomic reproducing to work on the healthy benefit and usefulness of pigmented rice. This survey gives a report on the dietary benefit and medical advantages of pigmented rice grain, exploiting both native and present day information, while likewise portraying the current methodologies taken to unraveling the hereditary premise of pigmentation.

Hostile to oxidant Activity

Dietary enemies of oxidants address a powerful method for fighting the aggregation of destructive responsive oxygen species and of adjusting the redox status of the body. Examination of concentrates produced using pigmented rice grain has shown that the phenolic intensifies tocopherol and anthocyanin are proficient neutralizers of receptive oxygen species, while creature tests have demonstrated that these mixtures are bioavailable. A few investigations have shown that the raised enemy of oxidation movement displayed by pigmented rice grains (most uniquely by dark rice) can be utilized to alleviate the fiery reaction

Hostile to diabetic Activity

The grain of some customary pigmented rice assortments have shown to be powerful in supporting glucose homeostasis, and are consequently

valuable for the administration of diabetes mellitus. Not at all like white rice grain utilization, which raises blood glucose levels, consuming pigmented grain can lessen blood glucose levels. Concentrates of pigmented rice grain and wheat have been displayed to successfully hinder the action of endogenous α-amylase and α-glucosidase, accordingly repressing the transformation of starch to glucose in the small digestive tract, which goes about as a wellspring of safe starch to be used by stomach microbiota in the colon. While removes produced using both red and purple grain have been accounted for to restrain α-glucosidase movement, just the previous was successful in likewise hindering α-amylase action. The anthocyanins found in the entire grain of dark rice went about as a strong inhibitor of β-glucosidase, consequently deferring the assimilation of sugars. Concentrates of dark rice grain have additionally been displayed to prompt the maintenance and recovery of pancreatic beta cells. Generally speaking, the counter diabetic impacts of pigmented rice appear to emerge from a synergistic impact of anthocyanin, proanthocyanidin, vitamin E, γ-oryzanol, and different flavonoids Black rice removes decreased blood glucose levels more rapidly than did extricates from red rice, a distinction which was ascribed to the presence of cyanidin 3-glucoside, a compound which enacts insulin awareness, glucose take-up, and adiponectin discharge. In any case, large numbers of the dark rice are low in its amylose content and after processing the vast majority of the anthocyanins collected in aleurone will be lost, subsequently not really would have low GI property when consumed as processed rice.

Objectives.

- Identify the GI in Rice
- Investigating the various genotype in rice
- Health benefits of in rice in comparison with various rice's.

Literature Review

Maria Krishna de Guzman (2017) Rice lines with more slow starch absorbability give valuable open doors in alleviating the worldwide ascent in type II diabetes and related non-transmittable sicknesses. Notwithstanding, evaluating for low glycemic list (GI) in rice rearing projects is beyond the realm of possibilities because of time and cost imperatives. This study assessed the possibility of utilizing in vitro cooked grain amylolysis, starch activation designs during seed germination, and variety in starch construction and creation in the full grown seed to separate examples of starch edibility. Preparation examples of complete starch, safe starch, amylose and amylopectin chains, and free sugars during seed germination uncovered that the interaction is comparable to assimilation in the human gastrointestinal plot. The mix of these biochemical markers can be utilized as an elective measure to foresee GI. Moreover, transcriptome investigation of put away mRNA records in high and low GI lines identified contrasts in starch digestion and affirmed the significance of seed stockpiling pathways in impacting absorbability. Pathway investigations upheld by metabolomics information uncovered that safe starch, cell divider non-starch polysaccharides and flavonoids conceivably add to more slow edibility. These new bits of knowledge can direct accuracy reproducing projects to deliver low GI rice with adequate cooking quality to assist with relieving the weight of diet-related way of life infections.

Ming MIAO (Oct 2013) The connection between sugar admission and wellbeing is turning out to be progressively significant for customers, especially in the space of glycemic record (GI) and expanded

energy-delivering starches. According to a physiological perspective, gradually absorbable starch (SDS) conveys a sluggish and supported arrival of blood glucose alongside the advantages coming about because of low glycemic and insulinemic reaction. SDS has been embroiled in a few medical issues, including diabetes, weight, and cardiovascular infections (metabolic conditions). It might likewise have business potential as a clever practical fixing in an assortment of fields, like sustenance, medication, and agribusiness. The current audit surveys this type of processing by breaking down strategies to get ready and assess SDS, factors influencing its change, its medical advantages, and its applications.

Sang-Kyu Lee (2007) ADP-glucose pyrophosphorylase (AGP) catalyzes the first dedicated advance of starch biosynthesis in quite a while. To distinguish AGP isoforms fundamental for this biosynthetic cycle in sink and source tissues of rice plants, we examined the rice AGP quality family which comprises of two qualities, OsAGPS1 and OsAGPS2, encoding little subunits (SSU) and four qualities, OsAGPL1, OsAGPL2, OsAGPL3 and OsAGPL4, encoding enormous subunits (LSU) of this protein heterotetrameric complex. Subcellular restriction concentrates on utilizing green fluorescent protein (GFP) combination develops demonstrate that OsAGPS2a, the result of the leaf-special record of OsAGPS2, and OsAGPS1, OsAGPL1, OsAGPL3, and OsAGPL4 are plastid-designated isoforms. Conversely, two isoforms, SSU OsAGPS2b which is a result of a seed-explicit record of OsAGPS2, and LSU OsAGPL2, are restricted in the cytosol. Examination of osagps2 and osagpl2 freaks uncovered that an injury of one of the two cytosolic isoforms, OsAGPL2 and OsAGPS2b, makes a contracted endosperm due a noteworthy decrease in starch blend. In leaves, be that as it may, just the osagps2 freak appears to seriously lessen the temporary starch content. Strangely, the osagps2 freak was indistinct from wild sort during vegetative plant development. Western blotch examination of the osagp freaks and wild sort plants showed that OsAGPS2a is a SSU isoform fundamentally present in leaves, and that OsAGPS2b and OsAGPL2 are the major SSU and LSU isoforms, individually, in the endosperm. At last, we propose a spatiotemporal complex model of OsAGP SSU and LSU isoforms in leaves and in creating endosperm of rice plants.

MATERIALS AND METHODS

The present investigations were conducted at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Directorate of Rice Research, Rajendranagar, Hyderabad and Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India during the years 2014 to 20.

D2 ANALYSIS

Observations were made on 53 genotypes for thirteen characters and the data were subjected to D2 analysis.

MATERIALS

Seeds of 53 genotypes collected from various place were utilized for the study. The details of the materials are presented in Table 1.

METHODS

Field Plot Technique

Seeds of the 53 genotypes were sown in raised nursery beds during Late Samba(September-January), 2010. The seedlings were transplanted to the main field at the rate of one seedling per hill, after 25 days, with the spacing of 20 cm between rows and 15 cm between plants ina row. A uniform population of 20

plants, in a row of 3 m length, was maintained. The rows were laid in randomized block design, replicated thrice (Plate 1).

Table 1. List of genotypes selected for D2 analysis

Genotype code	Varieties/ Cultures	Origin
G1	ADT 36	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G2	ADT 37	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G3	ADT 38	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G4	ADT 39	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G5	ADT 40	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G6	ADT 41	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G7	ADT 42	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G8	ADT 43	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G9	ADT 44	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G10	ADT 45	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G11	ADT 46	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G12	ADT 47	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G13	ADT 48	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G14	ADT 49	Tamil Nadu Rice Research Institute (TRRI), Aduturai, Tamil Nadu, India.
G15	CR 1009	Central Rice Research Institute (CRRI), Cuttack, Orissa, India.
G16	BPT 5204	Agricultural college, Bapatla, Andhra Pradesh, India.
G17	IR 64	International Rice Research Institute (IRRI), Philippines.
G18	IMPROVED WHITE PONNI	Paddy Breeding station, Coimbatore, Tamilnadu, India.
G19	TRY-1	Agricultural College and Research Institute, Trichy, Tamil Nadu, India.
G20	TRY-2	Agricultural College and Research Institute, Trichy, Tamil Nadu, India.
G21	TRY-3	Agricultural College and Research Institute, Trichy, Tamil Nadu, India.
G22	CSR-30	Central Saline Soil Research Institute (CSSRI), Karnal, Haryana, India.
G23	AURC39	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G24	CO 49	Paddy Breeding station, Coimbatore, Tamil Nadu, India.
G25	AURC1	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G26	AURC3	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G27	AURC4	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G28	AURC5	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G29	AURC6	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G30	AURC7	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G31	AURC8	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G32	AURC9	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G33	AURC10	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G34	AURC11	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G35	AURC12	Plant Breeding Farm, Faculty of

		Agriculture, Annamalai University, Tamil Nadu, India
G36	AURC14	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G37	AURC15	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G38	AURC16	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G39	AURC18	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G40	AURC20	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G41	AURC22	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G42	AURC23	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G43	AURC25	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G44	AURC26	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G45	AURC28	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G46	AURC29	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G47	AURC30	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G48	AURC31	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G49	AURC34	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G50	AURC35	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G51	AURC36	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G52	AURC37	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India
G53	AURC38	Plant Breeding Farm, Faculty of Agriculture, Annamalai University, Tamil Nadu, India

Observations Recorded

Thirteen characters were recorded on single plant basis in ten randomly selected plants in each of the genotype per replication. The following economic characters were studied for D2 analysis.

Days to first flower (DF)

The number of days taken from sowing to emergence of primary panicle in randomly selected plants in each genotype were recorded.

Plant height (PH)

The height of the plant was measured from the ground level upto the tip of the panicle and measured in centimeter.

Number of productive tillers per plant (NPT)

The total number of panicle bearing tillers were counted in eachhill at the time of harvest and recorded.

Panicle length (PL)

The length of the primary panicle of each plant from the neck ofthe panicle to the tip was measured and recorded in centimeter.

Filled grains per panicle (FGP)

The total number of fully developed and well filled grains in the primary panicle of each plant was counted and recorded.

Hundred grain weight (HGW)

The weight of 100 randomly selected grains in each plant was recorded and expressed in grams.

Grain length (GL)

Five well filled randomly selected grains were used to measure the length with Mitutoyo micrometer from each sample. The average was calculated and expressed in millimeter.

Grain breadth (GB)

Five well filled randomly selected grains were used to measure the breadth with Mitutoyo micrometer from each sample. The average was calculated and expressed in millimeter.

Grain L/B ratio (GLBR)

The ratio of grain length to grain breadth was computed as grain

L/B ratio.

Kernel length (KL)

Grains hulled in Satake dehusker were used to measure brown rice length with Mitutoyo micrometer. Five randomly selected kernels from each sample were measured, average worked out and expressed in millimeter.

Based on average length, kernels were classified as narrated by Standard Evaluation System (IRRI, 1996).

Grain size	Length (mm)
Extra long	> 7.50
Long	6.61 to 7.50
Medium	5.51 to 6.60
Short	< 5.50

Kernel breadth (KB)

Grains hulled in Satake dehusker were used to measure brown rice breadth with Mitutoyo micrometer. Five randomly selected kernels from each sample were measured, average worked out and expressed in millimeter.

Kernel L/B ratio (KLBR)

The ratio of kernel length to kernel breadth was computed as kernel L/B ratio.

Based on the ratio, the kernels were classified as narrated by Standard Evaluation System (IRRI, 1996).

Grain size	Length/Breadth ratio
Slender	> 3.01
Medium	2.01 to 3.00
Bold	1.01 to 2.00
Round	1.00 or less

Grain yield per plant (GYD)

The weight of dried and cleaned grains from a single plant was taken and expressed in grams.

STATISTICAL ANALYSIS

Genetic divergence

Mahalanobis D2 statistic was used for estimating the genotypic divergence among fifty three genotypes. The D2 statistic between the populations as estimated from the sample on the basis of 'P' character is,

$$D^2P = \sum_{i=1}^{P}\sum_{j=1}^{P}(\lambda ij)\sqrt{i}\sqrt{j}$$

Where,

ij = Reciprocal matrix to the pooled common dispersion matrix obtained from the error matrix.

i = Difference in mean values for the ith character of the two populations. j = Difference in mean values for jth character of the two populations.

Accordingly error variance, covariance matrix was obtained. The correlated variables were transformed into uncorrelated variables by pivot condensation method as given by Rao (1952). The actual values of D2 between any two variables were obtained by squaring and adding differences corresponding to the transformed mean values of the two genotypes.

Clustering pattern

For grouping the genotypes into different clusters, the criterion suggested by Rao (1952) was followed. Any two populations belonging to the same cluster on the average should show smaller D2 than those belonging to different clusters. To start with, two closely associated types with the lowest D2 values were selected and a third type which had the smallest average D2 from the first two was derived. Similarly, the fourth one was chosen to have the smallest average D2 from the first three and so on. If at any stage, the average D2 of a group, from these already included appeared to be high, it was considered that the group does not fit in with the former cluster and hence, taken to be outside the first cluster. The group of first cluster was then omitted and the rest treated in the similar manner.

LINE X TESTER ANALYSIS

PARENTAL MATERIALS

Based on D2 analysis, from each cluster high yielding genotypes were considered for lines (Six lines). Among the fifty three genotypes, five popular varieties were randomly selected as testers. The parents chosen as lines and testers are listed in Table 2.

METHODS

Crossing block

Staggered sowings of six lines and five testers were taken up during Navarai(January – April), 2011. The seeds were sown in raised nursery beds at ten days interval for synchrony in flowering. 25 days old seedlings were transplanted to the main field at the rate of one seedling per hill, adopting a spacing of 30 cm between rows and 20 cm between plants in a row and in between two genotypes 50 cm spacing was maintained. Crosseswere affected between six females and five male parents in line x tester (Kempthorne, 1957) fashion and totally 30 cross combinations were obtained by adopting hand emasculation and artificial pollination.

Table 2. List of genotypes selected for line x tester analysis

S.No.	Selected parents	Code
Lines		
1	AURC1	L1
2	AURC8	L2
3	AURC10	L3
4	AURC14	L4
5	AURC22	L5
6	AURC25	L6
Testers		
7	ADT36	T1
8	ADT39	T2
9	ADT43	T3
10	IR 64	T4
11	TRY 1	T5

Emasculation and pollination

The spikelets which are likely to open on the same day morning were selected in the female parent during early hours between 6.30 and 8.00 a.m. Immature and already opened spikelets i.e, the bottom and top portion of the panicle respectively were clipped off. The spikelets, which were likely to open on that day are selected and the top one third of the unopened spikelets in the panicle were clipped off using scissors, the anthers from these spikelets were removed by using fine forceps without damaging the stigma (Chaisang et al., 1967). The emasculated panicles were covered with long butter paper bag.

The panicles at anther dehiscence stage were collected from pollen parent and inserted through the top of the butter paper cover and brushed over the emasculated spikelets of female parent to effect cross pollination. Three panicles of male parent were used to dust one female panicle. Then the pollinated panicles were bagged to prevent contamination and labeled properly (Plate 2).

Thus six lines were crossed with all the five testers and the set seeds from 30 cross combinations were collected cross wise after complete physiological maturity and used as F1 hybrid seeds. Selfing of parents were also done and the parental seeds were collected, dried and stored carefully for further studies.

Plate 1. Field view of genetic divergence study

(a) (b) (c)

Plate 2. Crossing Techniques

(a). Emasculation, (b). Bagging, (c). Dusting

Plate 3. Field view of F1 crossing block

F1 hybrids and parents

The 41 genotypes, comprising of eleven parents (six lines and five testers) and thirty hybrids were raised in randomized block design with three replications during Samba (August-December), 2011. Each genotype was accommodated in a row of 3 m length. The seedlings were transplanted at the rate of one seedling per hill, after 25 days with the spacing of 20 x 15 cm. A uniform population of 20 plants in a row per replication was maintained. Normal agronomic practices and need based plant protection measures were adopted to raise the crop. Observations were recorded on ten randomly selected plants both in parents and hybrids per replication (Plate 3).

STATISTICAL ANALYSIS

Unit analysis

The mean values were computed for each genotype over three replications for each cross. The variances and the corresponding standard errors of the mean were computed

from the deviations of the individual values (Panse and Sukhatme, 1978).

Combining ability analysis

The analysis of combining ability was carried out following Kempthorne method (1957). The general combining ability of the parents and specific combining ability of the hybrids were assessed. The meansquares due to different sources of variation in each experiment as well as their genetic expectations were estimated as indicated in the ANOVA table given below:

ANOVA

Source	Degrees of freedom (df)	Mean sum of squares	Expectations of mean squares
Replications	(r - 1)		
Hybrids	(lt – 1)		
Lines	(l – 1)	M1	2e + r [Cov. (F.S.) – 2

			Cov. (H.S.)] + r t [Cov. (H.S.)]
Testers	(t – 1)	M2	□2e + r [Cov. (F.S.) – 2 Cov. (H.S.)] + r l [Cov. (H.S.)]
Lines □ testers	(l-1) (t-1)	M3	□2e + r [Cov. (F.S.) – 2 Cov. (H.S.)]
Error	(r-1) (lt-1)	M4	□2e
Total	(ltr – 1)		

where, r = number of replications
l = number of lines
t = number of testers

Cov. (F.S) = Covariance between full sibs
Cov. (H.S.) = Covariance between half sibs

Estimates of covariance of full sibs and that of half sibs were calculated from the genetic expectations of mean squares as:

$$\text{Cov. (F.S.)} = \frac{M_1 + M_2 + M_3 - 3M}{}$$

$$\text{Cov. (H.S.)} = \frac{M_1 + M_2 - 2M_3}{r(1+t)}$$

From the covariance of full sibs and covariance of half sibs, variances due to general combining ability (□2gca) and specific combining ability (□2 sca) were estimated as follows:

$$\sigma^2 gca = \text{Cov. H.S.}$$

$$\sigma^2 sca = \text{Cov. F.S.} - 2\,\text{Cov. H.S.}$$

Estimation of additive and dominance variance

Additive and dominance variances were estimated both under heterozygous (the inbreeding coefficient F = 0) and homozygous condition (the inbreeding co-efficient F = 1) with the formula.

$$\sigma^2 GCA = \left[\frac{1+F}{4}\right] \sigma^2 A$$

$$\sigma^2 A = \left[\frac{4}{1+F}\right] \sigma^2 GCA$$

$$\sigma^2 SCA = \left[\frac{1+F}{4}\right]^2 \sigma^2 D$$

$$\sigma^2 D = \sigma^2 SCA \left[\frac{2}{1+F}\right]^2$$

GENERATION MEAN ANALYSIS

Among the 30 hybrids evaluated, four superior ones were selected based on different combinations of gca effects of parents and sca effects of hybrids along with their superior per se performance for grain yield per plant.

List of crosses selected for generation mean analysis

Cross No.	Cross code	gca effect of line	gca effect of tester	sca effect for grain yield per plant	Parentage
1	L2/T1	High	High	Positive significant	AURC 8/ADT 36
2	L3/T3	High	Low	Positive significant	AURC 10/ADT 43
3	L5/T4	Low	Low	Positive significant	AURC 22/IR 64
4	L5/T5	Low	High	Positive significant	AURC 22/TRY 1

Generation building

F1 generation

The parents viz., L2, L3, L5, T1, T3, T4 and T5 were sown in crossing block and the following crosses were made during Navarai, 2012.

1. L2/T1
2. L3/T3
3. L5/T4
4. L5/T5

F2 generation

The reserve F1 seeds of the crosses L2/T1, L3/T3, L5/T4 and L5/T5 were sown during Navarai (January-April), 2012 and randomly selected few plants were selfed and F2 seeds were produced (Plate 4).

F3 generation

In Samba (August-December), 2012 randomly selected F2 plants of the crosses L2/T1, L3/T3, L5/T4 and L5/T5 were selfed and F3 seeds were produced (Plate 5).

Plate 4. Field view of F2 generation

Plate 5. Field view of F3 generation

The F1, F2 and F3 generations of the four crosses were raised during Navarai (January-April), 2013 along with their parents P1 and P2 in a randomised block

design with three replications. The crosses were first randomized in each block and different generations were randomized within the cross. The plot size for each cross was 6 x 3 m for each replication. Single seedling was planted per hill adopting a spacing of 20 cm between rows and 15 cm between plants in a row. Recommended crop management practices and need based plant protection measures were adopted.

The number of plants raised for each generation and the number of plants selected at random for recording observations in each of the four cross combinations are tabulated here under

Generation	Plants raised per replication	Total plants studied
P1	30	60
P2	30	60
F1	30	60
F2	240	600
F3	150	300

Conclusion

Fine mapped genetic regions associated with proanthocyanidins and anthocyanin needs to be undertaken to develop quality markers to support marker-assisted-selection breeding of these nutritional traits into high yielding rice backgrounds. A systems approach to study implication of diet based health benefits would require holistic understanding of the molecular basis of human health benefits of consuming grain pigmentation, enabling the identification of the modulators involved to overcome the prevailing double burden malnutrition and communicable diseases in the target communities. While several health benefits were shown to possess to consume pigmented rice, its texture and palatability is found to be poor and thus its acceptance rate is lower. To address this limitation, we need to explore the genetic variation for the retention of GI in the rice.

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