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Research Article

Selection indices for improving the selection efficiency of rice genotypes using grain quality traits

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Abstract
Association study and selection of best rice genotypes based on grain quality traits was experimented with 44 rice cultures. The study material comprised of 40 stabilised mutant lines of ADT 37 and ADT (R) 45 and four varieties. The grains with 11-13 per cent of moisture content were subjected for all grain quality estimation/quantification. It is observed that the amylose did not show any correlation with any of the milling properties as well the Alkali Spread Value. Protein has a negative correlation with Gel Consistency. Kernel breadth exhibited a negative correlation with most of the traits. Volume expansion has a good positive correlation with grain elongation after cooking. Upon comparison of selection indices *viz.,* Multiplicative Index, Index Free of Weights and Parameters, Base Index, Classical index, Index based on the sum of Ranks and Index based on gains desired, the multiplicative index has given higher gains for most of the traits. However the index based on the sum of ranks was found to give good weightage to all the important traits. Hence the genotypes *viz.,* ACM17006, ACM 18001, ACM18021, ACM18011, ACM18017 were found promising in this study based on the sum of ranks index.

Keywords
Paddy, Selection Index, Association, grain quality traits

INTRODUCTION

Rice (*Oryza sativa* L.) is the most staple food in Asian countries as 90% of the rice produced and consumed in Asia. Among the Asian countries, China and India alone contributes over 55 % of the global production. Stability in rice production is the key to attain food security. (Bandumula, 2018). To sustain the self-sufficiency, there is a need for the development of new varieties or hybrids with high yielding potential and capable of withstanding adverse conditions (Papademetriou, 2000). As the economic growth of India rapids, the standard of living also moves forward at a substantial rate. Nowadays, the consumer acceptance of a rice variety depends on the grain quality (Sharma and Khanna, 2020).The grain quality is a complex and polygenic group of traits that are influenced by the environment, and their interactions. Quality traits involves the appearances, milling quality, cooking quality, aroma and nutritional status which are based on the location, market demand, consumer preferences etc…(Juliano *et al*, 2019)

The practice of selection indices in the rice breeding program will enable the selection of best genotypes based on the combination of traits and economic weight attributed to them (Hazel, 1943; Smith, 1936). Currently, there are several approaches for obtaining selection indexes. The selection index proposed by Smith (1936) and Hazel (1943) proposed the idea of weightage of economically important traits based on the estimation of the weighing coefficient where the correlation between the index and trait coefficient is maximized. Mulamba and Mock (1978) proposed the classification of genotypes based on the improvement of the trait towards and the sum of traits that contribute to the additional improvement.

MATERIALS AND METHODS

The study was conducted at Tamil Nadu Rice Research Institute, Aduthurai during 2019-20. The study material comprised of 40 mutant lines obtained through gamma irradiation of rice varieties ADT 37 and ADT 45 using cobalt 60 as source of irradiation and four high yielding varieties **(Table 1)**. The trial was conducted in Randomized Block Design with two replications. All the recommended agronomical practices were followed for establishing a good crop. The plants were harvested at physiological maturity, threshed properly and sun-dried to the moisture content of 11-13 %. These seeds were used for the analysis of grain quality parameters includes hulling percentage, milling percentage, head rice recovery, kernel length (mm), kernel breadth (mm), L/B ratio, kernel length after cooking (mm), kernel breadth after cooking (mm), linear elongation ratio, breadth wise elongation ratio, gel consistency, Alkali spreading value, amylose (%) and protein (%). The milling parameters were recorded using Zaccaria huller. Kernel length and breadth were recorded by measuring ten grain length and breadth in the graph sheet.

Gel Consistency test was conducted by the method described by Cagampang *et al*. (1973). 100g finely powdered sample taken in a 13 X 100mm culture tube and 0.2 ml of thymol blue and 2ml of 0.2 N NaOH was added. Then the tubes were kept it in the boiling water bath for 8 min and allowed for cooling. The tubes were placed horizontally and the length of the gel was measured. Protein analysis was carried out in the Kelplus (Kjeldahl method approved by the American Association of Cereal Chemists). Gelatinization temperature was determined as described by Little *et al.* (1958) using alkali-spreading value. The alkali digestibility test is employed. Grains were soaked in 1.7% KOH and incubated in a 30^{o}C oven for 23 hours. Amylose content was determined by a simplified colorimetric method as described by (Juliano *et al*., 1981). The 100g of samples was taken in 100 ml volumetric flask and 1 ml of 95% ethanol and 9 ml of 1 N NaOH. Keep it in the boiling water bath for 20 min and cool it. Distilled water was added to make the volume up to 100 ml and 5 ml of that solution was taken in a 100 ml volumetric flask. To this, 2 ml of 0.2 % iodine and 1 ml of 57.5 % acetic acid were added and the volume was made to 100 ml. The absorbance was read in a spectrophotometer in 620 nm after 20 mins of dark condition.

The correlation was calculated for the given data using STAR software version 2.0.1 developed by IRRI. Selection indexes of Index Free of Weights and Parameters (Elston,1963), Base Index (Williams,1962), Classical index (Smith, 1936 and Hazel 1943), Index based on the sum of Ranks (Mulamba and Mock,1978) and Multiplicative Index (Subandi *et al*,1973) was performed by using GENES software.

1	ACM 18001
2	ACM 18002
3	ACM 18003
4	ACM18004
5	ACM18005
6	ACM18006
7	ACM18007
8	ACM18008
9	ACM18009
10	ACM18010
11	ACM18011
12	ACM18012
13	ACM18013
14	ACM18014
15	ACM18015
16	ACM18016
17	ACM18017
18	ACM18018
19	ACM18019
20	ACM18020
21	ACM18021
22	ACM18022
23	ACM18023
24	ACM18024
25	ACM18025
26	ACM18026
27	ACM18027
28	ACM18028
29	ACM18029
30	ACM18030
31	ACM18031
32	ACM18032
33	ACM18033
34	ACM17001
35	ACM17002
36	ACM17003
37	ACM17004
38	ACM17005
39	ACM17006
40	ACM17007
41	ADT 37
42	ADT 45
43	TPS 5
44	BPT 5204

Table 1 . List of Rice genotypes analyzed for Grain quality

RESULT AND DISCUSSION

The study on association pattern between 15 paddy grain quality traits was done to understand the correlation between each trait. (**Table 2**). The Hulling percentage has a highly significant and positive correlation with milling percentage (r=0.5834), head rice recovery (r=0.4672) and was also positively influenced by gel consistency(r=0.3233). The result of positive association between HRR with milling and hulling percentage is in accordance with the reports of Nayak *et al.*(2003); Nirmaladevi *et al.*(2015). A positive correlation of milling percentage with head rice recovery (r=0.4866), kernel length after cooking (r = 0.4613) and volume expansion (r= 0.2806) is of great importance to the breeders for selecting the genotypes with good cooking quality.

Table 2. Correlation coefficient for 15-grain quality parameters among 44 rice genotypes

	HP	MP	HRR	KL	KB	LB ratio	KLAV	KBAC	LER	BER	VE	GC	AMY	ASV	Protein
HP	1.0000	0.5834**	0.4672**	0.0372	-0.1394	0.2609	0.1654	-0.2249	0.0483	-0.0789	0.0688	0.3233*	-0.1263	-0.2128	-0.0488
MP		1.0000	0.4866**	-0.1071	0.0764	0.2612	0.4613**	-0.0761	0.2314	-0.3704**	0.2806*	0.1558	-0.2017	-0.3512**	-0.1478
HRR			1.0000	-0.0756	-0.3139*	0.1295	-0.1147	-0.3386*	0.0041	0.0736	-0.1756	0.2037	0.0660	-0.3517*	0.0146
KL				1.0000	-0.3740**	0.4766**	-0.2179	-0.2571	-0.7280**	0.2484	-0.3088*	-0.0922	0.0383	-0.0945	0.1920
KB					1.0000	-0.6739**	0.4297**	0.4336**	0.4708**	-0.7655**	0.5328**	-0.1580	-0.1203	0.1460	-0.2600
L.B ratio						1.0000	0.1762	-0.0157	-0.3230**	0.5024**	-0.0163	0.0404	-0.0363	-0.1098	0.2204
KLAC							1.0000	0.4561**	0.7211**	-0.3958**	0.6241**	-0.0058	-0.2167	0.0768	-0.1158
KBAC								1.0000	0.3151*	0.1190	0.3273*	-0.1736	-0.1708	0.1720	-0.0522
LER									1.0000	-0.3737**	0.4441**	0.0841	-0.1698	0.1410	-0.1749
BER										1.0000	-0.5233**	0.0453	0.0351	0.0154	0.3082*
VE											1.0000	-0.0267	0.0388	0.0553	-0.0966
GC												1.0000	-0.0449	-0.2581	-0.3485*
AMY													1.0000	-0.1364	-0.1611
ASV														1.0000	0.0766
protein															1.0000

HP – Hulling percentage; MP – Milling percentage ; HRR – Head rice recovery (percentage); KL – Kernel Length (mm); KB – Kernel Breadth (mm); LB ratio – Length Breadth Ratio; KLAC – Kernel Length After Cooking (mm); KBAC - Kernel Breadth After cooking (mm); LER- Linear elongation ratio; BER – Breadth wise elongation ratio ; VE – Volume expansion (ml) ; GC – Gel Consistency (cm); AMY – Amylose (%); ASV – Alkali Spread Value ; Protein (%)
*- Significant at 5% level ($P<0.05$) , **- Significant at 1% level ($P<0.01$)

Kernel length is positively and highly correlated with the length/breadth ratio (r=0.4766) thus confirming the findings of Nirmaladevi *et al.,* (2015); Kumar, 2015; Saif-ur-Rasheed *et al.*(2002). The trait kernel breadth has a positive and significant association with kernel length after cooking (r =0.4297), kernel breadth after cooking (r=0.4336), linear elongation ratio (r= 0.4708)(Rathi, *et al.,* 2010) and volume expansion (r=0.5328).

The analysis exhibited kernel length after cooking has a highly significant and positive correlation with linear elongation ratio (r=0.7211) (Khatun *et. al.*, 2003) and volume expansion (r= 0.6241). Similarly linear elongation ratio was highly significant and positive association with the volume expansion (r=0.4441) and Breadthwise expansion ratio had a positive significant association with protein content (r = 0.3082).

Milling percentage had a highly significant negative association with Breadth wise expansion ratio (r=-0.3704) and alkali spread value (r= -0.3512). Head rice recovery had a significant negative correlation with kernel breadth (r= -0.3139), kernel breadth after cooking (r= -0.3386) and Alkali spread value (r= -0.3517). Gel consistency had a significant negative association with protein content (r = -0.3485).

In this study, it is inferred that, volume expansion can be improved with selecting genotypes with good elongation after cooking either lengthwise or breadthwise as volume expansion exhibited positive significant correlations with these traits. Similarly in this study it was observed that the protein has positive significant correlation with BER hence it can adjudged that if breadthwise elongation is more than the genotype may have higher protein content. The amylose content is not associated with any other traits.

In this study, all variables manifested high heritability ranging from 85.7 to 100 per cent(**Table 3**). Highest heritability was noted for alkali spread value (100%), followed by gel consistency (99.96 %), head rice recovery (99.85%) , protein (99.84%), amylose (99.79%), hulling percentage (99.61%) and kernel length (99.44 %) . The lowest heritability was noted for kernel length after cooking (85.73), followed by volume expansion (93.53%) and kernel breadth after cooking (95.38%). These results indicated that there are wide genetic variability and greater possible genetic gain from these traits.

The genetic gain from all possible indexes showed a greater value in Multiplicative Index (Subandi *et al.,*1973) (72.5 %), followed by Index Free of Weights and Parameters (Elston,1963), Base Index (Williams,1962),

Table 3. Estimative of heritability percentage (h^2%) and percentage gains with selection (GS %) of 44 rice genotypes for 15 quality parameters

		GS%				
Variables	**h^2**	**IFWP**	**IBSR**	**MI**	**CI**	**BI**
HP	99.61	1.18	5.54	3.62	3.09	4.69
MP	97.07	-1.44	4.03	2.32	4.6	3.69
HRR	99.85	3.31	6.23	5.64	10.31	4.77
KL	99.44	-0.07	1.36	-0.35	-2.7	-1.96
KB	98.31	-20.05	-2.41	-11.73	-1.89	-2.45
LB ratio	98.73	23.07	3.16	13.81	-1.11	.41
KLAC	85.73	-0.26	3.22	0.74	0.9	2.89
KBAC	95.38	3.05	-.18	1.97	1.97	-.18
LER	98.41	-0.58	2.23	0.9	4.39	5.03
BER	98.48	28.84	1.43	16.94	4.15	2.64
VE	93.53	-2.88	3.21	-.45	-.45	-.45
GC	99.96	27.55	14.75	46.94	44.95	49.77
AMY	99.79	-5.24	-1.48	-6.55	-5.41	-5.51
ASV	100.0	7.06	-13.33	1.96	-8.24	-8.24
protein	99.84	4.72	9.33	-3.26	-6.98	-4.72
Genetic gain		68.26	37.09	72.5	47.58	50.38

HP – Hulling percentage; MP – Milling percentage; HRR – Head Rice Recovery (%); KL – Kernel Length (mm); KB – Kernel Breadth (mm); LB ratio – Length Breadth Ratio; KLAC – Kernel Length After Cooking (mm); KBAC - Kernel Breadth After cooking (mm); LER- Linear elongation ratio; BER – Breadth wise elongation ratio; VE – Volume expansion (ml); GC – Gel Consistency (cm); AMY – Amylose (%); ASV – Alkali Spread Value; Protein (%)

h^2 - Broad sense heritability ; IFWP - Index Free of Weights and Parameters (Elston,1963); IBSR - Index based on the sum of Ranks (Mulamba and Mock,1978); MI - Multiplicative Index (Subandi et al,1973); CI - Classical index (Smith, 1936 and Hazel 1943); BI - Base Index (Williams,1962).

Classical index (Smith, 1936 and Hazel, 1943), and Index based on the sum of Ranks (Mulamba and Mock,1978). The highest genetic gain obtained Multiplicative Index (Subandi *et al.*,1973) (72.5 %) were from gel consistency (46.94 %), followed by breadth wise elongation index (16.94 %) and LB ratio (13.81%). The lowest genetic gain obtained from this index selection were kernel length after cooking (0.74%), linear elongation ratio (0.90%), Alkali spread value (1.96 %) ,kernel breadth after cooking (1.97 %), milling percentage (2.32%), hulling percentage (3.62 %) and Head rice recovery (5.64 %). The predicted gains for other characteristics were kernel length (-0.35%), kernel breadth (-11.73) , volume expansion (-0.45), amylose(-6.55)and protein (-3.26%) .

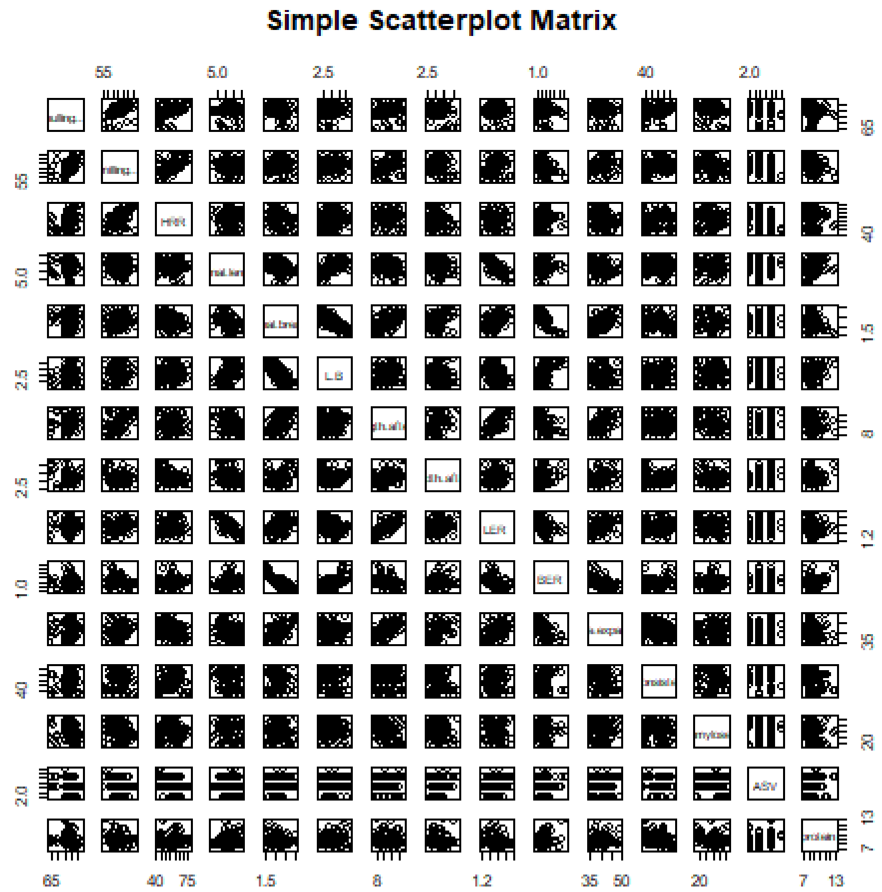

Fig. 1. Correlation coefficient of 15-grain quality parameter as scatter plot among 44 rice genotypes

This negative predicted gain indicates that the selection based on these traits causes a reduction in the total gain. Based on the multiplicative index, the genotypes that were selected are ACM18018, ACM18013, ACM 18001, ACM17006, ACM18025, ACM18022.

The genetic gains were predicted by the Base Index (Williams,1962). The highest genetic gain, from a total of 50.38 % was gel consistency (49.77 %) followed by linear elongation ratio (5.03 %), head rice recovery (4.77%), hulling percentage (4.69%) and milling percentage (3.69%). The lowest genetic gain was obtained for LB ratio (0.41%) followed by breadth wise elongation ratio (2.64%), kernel length after cooking (2.89%). The negative genetic gain obtained by kernel length (-1.96%), kernel breadth (-2.45%), kernel breadth after cooking (-0.18), volume expansion (-0.45), amylose (-5.51), alkali spread value (-8.24) and protein (-4.72%). The selection based on the characters like milling percentage, hulling percentage, head rice recovery, linear elongation ratio, and gel consistency results in greater genetic gain which is beneficial for selection. The genotypes that were selected based on this index are ACM 18001, ACM17006, ACM18025, ACM18022, ACM18019, ACM18006.

The selection index of Classical index (Smith, 1936 and Hazel 1943) has a total genetic gain of 47.58 % with the highest genetic gain of 44.95 % for gel consistency followed by 10.31 % for head rice recovery,4.6% for milling percentage, 4.39% for length elongation ratio, 4.15% for breadth wise elongation ratio and with the lowest genetic gain (0.9 %) for kernel length after cooking, 1.97 % for kernel breadth after cooking, and 3.09 % for hulling percentage. The negative gains from the smith and hazel index obtained for kernel length (-2.7%), kernel breadth (-1.89%), LB ratio (-1.11 %), volume expansion (-0.45), amylose (-5.41), protein (-6.98). The selection using this Index will have genotypes with greater head rice recovery, greater linear elongation ratio, and breadthwise elongation ratio. Having kernel length, kernel breadth, volume expansion, amylose and protein as selection traits will reduce the overall gain of the selection. The genotypes selected through this selection index are ACM 18001,ACM17003 , ACM18016, ACM18025, ACM18006, ACM17006.

The Index Free of Weights and Parameters (Elston,1963) has greater genetic gain compared with smith and hazel and Mulamba and mock indexes. Of the total genetic gain (68.26 %), the highest gain was for gel consistency (27.55%), followed by the Breadth wise elongation index (28.84%) and LB ratio (23.07%). And the lowest genetic gain obtained through this selection index was hulling percentage of 1.18%, kernel breadth after cooking of 3.05%, head rice recovery of 3.31%, protein of 4.72% and amylose of 7.06%. The negative genetic gain attributed by the following traits: milling percentage with -1.44%, kernel length with -0.07%, kernel length after cooking with -0.265, linear elongation ratio with -0.58%, volume expansion with -2.885, amylose with -5.24%. The selected genotypes using this index will have greater gel consistency, greater breadth wise elongation ratio, with greater LB ratio and have lower head rice recovery, Lower kernel breadth after cooking and a lower amount of amylose and protein content. The genotypes selected using this index are ACM18018, ACM18013, ACM18025, ACM17006 , ACM18022.

The other selection index involved is Index based on the sum of Ranks (Mulamba and Mock,1978) which is widely accepted. The total gain was 37.09 % which is lesser compared to all other indexes. The positive and highest gain was observed for gel consistency (14.76 %) followed by protein (9.33%), head rice recovery (6.23), hulling percentage (5.54%), milling percentage (4.03%), kernel length after cooking (3.22%), volume expansion (3.21%), LB ratio (3.16%) and the lowest gain is breadth wise elongation ratio (1.43%) followed by kernel length (1.36%), and linear elongation ratio (2.23%). The negative gain obtained is kernel breadth (-2.41%), kernel breadth after cooking (-0.18), amylose (-1.48%) and alkali spread value (-13.33%). The selected genotype will have a higher gel consistency, higher protein content, greater head rice recovery and good LB ratio, more kernel length elongation after cooking and volume expansion with low kernel length and linear elongation ratio. Selection based on the kernel breadth, kernel breadth after cooking, alkali spread value and amylose will result in the reduction of total gain. The genotypes selected are ACM17006, ACM 18001 , ACM18013,ACM18011, ACM18017.

In this study, the greater genetic gain was presented by Multiplicative index. Though the Multiplicative index has a higher genetic gain, the selection criteria have a negative gain for amylose and protein content which is an important factor for the selection of a genotype. Improvement in the quality parameters of rice will mainly focus on the protein content. Amylose is an inevitable factor for the selection as the customer preferences for good quality grain will also include the amylose factor, mostly as intermittent levels in regional areas. Considering other selection indexes, Index based on the sum of Ranks (Mulamba and Mock,1978), though it has a less genetic gain compared to others, the weightage given to the trait and combination of trait has given the desired results in the genotypes considering all criteria for the selection. Thus, the selection was followed based on the Index based on the sum of Ranks (Mulamba and Mock,1978).

The study conducted to identify the association of grain quality traits in paddy towards indirect selection of genotyes with improved cooking qualities, it was observed that the amylose was independent with other milling and cooking related traits. The selection based on kernel length was significant in improving the linear elongation after cooking, volume expansion and Head Rice Recovery. The gel consistency was negatively correlated with protein content in the paddy grains.
Different selection indices were compared and it was found that though multiplicative index showed a high genetic gain , it does not have desirable values for protein and amylose hence the other index *viz.,* Sum of ranks which has given equal weightage for all the traits taken for study. Hence the Sum of rank index method is considered for selection of genotypes accordingly the genotypes *viz.,* ACM17006, ACM 18001, C2T2D1-18-3, ACM18021, ACM18017 were found promising.

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