

Physicochemical Evaluation of Parental Germplasm of Quality Rice Breeding Program in Sri LankaAVC Abhayagunasekara¹, SS Paththinige¹, SP Rebeira¹, RLG Rajapasksha¹, NM Navarathna¹, DA Padmakanthi¹ and SW Abeysekara¹¹Rice Research and Development Institute, Batalagoda, Ibbagamuwa**Abstract**

Rice quality is considered as the second important trait in rice breeding programs after yield. Better quality rice varieties give better returns to the farmer. Therefore, rice lines with better yield as well as supreme quality is very important in quality rice breeding program. In the present study, thirty (30) promising quality rice lines from INGER program (IRRI) were evaluated for their morphological and physico-chemical traits. The dendrogram developed on Euclidean distance coefficients using 23 traits at 28.65 similarity level identified three main lineages and five clusters. There are 12 genotypes in linkage I, that can be classified as having the best physico-chemical attributes in grain quality traits of long slender, scented, 105 days' maturity group and having potential yield of 4 t/ha. Further, linkage II consist of 16 genotypes (IR02A477, IR03A477, IR03A568, IR04A381, IR07A167, IR09A102, IR09A105, IR10A108, IR04A395, IR 05A235, IR09A104, IR06N212, IR06N211, IRR1145, At306 and At405) of long slender, aromatic, which mature in 95-105 days and having 4-5 t/ha of yield potential. Linkage III consists of 3 genotypes (At362, IR07A127 and MA2) of long medium grains with 5 t/ha of potential yield and 105 days' maturity duration. Therefore, the present study reveals that the exotic genotypes (IR71146-97-1-2-1-3, IR04A212, IR04A216, IR11A172, IR04A285, IR07A166, IR09A101, IR10A107, IRR1156, IR75483-385-2-2, WAS 169-B-B-4-2-9 and WAS 169-B-B-4-2-3) have preferred grain quality traits and they can be readily used for quality rice breeding programs and biotechnological researched for the grain quality improvement of rice cultivation.

Keywords: Cluster, Correlation, Grain quality traits, Physico-chemical traits, Principle component***Corresponding author:** chandranihordi@yahoo.com**Introduction**

Rice is a staple food of over the half of the world's population especially in Asian region (FAO, 2004). The adaptation of rice cultivars to wide climatic conditions has led to the development of thousands of rice varieties having diverse quality features. It is a very complex trait consists of several components traits including grain appearance, milling quality, nutritional quality, cooking, eating quality and product development characteristics (Toriyama *et al.*, 2005). Further, grain quality has become an important issue affecting domestic consumption and international trade of rice. The assessment indexes of sensory quality of rice are mainly based on the color, appearance, smell, taste and other features which are identified by the examiner's sense organs and practical experience. The appearance of milled rice grain is an important quality attribute considered by consumers first. Other physico-chemical characteristics include grain length, breadth, L/B ratio, hulling and milling percentage. The gelatinization temperature (GT), gel consistency (GC) and amylose content (AC) are major rice traits, which are directly related to cooking and eating quality. Other cooking qualities are alkali spreading value (ASV), water uptake (WU), volume expansion ratio (VER)

and kernel elongation ratio (KER). Rice starch functionality depends on two major components; amylose and amylopectin. Amylose molecule determines the grain's gelatinization temperature, pasting behavior and viscoelastic properties which is an important component to be considered in quality of rice. Further, GT is responsible for cooking time, water absorption and it is the temperature at the starch irreversibly loses its crystalline order during cooking. The GC is responsible for softness while the AC for texture of cooked rice.

In rice breeding programs after yield, rice quality is considered as the 2nd most important trait. When rice breeding, rice lines with better yield and excellent quality is very important as better quality rice gives better returns to the farmers. With increasing the demand of consumers for quality rice, the attention of breeders has focused to develop high quality rice varieties with respect to cooking, eating and nutritional qualities. Systematic study and characterization of high quality germ plasm is not only important for utilizing the appropriate attribute based donors, but also essential in the present era for protecting the unique rice. Moreover, it is also an essential step to prevent adulteration of low priced, non-aromatic rice

with high priced aromatic rice and consequently dissemination of right information to the consumers. Therefore, in the present study, thirty (30) exotic and locally bred rice lines were evaluated for their morphological and physico-chemical traits to identify the quality parental lines for future breeding programs.

Materials and Methods

Out of thirty rice cultivars used in the present experiment, twenty-seven cultivars were taken from INGER (International Network for Genetic Evaluation of Rice), IRRI, Philippines with having diverse origin. Other three genotypes selected for the study were locally released commercial rice varieties.

Experiment was conducted at the experimental field at Rice Research and Development Institute (RRDI) of Batalagoda during the 2012/13 Mahaseason with randomized complete block design with two replicates. Each tested lines were planted as three row progenies with 15 X 20 cm plant spacing. DOA recommendations for fertilizer application, pest and disease control were practiced. Characterization of different morphological traits from seedling stage to the harvest stage of the crop based on IRRI standard evaluation system of rice. Leaf length, leaf width, flag leaf length, plant height, number of productive tillers per plant, days to 50% flowering, days to maturity, panicle length and grain yield were recorded as quantitative parameters while leaf blade pubescence, leaf blade color, leaf blade intensity of green color, leaf blade attitude, ligule color, ligule shape, collar color, auricle color and inter node color were the recorded as qualitative parameters.

For phenotyping of grain quality traits, mature seeds from each genotype were harvested individually and dried. Then the seeds were dehulled for evaluation of the following phenotypic characters at the grain quality laboratory, RRDI, Batalagoda.

Data collection

Grain length (grain size) and grain width of 10 random sample of whole rice grains from each 30 genotypes measured manually and then average length and width were used as the length and width (mm) for analysis. Grain length width ratio (grain shape) was obtained from the measurements of grain length divided by grain width. Aroma was determined by the method described by Tragoonrung *et al.*,

(1996). Amylose content was determined through measuring blue value of rice varieties as described by Juliano, (1971). Gelatinization temperature was assessed using standard alkali digestion and spreading scores (Little *et al.*, 1958) and gel consistency was measured as described by Cagampang *et al.*, (1973). Translucency/chalkiness of the samples were visually observed and recorded for the presence of white patches in the kernels. Hulling and milling values were evaluated as the methods described in rice quality training manual published by IRRI.

Data analysis:

All recorded agro-morphological and physicochemical traits were analyzed by numerical taxonomic techniques using two complementary procedures: cluster and principal component analyses. To avoid effects due to scaling differences, means of each trait were standardized prior to cluster and principal component analyses using Z-scores. Estimates of Euclidean distance coefficients were produced for all pairs of cultivars. The consequential Euclidean dissimilarity coefficient matrices were used to estimate the relationships between the cultivars with a cluster observation using ward linkage method (Minitab 15). Principal component analysis was also performed with the same data matrix.

Results and Discussion

Phenotypic variation:

Basic statistics for 23 morpho-physico chemical traits is presented in Table 1. A reasonable amount of genetic variation was displayed for the traits evaluated. Seed length, brown rice percentage and total milled rice percentage were the characters with less than 5% coefficient of variances (CV) observed. However, the majority traits showed above 10% CV value and the highest was 52.31% (Presence of white bellies in the whole grain). Coefficient of variance of qualitative traits were also high; leaf blade color, leaf blade intensity of green color, inter node color and seed shape recorded more than 25% of CV.

Plant height varied from 47.5 cm to 76.85 cm of the tested genotypes. Days taken to 50% flowering ranged 58-79 days and coefficient of variation was 7.92. Days to maturity exhibited high range (93-114 days) with 5.19% of CV. Most of test edgeno types belong to 90 to 105 days' maturity group. Flag leaf area with its angle is important contributing factor for plants optimum photosynthesis. Maximum flag leaf

of sixteen cultivars combining cluster III and IV. All cultivars in this group were long slender, aromatic, intermediate translucency and gelatinization temperature and consists of 2-3 white bellies. Seed length varies from 6-6.5 mm while seed width was 1.5 - 2.0 mm; subsequently length width ratio varies as 3.5-4.0. These cultivars were characterized by 95-105 days' maturity group. Average yield was 4-5 t/ha, BR% is over 80% and 70-74% TMR. Lineage-III consisted of a single cluster (V) and

contributed to PC1. Other tested traits were negatively contributed to the principal component-1.

Correlation among grain quality traits

In this study, the grain length had significant and positive association with grain length-width ratio; Seed width has significant and negative association with grain length-width ratio. This result is similar to the findings of Begum (2006) and Chauhan (1998). In contrast,

Table 2: Description of genotypes in clusters

Linkage	Cluster	Number of genotypes	Genotype names
I	Cluster- I	5	IR71146-97-1-2-1-3, IR04A216, IR754833, IR04A285, IR11A172
	Cluster- II	7	WAS 169-B-B-4-2-9, WAS 169-B-B-4-2-3, IR07A166, IR09A101, IR10A107, IRR1156, IR02A477
II	Cluster- III	6	At 306, IR09A102, IR09A104, IR09A105, IR03A477, IR75483-385-2-2
	Cluster- IV	10	IR04A381, IR04A395, IR05A235, IR07A167, IR10A108, IR06N211, IR06N212, IRR1145, At 405
III	Cluster- V	3	MA2, At 362, IR07A127

comprising of long medium grains of 3 cultivars. Average yield of this group was 5 t/ha.

It was taken 65 days to flowering and 105 days taken to maturity. Chemical attributes of this lineage was low GT, intermediate translucency and consists of 1-2 white bellies. Brown rice % was 80%, 75-80 % of TMR and 20% of hull.

In general, long grains are preferred in the Indian subcontinent, but in Southeast Asia, the demand is for long medium rice. There is a high demand for long grain rice in the national market. Sharma (2002) mentioned that the aromatic cultivars possessed as lender shape compared with the medium-slender shape of non-aromatic cultivars.

Principal component analysis

The results of principal component analysis showed that the first eight PCs are having greater than 1 eigen values accounted for 79.91% of the total variation. The combination of the first and second principal components explained the 37.21% of the total variation (Table 3). Number of culms per plant, average yield, brown rice%, total milled rice %, seed width, seed shape, leaf blade pubescence, leaf blade color and inter node color were the traits that more positively

there is no any association between kernel size and shape. It had significant negative association between grain width and grain length width ratio. BR% and HULL% followed the significant and negative association with total milled rice%, while the BR% and TMR% correlation is significantly positive.

Table 3: Principal components and variance of tested genotypes

Component	Extraction Sums of Squared Loadings		
	Total	% of Variance	Cumulative %
1	4.82	20.09	20.09
2	4.10	17.11	37.21
3	2.30	9.61	46.83
4	2.00	8.34	55.17
5	1.64	6.87	62.05
6	1.43	5.95	68.00
7	1.38	5.75	73.76
8	1.23	5.15	78.91

Extraction Method: Principal Component Analysis - 8 components extracted

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Table 4: Genotypic and phenotypic correlation coefficient among rice grain quality traits

TRAITS	SDLEGT	SDWDT	LWDR	BR	HULL	TMR	SSPE	WBELY	TRANS	GELATI
SDLEGT	1.000									
SDWDT	-.356	1.000								
LWDR	.658*	-.934*	1.000							
BR	-.342	.304	-.373	1.000						
HULL	.397	-.263	.368	-.945*	1.000					
TMR	-.522*	.350	-.482	.887*	-.918*	1.000				
SSPE	-.071	.352	-.290	.187	-.170	.168	1.000			
WBELY	.289	.203	-.071	-.013	.050	-.056	.180	1.000		
TRANS	-.160	-.337	.212	-.084	.097	-.033	-.070	-.135	1.000	
GELATI	.419	-.232	.328	.012	.065	-.124	-.334	.131	-.239	1.000

*= 5% level of significant

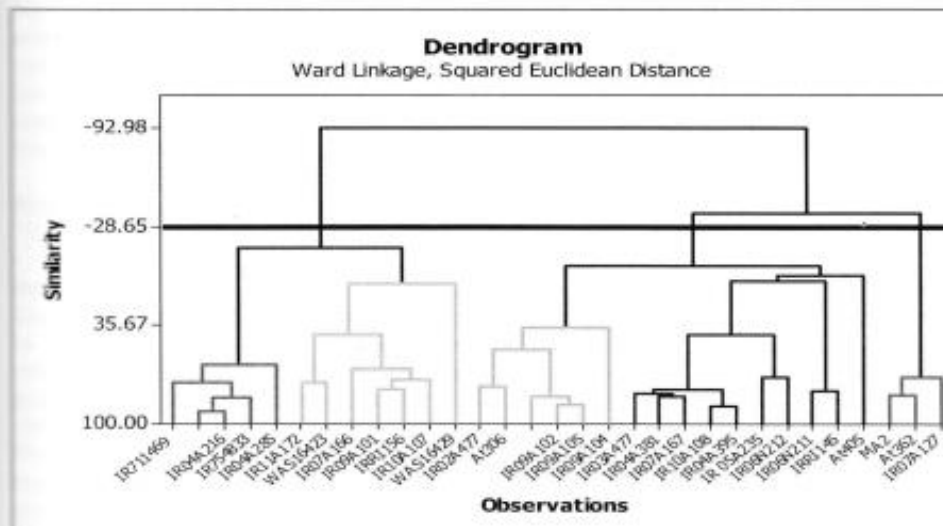


Figure 1: Dendrogram based on 23 morpho-physicochemical traits of 30 genotypes

Conclusion

This study was concentrated on the morphological, physico-chemical attributes and correlation among grain quality traits. There are 12 genotypes which are belong to linkage I, can be suggested as having the best physico-chemical attributes among tested genotypes. Those are long slender, scented genotypes which are matured in 105 days and having 4 t/ha potential yield. Further, linkage II, consists of 16 genotypes of long slender, aromatic which are matured in 95-105 days and 4-5 t/ha of potential yield. Linkage III consists of 03 genotypes of long medium grains with potential yield of 5 t/ha and matured in 105 days. Correlation analysis always helps to the

researches to select better rice varieties for consumer preferences. Results of the correlation analysis revealed that the grain length had significant and positive association with grain length-width ratio; In contrast, there is no any association between kernel size and shape. Therefore, the present study revealed that genotypes in lineage I (IR71146-97-1-2-1-3, IR04A212, IR04A216, IR11A172, IR04A285, IR07A166, IR09A101, IR10A107, IRR1156, IR75483-385-2-2, WAS 169-B-B-4-2-9 and WAS 169-B-B-4-2-3), consists of exotic genotypes have preferred quality traits and it could be readily used for quality improvement of rice breeding programs and biotechnological researches.

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