Original Research Article

Diversity and Multi-variate analysis of Basmati and non-Basmati rice genotypes over two seasons using organo-leptic traits

---

ABSTRACT

Investigation on multi-variate analysis was done with Mahalanobis' D^2 statistic, Principal Component Analysis (PCA), genetic variability studies and Pearson's correlation coefficient analysis among fifty-one rice genotypes over two consecutive seasons i.e., Kharif 2021 and Rabi 2021. It led to the clustering of the genotypes into ten clusters with maximum intra cluster distance found in cluster III and inter cluster distance between clusters III and X. PCA led to six principal components that had eigen values greater than one, explaining cumulative of 76.77% of the total variation. Based on the per se performance, D^2 analysis and PCA, it was found that the genotypes, Improved white ponni, CO 52, VGD 1, BPT 5204, RNR 15048, Pusa Basmati 1121 and Pusa Basmati 1 were highly divergent due to the large genetic distance from the genotypes viz., TRY 3, TPS 5, Palawan, Azucena and Khao do ngoi for both grain yield and organoleptic traits indicating the possibilities for the potential use of these parents in future breeding programme aimed at improvement of grain yield and desirable organoleptic traits . Linear elongation ratio was positively correlated with amylose content, kernel length, L/B ratio and kernel length after elongation but negatively correlated with kernel breadth, kernel breadth after cooking, water uptake ratio and volume expansion ratio and hence indirect selection for longer grains and intermediate to high amylose content would improve LER inspite of the seasonal influence. These traits attribute to the selection of genotypes with desirable cooking quality that fetches premium price in the market in particular to that of non-basmati genotypes.

Keywords: Rice, Diversity, seasonal influence, PCA, Variability, Correlation, Physico-chemical traits

1. INTRODUCTION

"Rice is life" is a phrase that best describes Rice to be the principal food grain crop, which plays a pivotal role in satisfying the nutritional needs of more than half of the world's production. World rice production accounts to 525.96 million tonnes from a global acreage of 165.25 million ha during the year 2021 – 22 [1]. Rice is cultivated in India in an area of about 463 lakh ha producing 129.47 million ha with an average productivity of 2798 kg/ha according during 2021 – 22. In Tamil Nadu, Rice is produced in an area of 22.17 lakh ha producing about 79.07 lakh tonnes with an average productivity of 3566 kg/ha [2].The per capita net availability of rice per day was 196 g/day and 73.3 kgs/year in India [3]. In the majority of Asian countries, the day is incomplete without rice. It is predicted that the world's need for rice would increase from 450 million tonnes in 2011 to around 490 million tonnes in

2020 and roughly 650 million tonnes by 2050, *i.e.,* a 40% increase in rice production to keep up with the world's population growth [4].

There has been an upsurge in the demand for premium rice internationally in the recent years. Determining consistent attributes of grain quality becomes increasingly challenging owing to the diversity of customer demand in Asia and around the world caused by varied demographics and culture [5]. While European customers prefer long grain and non-aromatic rice, Middle Eastern consumers strongly favour long grain, well milled rice with strong aroma [6]. Between 2021 and 2022, 3.9 million tonnes of basmati rice were exported at a cost of Rs. 26390 crores (897 USD/tonne), whereas 17.29 million tonnes of non-basmati rice were exported at a cost of Rs. 45725 crores (355 USD/tonne) [7]. This statistic reveals that the most crucial quality characteristic that set the highly priced basmati rice apart from other non-basmati rice is cooked kernel elongation

Superfine slender grains with excellent cooking quality, pleasant aroma and high cooked kernel elongation while cooking will get exceptional price in both the domestic and international markets [8]. The best indications of grain quality are the physico-chemical and cooking qualities. Majority of consumers prefer rice with soft to medium gel consistency, an intermediate amylose content and an intermediate gelatinization temperature [9, 10]. Hence, Rice grain appearance and grain quality have emerged as rice breeders' top concerns as a result of the intensifications of various dietary needs and living standards of worldwide populations [11].

India has a diverse source of rice germplasm both at inter-specific and intra-specific level [12]. Analysis of genetic diversity aids in both the maintenance and usage of desired variation in breeders' operations as well as the selection of acceptable parents for breeding programmes. Additionally, it advances breeders knowledge of the crop evolutionary pattern. Hence the present investigation was taken up with fifty-one rice genotypes to detect the cultivars with good yielding capacity and desirable cooking quality. This study also aimed at determining the factors that are attributable to the yielding behaviour and the components required for building desirable organoleptic traits.

2. MATERIAL AND METHODS

2.1 Field Experiment

A total of fifty-one rice genotypes comprising of traditional landraces, released varieties and pre-releasee cultures were collected as pure seeds from respective locations and evaluated in two seasons *i.e., Kharif* 2021 and *Rabi* 2021 in two replications following Randomized Block Design as presented in Table 1. The experimental material was raised at a spacing of

20 x 20 cm. Single seedling per hill was maintained. The recommended practice of cultivation was provided during the entire crop growth period. Observations on biometrical traits *viz.,* days to fifty per cent flowering, plant height (cm), panicle length (cm), number of productive tillers per plant, number of filled grains per panicle, thousand grain weight (g) and single plant yield (g) were recorded in five randomly tagged plants in each genotype in each replication.

Table 1: List of rice genotypes used for phenotypic diversity for biometrical and physico-chemical traits

S.No.	**Code**	**Genotype name**	**Parentage**	**Type**	Grain type
1	G1	AD 16024	Turant Dhan x IET 22075	Culture	Short bold
2	G2	AD 16028	ADT 56	Culture	Short slender
3	G3	AD 16052	IET 22075 x ADT 48	Culture	Short slender
4	G4	AD 17020	ADT 43 x JGL 384	Culture	Short slender
5	G5	AD 17037	WGL 14377 x MDU 5	Culture	Short slender
6	G6	AD 18538	ADT (R) 46 x AD 09391	Culture	Medium slender
7	G7	AD 18545	ADT (R) 46 x AD 09391	Culture	Short bold
8	G8	AD 18573	ADT (R) 45 x ACK 03002	Culture	Short bold
9	G9	AD 18600	ADT 39 x NDR 359	Culture	Short bold
10	G10	AD 19055	ADT 49 x MTU 1150	Culture	Long slender
11	G11	AD 19224	ADT 43 x BPT 5204	Culture	Short slender
12	G12	ADT 37	BG 280 – 12 x PTB 33	Variety	Short bold
13	G13	ADT 43	IR 50 x White Ponni	Variety	Long slender
14	G14	ADT 53	ADT 43 x JGL 384	Variety	Long slender
15	G15	ADT 54	Improved White Ponni x Bansakthi	Variety	Long slender
16	G16	ASD 16	ADT 31 x CO 39	Variety	Short bold
17	G17	AZUCENA	-?	Tropical *japonica*	Long bold
18	G18	BPT 5204	GEB 24 / TN1 / Mahsuri	Variety	Short slender
19	G19	*Burma Kavuni*	-?	Landrace	Short bold
20	G20	CB 12122	BPT 5204 x CO 48	Culture	Medium slender
21	G21	CB 13132	CO 49 x KJTCMS4	Culture	Medium slender
22	G22	CB 15114	*Rasakadam* x IET 19865	Culture	Short slender
23	G23	CB 15569	ADT 45 x CB 04110	Culture	Short slender
24	G24	CB 15714	ADT 43 x GEB 24	Culture	Short slender
25	G25	CB 15801	ADT 45 x Improved White Ponni	Culture	Medium slender

Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left

26	G26	CB 16605	CO 51 x JGL 17211	Culture	Short slender
27	G27	CB 16723	CB 08504 x Pusa Basmati 1	Culture	Long slender
28	G28	CB 17528	CO 51 x WGL 536	Culture	Long slender
29	G29	CB 19132	CB 05022 x CB 05219	Culture	Medium slender
30	G30	CO 51	ADT 43 x RR 272 – 1745	Variety	Medium slender
31	G31	CO 52	BPT 5204 x CO (R) 50	Variety	Short slender
32	G32	*Gedumani*	-?	Landrace	Short bold
33	G33	Improved White Ponni	Taichung 65 x 2 MayangEbos*80	Variety	Short slender
34	G34	*Kaatuyanam*	-?	Landrace	Medium slender
35	G35	*Karuppu Kavuni*	?-	Landrace	Short bold
36	G36	*Kavuni*	?-	Landrace	Long slender
37	G37	KHAO DO NGOI	?-	Tropical *japonica*	Long bold
38	G38	*Ottadai*	?-	Landrace	Short bold
39	G39	PALAWAN	?-	Tropical *japonica*	Short bold
40	G40	Pusa Basmati 1	Pusa – 150 x Karnal Local	Variety	Long slender
41	G41	Pusa Basmati 1121	Pusa 614 – 1 – 2 x Pusa 614 – 2 – 4 – 3	Variety	Extra-long slender
42	G42	RNR 15048	MTU 1010 x JGL 3855	Variety	Short slender
43	G43	*Sivappumalli*	?-	Landrace	Short bold
44	G44	*Thailand Kavuni*	?-	Landrace	Short bold
45	G45	*Thirupathisaram*	?-	Landrace	Long bold
46	G46	TN 1	DGWG x Tsai – yuan – chung	Variety	Short bold
47	G47	TPS 5	ASD 16 x ADT 37	Variety	Long bold
48	G48	TRY 1	IR578 – 172 – 2 – 2 x BR – 1 – 2 – B – 1	Variety	Short bold
49	G49	TRY (R) 2	IET6238 x IR36	Variety	Short bold
50	G50	TRY 3	ADT 43 x Jeeraga Samba	Variety	Short bold
51	G51	VGD 1	ADT 43 x Jeeraga Samba	Variety	Short bold

Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left
Formatted: Left

2.2 Analysis of Physico-chemical traits

The harvested seeds were processed using laboratory huller, laboratory polisher and pound using a mixer to assess the physico-chemical traits viz., kernel length (mm), kernel breadth (mm), kernel L/B ratio, KLAC (mm), kernel breadth after cooking (mm), linear elongation ratio, breadthwise elongation ratio, amylose content (%), gel consistency (as gel length measured in mm), alkali spreading value, water uptake ratio and volume expansion ratio. KL and KB were recorded by arranging ten randomly selected dehulled rice in a graph sheet, the value was averaged and recorded in mm. Kernel L/B ratio was computed by finding the ratio between the length and breadth of dehulled kernel[13]. Ten unbroken milled grains were measured for their length and breadth before cooking, pre-soaked in water for 20 minutes and boiled till the grains are cooked. Excess water was drained, the length and breadth of the cooked kernels were logged by arranging them in a laminated graph sheet[13]. LER and BER were calculated as the ratio of mean length/breadth of cooked rice to mean length /breadth of milled rice respectively [14]. AC was determined in the rice flour by the simplified calorimetric method as described by Sowbhagya and Bhattacharya [15]. Incubating six kernels of whole rice in 10 ml of 1.7% KOH for 23h as per Little [16] to assess the ASV and their degree of spreading was measured using a 7-point scale. Gel consistency test was performed by dispersing 100mg rice flour in 0.2 ml of 95% ethanol containing 0.025% thymol blue in test tube followed by adding 2 ml of 0.2N KOH. The contents were heated in boiling water bath (8 minutes), normalized in room temperature (5 minutes), cooled in an ice-water bath (15 minutes) and laid in a laminated graph sheet for 1h. The length of gel was measured and classified as per Cagampang, Perez [17].WUR was estimated as the ratio of final cooked weight to uncooked weight [18]. VER was estimated as the ratio between cooked volume to the uncooked volume [19].

2.3 Statistical analysis

Analysis of variance (ANOVA) was computed as pooled ANOVA using STAR software 2.0.1 and the traits were analyzed for mean, critical difference (CD), genotypic coefficient of variation (GCV %), phenotypic coefficient of variation (PCV %), heritability (%) and genetic advance as percentage of mean (GAM %). The mean data recorded for various biometrical and physico-chemical traits were assessed for phenotypical diversity using Mahalanobis D^2 statistic [20]and Principal Component Analysis (PCA). This was performed using TNAUSTAT software[21]and PCA was performed using the R (4.3.0) packages *viz.,*FactoMineR, factoextra, tidyverse, devtools, ggplot2 and ggbiplot. Correlation analysis was performed using the R (4.3.0) packages *viz.,* corrplot and ggcorrplot.

3. RESULTS AND DISCUSSION

3.1 Per se performance and Genetic variability studies

The combined analysis of variance (ANOVA) revealed significant genotype mean sum of squares attributable to fifty-one rice genotypes for every trait studied, significant season mean sum of squares for every trait except TGW, and significant genotype x seasons interaction for every trait except TGW and KB (Table 2.). This finding implies that all genotypes for yield-related characteristics and physico-chemical traits exhibit a spectrum of genetic variability. Earlier researchers[22, 23] had also noted a significant level of genetic variability in the experimental material for the studied grain yield and quality traits. Pooled estimates of mean, range, variability, heritability and genetic advance as per cent of mean for all the studied yield and grain quality traits in both the seasons were given in Table 3.

Table 2: Analysis of variance for biometrical and physico-chemical traits estimated over two seasons

Characters	Genotypes	Seasons	Genotypes x Seasons	Error
df	50	1	50	100
DFF	553.93**	___68.25**	_5.186**	_2.12
PH	1585.14**	___41.76*	10.732*	_9.67
PL	__17.56*	__13.08**	__1.04**	_1.88
NPT	__36.39**	____7.10**	__6.23*	_1.91
NFG	6910.51**	__33.82**	__8.61**	32.36
TGW	__58.21**	1__5.01	__0.01	_0.39
SPY	_183.53**	2388.39**	234.00**	_1.55
KL	__55.14**	2137.11**	_70.38*	0.004
KB	___0.95**	__0.003*	0.0013	0.004
L/ B RATIO	___1.76**	__0.003*	_0.001*	0.006
KLAC	__17.33**	___0.04*	__0.01*	_0.02
KBAC	2088.32**	_120.00**	_54.31*	0.003
LER	___5.52*	___0.24**	0.0003*	0.0005
BER	1920.10**	_155.15**	_55.72*	0.002
AC	2805.65**	__87.41**	_77.35**	_1.05
GC	4199.09**	2294.42**	318.26**	86.16
GT	_478.01**	__96.52**	__4.72**	__0.20
WUR	___6.25**	___2.73**	__0.07*	__0.02
VER	___4.90**	___1.47**	__1.13*	__0.03

** - significant at 1% level and * - significant at 5% level

Table 3a: Pooled estimates of mean and variability of fifty-one diverse rice genotypes for biometrical and physico-chemical traits

Genotype	DFF	PH	PL	NPT	NFG	TGW	SPY	KL	KB	L/ B	KLAC	KBAC	LER	BER	AC	GC	GT	WUR	VER
AD16024	96.00	95.62	23.91	14.78	129.50	24.26	25.48	5.13	2.14	2.40	8.83	2.73	1.72	1.28	21.89	78.79	3.25	2.39	3.90
AD16028	93.50	97.89	24.66	14.35	139.68	20.03	26.68	5.48	1.68	3.27	9.88	2.48	1.80	1.48	20.04	80.29	4.00	2.35	4.32
AD16052	82.00	83.52	20.12	12.99	159.39	21.25	23.03	5.83	1.48	3.95	9.73	2.64	1.67	1.79	18.96	80.93	3.00	3.77	3.85
AD17020	93.25	102.67	21.41	11.79	131.56	23.97	22.17	5.68	1.69	3.37	7.73	2.73	1.36	1.62	18.33	73.09	4.00	2.86	3.95
AD17037	95.00	98.10	23.62	16.39	149.94	21.60	24.35	5.83	1.53	3.83	9.25	2.91	1.59	1.91	18.02	78.42	3.25	4.04	4.07
AD18538	82.75	116.30	23.86	14.97	136.35	26.59	22.38	5.13	1.98	2.60	9.26	2.83	1.81	1.43	22.31	71.69	4.75	2.71	3.81
AD18545	88.25	113.09	24.79	13.78	155.08	26.83	24.04	5.15	2.08	2.49	9.33	2.26	1.81	1.09	18.00	83.13	3.75	4.35	4.54
AD18573	85.50	109.05	24.25	15.00	156.24	24.11	22.56	5.10	2.08	2.48	8.16	2.73	1.60	1.32	18.10	86.53	3.00	3.02	4.01
AD18600	88.00	102.63	22.28	11.84	138.53	22.60	25.33	5.01	2.04	2.46	8.60	2.60	1.72	1.28	21.99	85.33	4.75	4.23	3.67
AD19055	84.50	95.12	23.34	14.95	128.10	21.35	24.09	6.08	1.98	3.08	9.64	2.68	1.59	1.36	21.58	76.89	4.75	2.89	4.18
AD19224	84.75	91.72	23.11	14.06	146.12	21.36	25.04	5.54	1.68	3.31	9.25	2.88	1.67	1.72	21.34	74.02	4.00	2.13	3.90
ADT37	83.75	105.72	22.04	14.74	185.83	22.89	33.48	5.14	2.66	1.94	7.78	2.89	1.52	1.09	21.77	81.88	3.25	3.41	5.52
ADT43	82.00	91.72	20.23	19.01	136.21	16.69	40.78	6.28	1.98	3.17	8.20	2.68	1.31	1.35	23.43	72.26	4.75	3.72	3.76
ADT53	94.00	103.19	21.58	22.41	115.55	15.14	37.19	6.40	2.14	3.00	9.73	2.83	1.52	1.32	23.55	68.96	3.75	3.56	4.02
ADT54	110.00	93.62	25.38	21.49	161.38	17.25	31.41	6.16	1.98	3.12	10.15	2.80	1.65	1.42	22.78	69.52	4.75	3.39	3.70
ASD16	87.50	102.46	23.58	16.96	246.92	23.75	28.33	5.39	2.79	1.94	8.15	3.69	1.51	1.32	24.38	86.33	4.50	4.26	5.48
AZUCENA	112.75	133.03	22.36	19.63	110.68	24.07	44.03	6.14	3.18	1.93	7.58	3.30	1.24	1.04	7.54	88.97	4.50	3.05	5.48
BPT5204	112.00	101.20	21.47	14.19	189.08	18.34	19.87	5.43	1.78	3.06	10.50	2.83	1.94	1.59	21.21	87.72	4.25	2.34	3.41
BURMA KAVUNI	113.50	139.58	20.27	13.78	95.14	24.78	20.55	5.63	2.63	2.14	7.23	3.23	1.29	1.23	26.43	65.17	1.75	2.82	4.28
CB12122	81.00	109.82	24.12	14.52	124.46	22.02	26.60	5.77	2.06	2.80	10.19	2.36	1.77	1.15	20.97	88.94	4.25	2.94	4.09

Comment [H1]: This Table need to be improved and subsquently to be lebelled a, b and c

Formatted Table

Genotype	DFF	PH	PL	NPT	NFG	TGW	SPY	KL	KB	L/ B	KLAC	KBAC	LER	BER	AC	GC	GT	WUR	VER
CB13132	88.00	105.04	26.24	16.00	131.20	24.72	23.01	5.25	1.88	2.81	9.92	2.56	1.89	1.37	20.96	74.29	3.25	2.59	3.61
CB15174	106.50	96.60	22.43	11.93	162.00	22.77	23.00	5.88	1.68	3.51	10.46	2.48	1.78	1.48	19.76	76.96	4.75	2.15	4.35
CB15569	92.25	95.65	22.75	15.06	138.89	17.19	25.47	5.33	1.25	4.26	8.53	2.63	1.60	2.10	21.55	73.31	4.75	3.48	4.32
CB15714	84.75	101.38	23.54	17.45	127.87	27.94	24.12	5.78	1.58	3.68	10.51	2.38	1.82	1.52	23.43	87.76	3.75	2.11	4.11
CB15801	85.50	97.77	18.53	13.08	121.41	21.08	25.38	5.57	1.96	2.84	9.16	2.80	1.65	1.43	18.75	87.13	4.75	4.09	3.78
CB16605	81.25	95.17	21.20	15.97	173.79	24.44	24.38	5.53	1.75	3.16	9.74	2.74	1.76	1.57	22.92	86.08	4.25	1.92	4.00
CB16723	84.50	99.78	20.75	12.31	170.34	22.53	22.60	6.10	1.98	3.09	9.88	2.86	1.62	1.45	20.57	71.33	3.75	2.91	4.37
CB17528	82.50	104.68	22.79	16.51	151.37	27.48	26.34	6.53	2.08	3.15	11.65	2.68	1.79	1.29	18.37	78.16	4.75	1.69	4.41
CB19132	97.00	136.80	24.10	18.18	171.45	23.62	26.06	5.40	1.98	2.73	10.05	2.63	1.86	1.33	22.95	74.46	4.75	1.71	3.94
CO51	83.00	91.07	21.72	16.02	142.62	22.91	33.93	5.48	1.98	2.77	9.65	2.98	1.76	1.51	22.37	81.24	3.25	2.06	3.81
CO52	110.50	117.91	24.50	22.74	177.67	16.94	39.39	5.61	1.80	3.12	10.23	3.23	1.82	1.79	21.46	87.30	4.25	4.50	3.99
GEDUMANI	98.00	132.63	22.72	11.98	99.45	21.09	20.92	5.64	2.33	2.43	8.03	3.18	1.43	1.37	23.53	61.39	1.75	2.69	4.01
Improved White Ponni	108.00	142.94	24.06	17.19	230.61	16.71	43.40	5.58	1.75	3.19	10.80	2.83	1.94	1.62	23.21	87.15	5.00	2.09	3.78
KAATUYANAM	93.25	135.00	22.10	10.59	84.41	25.55	18.58	5.75	2.18	2.65	8.55	3.28	1.49	1.51	26.29	58.55	1.75	1.73	3.87
KARUPPU KAVUNI	112.75	172.54	21.23	12.18	86.47	24.05	21.75	5.46	2.56	2.14	7.53	3.24	1.38	1.27	23.67	60.92	1.75	3.11	4.07
KAVUNI	113.00	152.57	20.21	12.42	105.97	26.16	19.19	6.23	2.38	2.63	10.04	3.14	1.61	1.32	22.67	65.30	1.00	3.64	4.55
KHAO DO NGOI	105.50	105.14	19.30	13.01	65.56	21.35	23.51	6.08	3.13	1.95	7.93	3.93	1.30	1.26	8.65	87.36	3.50	3.85	5.32
OTTADAI	104.75	133.15	21.74	12.06	97.90	23.63	19.18	5.91	2.53	2.34	8.43	3.45	1.43	1.37	27.03	57.54	1.00	1.93	3.95
PALAWAN	115.50	137.04	23.02	15.61	106.20	26.30	19.76	5.13	3.08	1.67	6.13	3.15	1.20	1.02	8.68	77.00	4.50	3.34	5.76
PB1	101.50	89.49	24.64	13.98	133.00	22.58	32.50	7.38	1.90	3.89	15.03	2.58	2.04	1.36	19.51	72.10	4.50	1.80	4.11
PB1121	98.75	113.16	26.45	14.4	111.	26.	30.9	8.0	1.8	4.3	19.6	2.38	2.4	1.2	21.7	82.6	3.2	4.31	4.57

Formatted Table

Genotype	DFF	PH	PL	NPT	NFG	TGW	SPY	KL	KB	L/ B	KLAC	KBAC	LER	BER	AC	GC	GT	WUR	VER
				2	16	91	6	9	8	2	3		3	7	9	2	5		
RNR15048	97.00	96.24	25.56	15.41	206.60	12.79	21.31	5.63	1.81	3.10	8.53	2.50	1.52	1.38	23.17	88.05	3.75	4.15	4.07
SIVAPPUM ALLI	102.25	152.28	22.02	10.78	128.38	21.86	17.10	5.13	2.35	2.18	7.43	3.06	1.45	1.30	25.59	64.07	2.00	2.50	3.80
THAILAND KAVUNI	116.75	128.59	21.16	11.61	87.25	25.61	20.70	5.61	2.45	2.29	7.91	3.13	1.41	1.28	24.94	64.39	2.75	3.09	4.07
THIRUPAT HISARAM	117.50	135.16	25.00	11.62	93.95	22.58	23.43	6.16	2.58	2.39	7.63	3.43	1.24	1.33	23.68	67.33	1.25	3.99	4.81
TN1	86.25	108.71	22.05	15.43	87.92	24.11	26.35	5.77	2.99	1.93	8.68	3.48	1.50	1.17	21.72	83.08	3.75	1.84	5.28
TPS5	87.75	98.30	24.97	14.46	258.91	21.95	40.23	6.03	3.13	1.93	8.46	3.43	1.40	1.10	20.84	78.58	3.00	2.81	5.25
TRY1	109.50	95.65	21.98	16.92	129.63	22.31	22.55	5.50	2.85	1.93	7.96	2.96	1.45	1.04	23.08	82.85	3.25	3.04	4.88
TRY2	111.75	91.46	22.69	16.16	137.93	23.09	22.96	5.88	2.99	1.97	8.46	4.14	1.44	1.39	21.70	85.68	4.00	2.75	5.12
TRY3	110.50	114.88	24.49	23.31	158.24	26.73	35.68	4.94	2.63	1.88	6.24	2.88	1.27	1.10	23.16	87.19	3.50	2.00	5.75
VGD1	96.00	93.30	25.26	17.65	219.68	8.83	35.27	3.73	1.63	2.29	7.53	2.89	2.02	1.78	22.78	79.18	4.00	2.28	4.11
Maximum	117.50	172.54	26.45	23.31	258.91	27.94	44.03	8.09	3.18	4.32	19.63	4.14	2.43	2.10	27.03	88.97	5.00	4.50	5.76
Minimum	81.00	83.52	18.53	10.59	65.56	8.83	17.10	3.73	1.25	1.67	6.13	2.26	1.20	1.02	7.54	57.54	1.00	1.69	3.41
Pooled Mean	96.71	110.90	22.85	15.17	141.83	22.25	26.60	5.69	2.17	2.75	9.21	2.92	1.61	1.39	21.20	77.39	3.60	2.94	4.30
C.D. 5%	2.04	4.34	1.92	1.93	7.95	0.87	1.74	0.09	0.08	0.11	0.17	0.08	0.03	0.06	1.43	12.97	0.63	0.18	0.24
C.D. 1%	2.69	5.74	2.53	2.55	10.49	1.15	2.30	0.12	0.11	0.14	0.23	0.11	0.04	0.08	1.89	17.12	0.83	0.24	0.32
GCV (%)	12.15	17.90	7.32	19.35	29.24	17.10	25.36	11.04	22.43	24.03	22.59	13.56	15.20	16.35	18.26	9.84	29.50	27.99	13.94
PCV (%)	12.24	18.11	9.47	21.39	29.51	17.33	25.79	11.10	22.61	24.20	22.63	13.71	15.25	16.66	18.88	15.51	32.04	28.34	14.50
h^2 (bs) (%)	98.48	97.60	59.78	81.83	98.15	97.37	96.70	98.99	98.48	98.65	99.65	97.86	99.23	96.26	93.47	40.24	84.76	97.51	92.46
GAM (%)	24.83	36.42	11.66	36.06	59.67	34.77	51.38	22.63	45.86	49.17	46.44	27.63	31.18	33.04	36.37	12.86	55.95	56.95	27.62

Formatted Table

Among the studied genotypes, the culture AD 16052 (83.52 cm) was the dwarf genotype while the landrace *Karuppu Kavuni* (172.54 cm) was the tallest genotype. The yield related traits, PL ranged from 18.53 cm (CB 15801) to 26.45 cm (Pusa Basmati 1121), NPT ranged from 10.59 (Kaatuyanam) to 23.31 (TRY 3), NFG ranged from 65.56 (Khao Do Ngoi) to 258.91 (TPS 5) and TGW ranged from 8.83 g (VGD 1) to 27.94 g (CB 15714). The SPY showed a wide difference from 17.10 g (*Sivappumalli*) to 44.03 g (Azucena) with an average yield of 26.60 g.

Regarding the grain physico-chemical traits, the genotypic variation for KL varied from 3.73 mm (VGD 1) to 8.09 mm (Pusa Basmati 1121) with an overall average of 5.69 mm while the KB showed a variation from 1.25 (CB 15669) mm to 3.18 mm (Azucena) with a pooled mean of 2.17 mm. The genotypes under study allowed for a well-rounded categorization of grain form, including short bold (18), short slender (13), medium slender (7), long slender (7), long bold (4), and extra-long slender (2). LER ranged from 1.2 to 2.43 times while the breadthwise elongation ratio was from 1.02 to 2.10. Based on the AC of the rice grains, the genotypes were categorized into four groups: extremely low (3), low (9), moderate (36) and high (3). The genotypes were divided into the soft (49) and medium (2) gel categories based on a GC test. The experiment led to the classification genotypes as per their ASV as low (8), low to medium (17), medium (23) and high (3).

Any crop improvement plan that aims to increase yield and improve the physico-chemical traits must have a thorough understanding of genetic diversity within the population that is already available. Therefore, it is crucial to understand genetic variability that is apportioned from the environmental influences. The findings of the current investigations showed that every trait under study had a higher PCV than GCV. The difference between the PCV and GCV was remarkably small, indicating that all these traits were not significantly influenced by the environment except for GC which showed a substantial difference confirming the influence of environment in determining this trait.

High PCV and GCV were seen in the traits *viz.,* NPT, NFG, SPY, KB, L/B ratio, KLAC, ASV and WUR, while the traits, DFF, PH, TGW, KL, KBAC, LER, BER, AC and VER showed moderate PCV and GCV and low PCV and GCV was shown by PL. This was parallel to the findings of Sudeepthi, Srinivas [24] for NPT and TGW, Sujitha, Pillai [25] for DFF, PH, TGW and KL, Kumar, Kumar [26] for DFF, KBAC, LER, BER, VER, L/B, KLAC and WUR, Sadhana, Raju [27] for NFG, KL, KBAC and LER, Lakshmi, Shanmuganathan [28] for NFG, NPT, SPY, DFF and PH, Bhargavi, Suneetha [29] for AC and ASV and Bhargavi, Suneetha [29] for NFG, NPT, SPY, L/B, KL, KBAC, LER, BER and VER. Contrary findings by Sadhana, Raju [27] and Maurya, Dwivedi [30] for KB were found. The likelihood of choosing a suitable genotype will increase if a given crop species has a large range of genetic variability. High genetic variability is indicated by a moderate to high PCV and GCV and this does give a greater scope for simple selection for improving the traits. Low PCV and GCV estimates of PL suggest a restricted genetic background for the trait. Improvement in these traits could be brought out by hybridization or induced mutagenesis to widen the genetic base followed by selection in later generations.

Despite the fact that heritability estimates offer an indication of the relative worth of selection based on phenotypic expression, heritability and genetic advance when considered together provides more reliable information in forecasting the outcome of selection. The heritability and the genetic advance as per cent of mean were reported to be high for all the studied traits except PL and GC which showed moderate heritability and genetic advance. Similar results were obtained by earlier workers like Sujitha, Pillai [25] for PL, NPT, NFG, TGW, KL and KB, Kumar, Kumar [26] for PL, NPT, NFG, TGW, KL, KB, L/B, KLAC, KBAC, LER and BER, Bhargavi, Shanthi [31] and Lakshmi, Shanmuganathan [28] for DFF, PH and SPY, Bhargavi, Suneetha [29] and Singh [32] for GC, ASV, WUR and VER, Singh, Snehi [33] and Mahesh, Ramesh [34] for AC and Dinkar, Kumar [35] for L/B, KLAC, KBAC and LER, whereas contrary findings for GC were given by Singh [32] and Kumar, Manhar [36]. High heritability in conjunction with high genetic advance indicates that selection may be effective since the heritability is most likely due to additive gene effects.

3.2 Mahalanobis' Diversity Analysis

The most crucial instrument in the arsenal of every plant breeder is diversity since it allows for the creation of variation and selection such that without which no varietal development could not be achieved. In the present study, using Mahalanobis' D^2 statistics, the phenotypic distance matrix was constructed among fifty-one genotypes using the 19 yields and yield contributing traits along with physico-chemical traits. Using the toucher clustering technique, genotypes were grouped into ten clusters with a cut-off value of 4101.045. Cluster I was the largest, comprising 25 genotypes, displaying its relatedness followed by Cluster III (11 genotypes), Cluster II (6 genotypes), Cluster IV and VI (2 genotypes). Clusters V (*Kavuni*), VII (Pusa Basmati 1), VIII (VGD 1), IX (*Thirupathisaram*) and X (Pusa Basmati 1121) were solitary clusters with one genotype in each cluster that showed their uniqueness for the studied traits (Table 4). The maximum contribution in the manifestation of genetic divergence was exhibited by L/B ratio (48.55%) followed by KB (17.88%) and other traits to follow (33.57%) (Fig. 1). Though both the basmati genotypes share many common features, they remain in separate clusters owing to the fact that they are derived from different genetic background. *Kavuni* stands solitary most of the times due to their exceptional nutritional quality and morphological features despite its poor yielding ability.

Table 4: Distribution of fifty-one genotypes based on biometrical and physico-chemical traits as computed by Mahalanobis' D^2 analysis

Clusters	**Number of genotypes**	**Details of genotypes**
Cluster I	25	AD 16024, CB 13132, AD 18545, AD 18573, ADT 37, CB 12122, AD 16052, AD 18600, RNR 15048, CB 16723, AD 19055, CO 51, TN 1, AD 18538, AD 16028, AD 17020, AD 19224, *Sivappumalli*, AZUCENA, TPS 5, TRY 1, ADT 53, CB 15801, TRY (R) 2, ADT 54
Cluster II	6	AD 17037, CB 19132, CB 17528, BPT 5204, CB 16605, CB 15569
Cluster III	11	ADT 43, CB 15114, *Thailand Kavuni*, CB 15714, *Burma Kavuni*, ASD 16, *Gedumani*, *Kaatuyanam*, *Ottadai*, PALAWAN, *Karuppu Kavuni*
Cluster IV	2	CO 52, Improved White Ponni
Cluster V	1	*Kavuni*
Cluster VI	2	KHAO DO NGOI, TRY 3
Cluster VII	1	PUSA BASMATI 1
Cluster VIII	1	VGD 1
Cluster IX	1	*Thirupathisaram*
Cluster X	1	PUSA BASMATI 1121

(Tocher cut off value = 4101.045)

Comment [H2]: Centre Ctrl +E is not fine please change

Formatted: Left

Formatted: Left

Formatted: Left

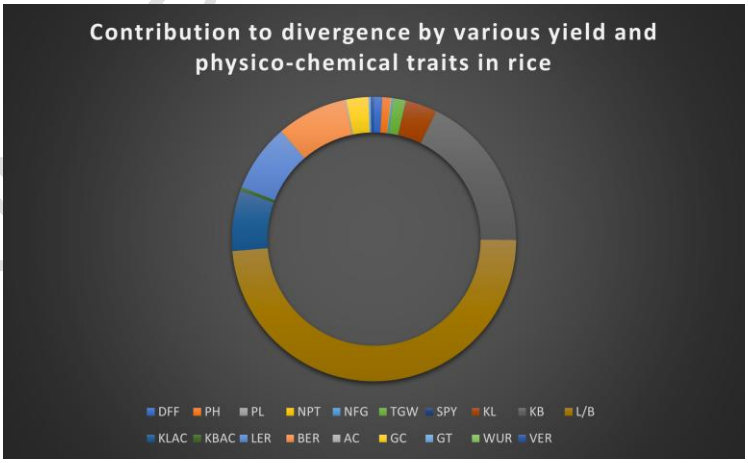


Fig. 1:~~-~~ Contribution to divergence by various yield and physico-chemical traits in rice

The intra and inter-cluster distances of clusters derived from computed D^2analysis showed the statistical difference among 51 genotypes. The maximum inter cluster distance was found between the clusters III and X (83850.971) (Table 5), where cluster X was solitary cluster and reported to have all the desired physical grain dimensional properties attributing to kernel elongation which was evident from their high cluster means for PL, KL, KLAC, L/B ratio, LER and WUR (Table 6). This was followed by the inter cluster distance between cluster VI and X, which were significantly divergent for the kernel dimensions i.e., cluster VI contained genotypes with bold grains and low LER while the cluster X contained extra-long slender genotype with high kernel elongation. Hence, selection of genotypes within these clusters (clusters X, III and VI) holds great promise as parents for obtaining promising elite lines through inter-varietal hybridization and also to create further variability for these traits [37]. The maximum intra cluster distance was observed in cluster III (3137.756) that contained mostly landraces, along with some released varieties, genetically stabilized cultures and a tropical *japonica* genotype, indicating wide genetic variation among the genotypes belonging to these clusters. The chances of developing good segregants by crossing the genotypes of the same cluster showing high values for intra-cluster distance is very high [22, 37]. Cluster IV could be adjudged to have high cluster means for yield related traits (NPT and SPY) while Cluster X had desirable organo-leptic traits (KL, KLAC, L/B ratio, LER and WUR) along with PL as evidenced from the Table 6.

Table 5: Average inter and intra (bold values) cluster distances of ten clusters computed from Mahalanobis' D^2 analysis using fifty-one genotypes for biometrical and physico-chemical traits

Cluster Number	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**
I	**2415.713** **(49.150)**	3992.769 (63.188)	4914.137 (70.101)	8747.742 (93.529)	4247.389 (65.172)	19158.184 (138.413)	6611.300 (81.310)	26045.490 (161.386)	14440.667 (120.169)	28149.548 (167.778)
II		**2099.488** **(45.820)**	10381.541 (101.890)	3233.584 (56.865)	5450.171 (73.825)	31846.480 (178.456)	5450.578 (73.828)	16892.819 (129.972)	25081.136 (158.370)	18012.788 (134.212)
III			**3137.756** **(56.016)**	18715.787 (136.806)	5465.851 (73.931)	10710.509 (103.492)	10422.840 (102.092)	37870.160 (194.603)	6134.569 (78.323)	83850.971 (289.570)
IV				**1046.623** **(32.352)**	10733.635 (103.603)	45669.402 (213.704)	9926.005 (99.629)	15140.174 (123.045)	38352.695 (195.838)	9883.5804 (99.416)
V					**0.000** **(0.000)**	23904.255 (154.610)	5974.423 (77.294)	24213.622 (155.607)	12570.794 (112.120)	30054.699 (173.363)
VI						**1172.149** **(34.237)**	28572.113 (169.033)	69896.035 (264.379)	5101.730 (71.426)	72385.617 (269.046)
VII							**0.000** **(0.000)**	10897.045 (104.389)	21179.139 (145.531)	34881.468 (186.766)
VIII								**0.000** **(0.000)**	59804.947 (244.550)	33495.219 (183.017)
IX									**0.000** **(0.000)**	44352.688 (210.601)
X										**0.000** **(0.000)**

Table 6: Cluster mean value of ten clusters computed from Mahalanobis' D^2 analysis using fifty-one rice genotypes for biometrical and physico-chemical traits

CLUSTER	DFF	PH	PL	NPT	NFG	TGW	SPY	KL	KB	L/B	KLAC	KBAC	LER	BER	AC	GC	GT	WUR	VER
Cluster I	91.24	102.84	22.90	15.123	144.958	21.959	25.934	5.604	2.188	2.671	8.964	2.865	1.605	1.344	20.735	79.511	3.800	3.202	4.427
Cluster II	93.000	104.767	22.338	16.183	162.401	22.228	28.402	5.683	1.729	3.361	9.967	2.750	1.755	1.636	20.852	80.200	4.333	2.700	4.175
Cluster III	100.773	123.939	21.672	13.199	121.211	23.987	23.483	5.686	2.347	2.537	8.293	3.082	1.455	1.334	22.711	62.707	3.227	2.984	4.487
Cluster IV	108.250	129.370	24.978	20.355	202.653	16.628	41.975	5.600	1.800	3.113	10.625	3.050	1.898	1.693	22.318	96.800	4.500	3.465	4.035
Cluster V	111.500	152.165	20.400	11.530	105.065	26.255	19.235	6.250	2.350	2.665	10.050	3.150	1.605	1.340	23.275	52.650	1.000	3.810	4.700
Cluster VI	107.500	110.640	22.20	18.820	110.670	24.060	30.170	5.530	2.890	1.910	7.100	3.430	1.290	1.180	16.630	89.730	3.500	3.100	5.690
Cluster VII	101.500	98.025	23.845	14.030	130.410	22.095	32.930	7.390	1.925	3.835	15.025	2.550	2.035	1.325	20.015	63.200	4.000	1.970	4.260
Cluster VIII	95.000	93.475	26.215	17.875	216.680	8.800	36.285	3.750	1.650	2.275	7.550	2.950	2.015	1.785	23.055	80.850	4.000	2.450	4.260
Cluster IX	118.000	134.540	25.620	7.835	94.025	22.900	24.015	6.150	2.550	2.410	7.650	3.450	1.245	1.355	23.185	58.825	1.000	4.160	4.960
Cluster X	98.000	111.830	26.525	14.720	108.255	26.685	30.930	8.100	1.875	4.320	19.650	2.375	2.425	1.265	21.970	86.850	3.000	4.480	4.720

Comment [H3]: Improve this table

Formatted Table

3.3 Principal Component Analysis (PCA)

The multivariate method of principal component analysis is widely used for assessing genetic diversity and identifying the most important traits that account for the greatest variation among the genotypes [23]. In PCA, data standardization made characteristics equally contribute to the divergence studies regardless of the units used [38]. It is noteworthy that similar trend was noticed in the results of PCA done in both the season as reported by Gunasekaran, Seshadri [39]. Scree plot graph as depicted in Fig. 2 explained the percentage of variance associated with each principal components (PCs) obtained by drawing a graph between Eigen values and principal component numbers. The top six PCs with eigen values greater than one was found to account for 76.77% variation among the genotypes (Table 7). PC1 accounted for 28.9% of the total variability and positively associated with days to 50 per cent flowering, PH, TGW, KB, KBAC, WUR and VER. The second PC accounted for 15.8% of the total variation and positively defined by days to 50 per cent flowering, PH, TGW, KL, L/B ratio, KLAC, LER, BER and amylose content. The third PC contributed to 10.9% of the total variation and positive loadings to this PC were given by the traits *viz.,* DFF, PL, NPT, TGW, SPY, KL, KB, L/B ratio, KLAC, LER, AC, GC, ASV, WUR and VER. This PC was contributed positively by most of the physico-chemical and yield-related traits as reported by Kesh, Battan [23] who gave PC1 with positive loadings by most of the traits particularly the grain quality traits.

Table 7: Eigenvalue, percentage of variation, cumulative percentage, and eigenvector value for the first 10 principal components**.**

	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**	**PC10**
Standard deviation	2.343	1.733	1.436	1.236	1.205	1.026	0.926	0.851	0.775	0.691
Eigen value	5.492	3.002	2.063	1.527	1.451	1.052	0.857	0.724	0.600	0.477
Percentage of variance	28.905	15.799	10.856	8.038	7.637	5.539	4.509	3.809	3.160	2.512
Cumulative percentage of variance	28.905	44.704	55.56	63.598	71.234	76.773	81.282	85.092	88.251	90.763
DFF	0.212	0.016	0.057	0.397	-0.368	-0.149	-0.348	0.006	0.262	0.132
PH	0.252	0.193	-0.011	0.374	0.002	-0.218	-0.167	-0.251	0.177	0.281
PL	-0.114	-0.135	0.153	0.429	0.143	-0.533	0.037	0.240	-0.455	-0.147
NPT	-0.140	-0.391	0.118	0.077	-0.084	0.122	-0.347	-0.183	-0.321	0.386
NFG	-0.213	-0.338	-0.121	0.180	0.089	-0.043	0.253	0.175	0.033	-0.031
TGW	0.176	0.174	0.309	-0.162	0.441	-0.043	-0.027	0.135	0.071	0.467
SPY	-0.203	-0.302	0.057	0.297	-0.173	0.319	-0.017	-0.145	0.209	-0.196
GL	-0.039	0.209	0.530	0.014	-0.254	0.331	0.053	0.015	-0.212	-0.077
GB	0.367	-0.208	0.177	0.065	0.039	0.158	0.099	-0.010	0.005	-0.102
L/B	-0.339	0.256	0.105	-0.109	-0.199	0.001	-0.093	0.125	-0.144	0.124
GLAC	-0.257	0.192	0.462	0.157	-0.029	0.085	0.094	0.047	0.133	-0.003
GBAC	0.298	-0.131	-0.069	0.116	-0.236	0.291	0.154	0.441	0.053	0.177
LER	-0.339	0.095	0.182	0.201	0.144	-0.118	0.072	0.071	0.356	-0.002
BER	-0.252	0.135	-0.326	-0.040	-0.308	-0.013	-0.073	0.483	-0.017	0.326
AC	-0.141	0.086	-0.230	0.362	0.262	0.364	0.339	-0.257	-0.229	0.411
GC	-0.174	-0.375	0.143	-0.155	0.092	-0.104	0.154	0.078	0.487	0.238
GT	-0.229	-0.266	0.043	-0.252	0.064	0.009	-0.445	-0.168	-0.044	0.079
WUR	0.015	-0.088	0.100	-0.212	-0.496	-0.375	0.512	-0.385	-0.070	0.245
VER	0.236	-0.309	0.284	-0.077	0.022	-0.023	0.044	0.277	-0.174	0.1199

Comment [H4]: Avoid Centre Ctrl +E

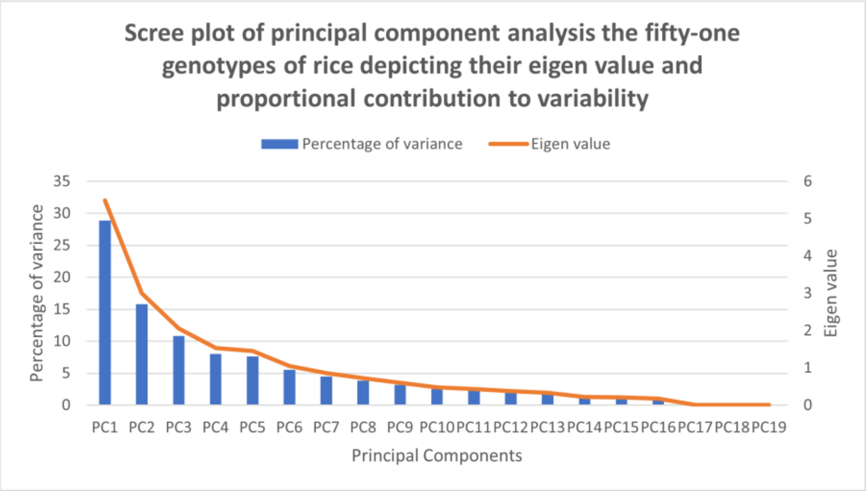


Fig. 2: Scree plot of principal component analysis the fifty-one genotypes of rice depicting their eigen value and proportional contribution to variability

From the PCA biplot (Fig. 3), maximum vector length was recorded by the trait L/B ratio and KB revealing its contribution to the divergence. It is evident from the vector angles that SPY was positively related (acute angle) by NPT and NFG while it was negatively correlated (obtuse angle) by PH and TGW. LER had close association (acute angle) with KL, L/B ratio, KLAC and AC, while it had negative association with KB, KBAC, GC, ASV, WUR and VER. The genotypes present close to the vectors of the same quadrant would be the best performing for those traits. The genotypes *viz.,* Pusa Basmati 1 and Pusa Basmati 1121 were found close to the trait vectors namely, KL, KLAC, L/B ratio, LER and AC revealing its uniqueness for those traits. The genotypes CO 52 and VGD 1 were found near the yield related trait vectors implying their high yielding behaviour. The genotypes, TRY 3, Palawan, Azucena, Khao do ngoi and TPS 5 were found in the quadrant where the trait vectors of KB, KBAC and VER were found. The genotypes of group 8 (Azucena, Khao do ngoi and Palawan), group 9 (ASD 16, TPS 5 and TRY 3) and group 10 (ADT 37, TN 1, TRY 1, TRY (R) 2) were having bold grains and yielded high cooked volume on cooking. *Japonica* types could be used in creating the new plant types that are fit to produce great yield potential inspite of their poor cooking quality especially in the tropical *japonica* types [40]. It was interesting to note that the tropical *japonica* types used in the present study stood out from the genotypes with desirable cooking qualities. The genotypes from group 3 (AD 16052, CB 15569, CB 15714, Pusa Basmati 1 and Pusa Basmati 1121) and group 5 (AD 16028, AD 17020, AD 17037, AD 18538, AD 19055, AD 19224, CB 12122, CB 13132, CB 15114, CB

Formatted: Line spacing: 1.5 lines

15801, CB 16605, CB 16723, CB 17528, CB 19132, CO 51) were composed of slender grains and found promising for cooking quality and AC. Genotypes contained in group 8, 9 and 10 were exactly found in the opposite quadrant where the genotypes contained in group 3 and 5 were present. Hybridization between the genotypes of these quadrants may lead to superior recombinants with transgressive segregation for both yield related and organo-leptic traits of rice. This is evident from both the results of Mahalanobis' D^2 analysis and that of Principal component analysis.

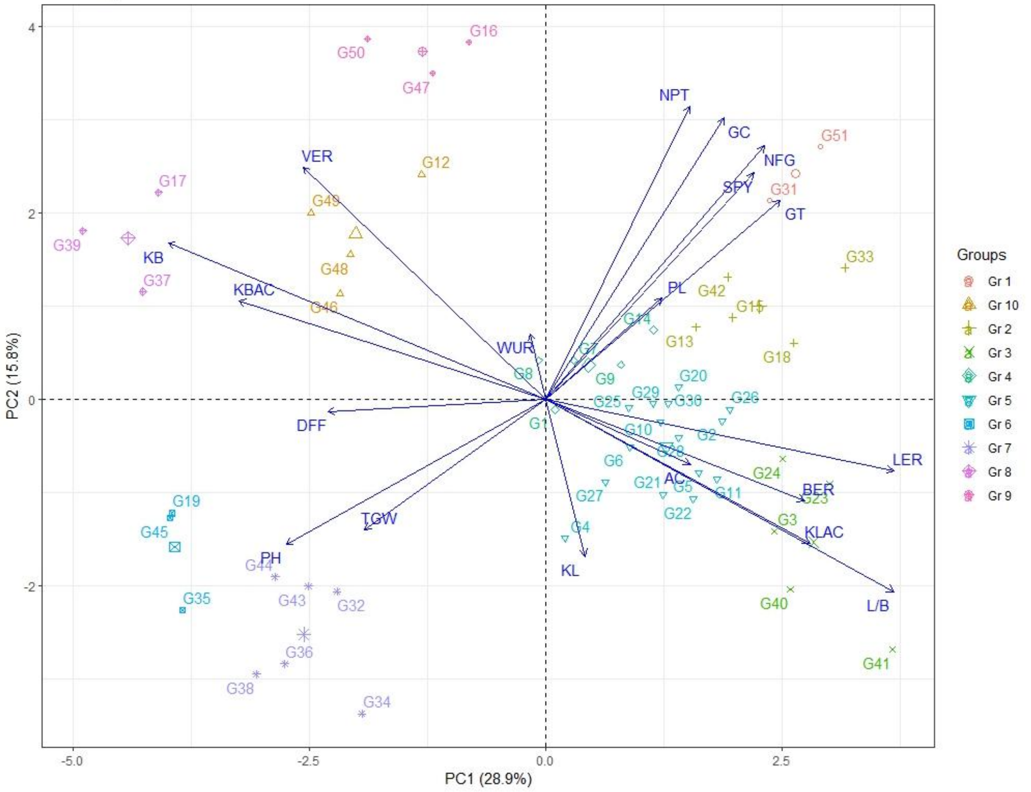


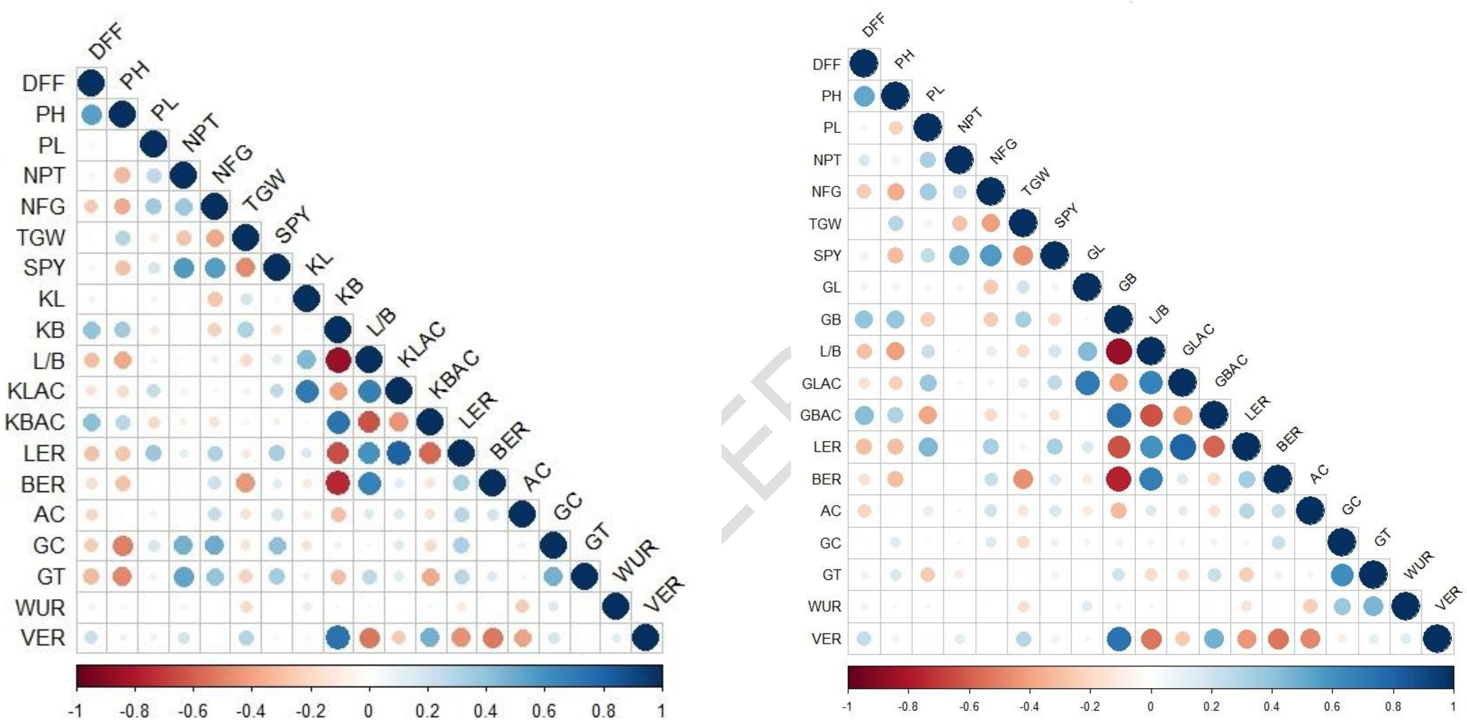
Fig. 3: PCA biplot of 50 rice accessions and 14 traits plotted by PC1 versus PC2 component.

3.4 Correlation analysis

Correlation analysis computes the mutual associations between numerous variables in plant breeding and identifies the constituent attributes that selection may rely on for the genetic enhancement of yield and physico-chemical traits. It was interesting to note that, both the seasons showed a more or less similar trend in the association among the studied traits

Formatted: Line spacing: 1.5 lines

(Fig. 4a and 4b). When yield related traits were taken into consideration, NFG had significant positive association with PL (r = 0.360), NPT (0.380) and SPY (r = 0.550) and significant negative association with PH (r = -0.370) and TGW (r = 0.390). Similar association trend was found in the study by Sudeepthi, Srinivas [24], Sujitha, Pillai [25] for PL, NPT, SPY and TGW and Kujur, Abhinav Sao [41] for PH. The SPY was having significant positive association with NPT (r = 0.560) and NFG (r = 0.550), while it had significant negative association with TGW (r = -0.480). The research yielded the above results due to the fact that increased panicle length and tillering ability accommodates a greater number of grains thereby increasing the grain yield while the compensatory mechanism lowers the test weight owing to reduced grain filling ability (Gunasekaran *et al.,* 2023). Balanced ideotype has to be achieved to get an overall compensatory physiological mechanism to improve the yield attributes [40].



(a) **(b)**

Fig. 4: Pearson's correlation matrix for the yield-related and grain quality traits studied during (a) *Kharif* 2021 and (b) *Rabi* 2021

~~With regard to physico-chemical properties, some noteworthy association between traits were found. KL had significant positive correlation with L/B ratio (r = 0.450) and KLAC (r = 0.700). KB showed significant positive association with KBAC (r = 0.730) but significant negative association with L/B ratio (r = -0.850), KLAC (r = -0.420), LER (r = -0.640) and BER (r = -0.760). L/B ratio and KLAC were~~

Regarding the physico-chemical properties, some noteworthy associations between traits were found. KL had significant positive correlation with L/B ratio (r = 0.450) and KLAC (r = 0.700). KB showed significant positive association with KBAC (r = 0.730) but significant negative association with L/B ratio (r = -0.850), KLAC (r = -0.420), LER (r = -0.640) and BER (r = -0.760). L/B ratio and KLAC were interdependent as evidenced by the strong positive association between them (r = 0.670).KL, KLAC, L/B ratio and LER are strongly in positive association implying the fact that selection of either of the traits would ultimately enhance the mean performance of the interdependent trait, while this pose a great logic in the resulted negative association of these traits with the KB, KBAC and BER as bold grains lower the L/B ratio and the length metrics of both the cooked and the uncooked grains [27, 29, 33, 35, 42-44].

LER had significant positive relation with KL (r = 0.160), L/B ratio (r = 0.590), KLAC (r = 0.810) and AC (r = 0.280), while it had strong negative association with KB (r = -0.640), KBAC (r = -0.580), WUR (r = -0.120) and VER (r = -0.450). LER's positive association with AC may be attributable to the fact that the branching starch molecules swell up while being cooked leading to sudden elongation lengthwise rather than breadthwise leading to high length kernel after cooking [45-47]. Earlier reports by various authors [46, 48] suggest that water uptake, volume expansion and linear elongation are positively correlated due to the fact that water uptake makes the kernel heavier and expandable leading to a good amount of cooked volume. It was clear from the current investigation that the kernel shape (L/B ratio) also influences the kernel elongation thereby water uptake leads to breadthwise expansion rather than lengthwise proving the negative association of water uptake and volume expansion with LER. This was supported by Ge, Xing [49] and Kumar, Manhar [36].

AC was negatively related to ASV (r = -0.160), water uptake (r = -0.260) and volume expansion ratio (r = -0.400). Water uptake and volume expansion decreases with increase in composition of amylose in rice grains. This was concomitant with the research findings of Mohapatra and Bal [48]. ASV had a strong positive association with GC (r = 0.470)which proves that genotypes with soft GC disperse well in alkaline medium and require low temperature to get gelatinized [50, 51] while it had a negative association with KB (r = -0.310) and KBAC (r = -0.380) that was against the findings of Pushpa *et al.* (2019). VER was in strong positive relation with KB (r = 0.740) and KBAC (r = 0.470), while it was negatively related to L/B ratio (r = -0.530), BER (r = -0.520) and AC (r = -0.400). This was in accordance with the results of Kumar, Manhar [36] for KB and KBAC and contrary to his results for L/B ratio and similar to the findings of Mohapatra and Bal [48].

Kharif (2021) revealed a temperature ranging from 23.4 to 31.7°C with an average of 27.6° C, relative humidity ranging from 27.1 to 82.1% with a mean humidity of 69.6%, 1 mm rainfall and 5.7 hours of sunshine. Also, the peak flowering time coincided with a temperature of 23° C and 57.1% RH while grain filling time accorded with the temperature of 27.3° C and 70.6% RH. *Rabi* 2021 season data showed a temperature ranging from 21.9 to 30.7° C with an average of 26.4° C, relative humidity ranging from 53.2 to 84.6% with an average humidity of 68.9%, 3.4 mm of rainfall and 6.2 hours of sunshine. Also, the peak flowering time coincided with a temperature of 20.7° C and 69.9% RH while grain filling time accorded with the temperature of 23.2° C and 61.6% RH. Even though there was a significant difference in the weather parameters during the experimental seasons, the genotypes exhibited consistent results in all the analysis done.

4. CONCLUSION

Per se performance identified the genotypes, VGD 1, CO 52, Improved white ponni, BPT 5204, RNR 15048, TRY 3, Azucena to be good yielders with better yield related traits, while Pusa Basmati 1, Pusa Basmati 1121, RNR 15048, Improved white ponni, BPT 5204, CB 15714, CB 12122 were found to have desirable cooking quality. It was interesting to find a large genetic distance between the genotypes, Improved white ponni, CO 52, VGD 1, BPT 5204, RNR 15048, Pusa Basmati 1121 and Pusa Basmati 1 and the genotypes *viz.,* TRY 3, TPS 5, Palawan, Azucena and Khao do ngoi as evident from the consistent results of D^2 analysis and Principal component analysis. Superior recombinants combining their yielding ability and anticipated cooking attributes can be derived from the hybridization between these genotypes especially making hybridization between the *indica* and the *japonica* types due to the large genetic distance between them. Simultaneous selection for the traits could be made for those with positive interdependencies. This goes with the positive significant association of single plant yield with number of productive tillers and number of filled grains per panicle, positive interdependence between linear elongation ratio, kernel length, L/B ratio, kernel length after cooking and amylose led to the discovery of selection tools for identifying elite cultivars with good yielding ability and physico-chemical attributes. Though the experiment was conducted over seasons, there was a similar trend in the clustering pattern and association analysis. This may aid in the selection for all the studied traits across seasons which could help in reducing the breeding cycle with proper planning. Thus, it is remarkable to conclude that hybridization between *indica* (with desirable organo-leptic properties) and *japonica* types (with novel plant types and yielding behaviour) would yield non-basmati genotypes which are comparable to the basmati genotypes and fetch premium price in the world rice market.

REFERENCES

1. Statista. World Rice acreage from 2012 to 2021: Statista; 2021 [Available from: https://www.statista.com/statistics/271969/world-rice-acreage-since-2008/#:~:text=This%20statistic%20shows%20the%20world,of%20rice%2Dcultivated%20area%20worldwide].
2. Indiastat. State/Seaon - wise Area, Production and Productivity of Rice in India (2021 - 2022) 2022 [Available from: https://www-indiastat-com/table/agriculture/state-season-wise-area-production-productivity-ric/1440252].
3. Indiastat. Per Capita Net Availability of Foodgrains in India (1951 to 2022) 2022 [Available from: https://www-indiastat-com/table/per-capita-availability/per-capita-net-availability-of-foodgrains-per-ann/6368].
4. Rajendran PA, Devi JN, Prabhakaran SV. Breeding for grain quality improvement in rice. Plant Breeding-Current and Future Views: IntechOpen; 2021.
5. Butardo VM, Sreenivasulu N, Juliano BO. Improving rice grain quality: State-of-the-art and future prospects. Rice grain quality: methods protocols2019. p. 19-55.
6. Singh R, Singh U, Khush G, Rohilla R. Genetics and biotechnology of quality traits in aromatic rices. Aromatic rices. 2000;5:47-70.
7. APEDA. Comparative statement for export of agri and processed food products (2021 - 2022) 2022
8. Kaur S, Panesar PS, Bera MB. Studies on evaluation of grain quality attributes of some basmati and non-basmati rice cultivars. Journal of Food Quality. 2011;34(6):435-41.
9. Bhattacharya K, Sowbhagya C. Water uptake by rice during cooking. Cereal Science Today. 1971;16(12):420-4.
10. Sidhu JS, Gill MS, Bains GS. Milling of paddy in relation to yield and quality of rice of different Indian varieties. Journal of Agricultural Food Chemistry. 1975;23(6):1183-5.
11. Bazrkar-Khatibani L, Fakheri B-A, Hosseini-Chaleshtori M, Mahender A, Mahdinejad N, Ali J. Genetic mapping and validation of quantitative trait loci (QTL) for the grain appearance and quality traits in rice (Oryza sativa L.) by using

Comment [H5]: The references should be arranged in aphabetical order while maintaining the numbering

recombinant inbred line (RIL) population. International Journal of Genomics. 2019;2019.

12. Bollinedi H, Vinod K, Bisht K, Chauhan A, Krishnan SG, Bhowmick PK, et al. Characterising the diversity of grain nutritional and physico-chemical quality in Indian rice landraces by multivariate genetic analyses. Indian Journal of Genetics. 2020;80(01):26-38.
13. IRRI. Standard evaluation system for rice: International Rice Research Institute; 1996.
14. Juliano B, Perez C. Results of a collaborative test on the measurement of grain elongation of milled rice during cooking. Journal of Cereal Science. 1984;2(4):281-92.
15. Sowbhagya C, Bhattacharya K. A simplified colorimetric method for determination of amylose content in rice. Starch-Stärke. 1971;23(2):53-6.
16. Little RR. Differential effect of dilute alkali on 25 varieties of milled white rice. Cereal Chem. 1958;35:111-26.
17. Cagampang GB, Perez CM, Juliano BO. A gel consistency test for eating quality of rice. Journal of the Science of Food Agriculture. 1973;24(12):1589-94.
18. Bhattacharjee P, Kulkarni PR, nutrition. A comparative study on the physical characteristics and cooking quality parameters of commercial brands of basmati rice. International journal of food sciences. 2000;51(4):295.
19. Pillaiyar P, Mohandas R. Hardness and color in parboiled rice produced at low and high temperatures. Journal of Food Science Technology. 1981;18:7-9.
20. Mahalanobis PC, editor On the generalized distance in statistics1936: National Institute of Science of India.
21. Manivannan N. TNAUSTAT-Statistical package. 2014.
22. Nagamani V, Shivakumar N, Nagaraja T. Genetic Diversity Analysis of Red Kernel Rice Genotypes using K-means Clustering for Grain Yield, its Components and Cooking Quality Traits. International Journal of Bio-resource Stress Management. 2022;13(8):845-53.
23. Kesh H, Battan KR, Khan M, Yadav S. Genetic diversity analysis of Basmati rice (*Oryza sativa*) genotypes for grain yield and quality traits. Journal of Agricultural Sciences. 2022;92(7):62 - 5.

24. Sudeepthi K, Srinivas T, Kumar BR, Jyothula D, Umar SN. Assessment of genetic variability, character association and path analysis for yield and yield component traits in rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding. 2020;11(01):144-8.
25. Sujitha R, Pillai MA, Kannan R, Shoba D. Genetic diversity and association studies in Rice (*Oryza sativa* L.). Journal of Pharmacognosy Phytochemistry. 2020;9(6):487-92.
26. Kumar A, Kumar S, Singh S, Prasad J, Jeena A, Upreti M. Studies on Genetic Parameters for Quality Traits and Yield Components in Basmati Rice (*Oryza sativa* L.). Int J Curr Microbiol App Sci. 2020;9(6):1525-32.
27. Sadhana P, Raju CD, Rao L, Kuna A. Studies on variability, correlation and path coefficient analysis for yield and quality traits in rice (*Oryza sativa* L.) genotypes. Electronic Journal of Plant Breeding. 2022;13(2):670-8.
28. Lakshmi M, Shanmuganathan M, Jeyaprakash P, Ramesh T. Genetic variability and diversity analysis in selected rice (*Oryza sativa* L.) varieties. Electronic Journal of Plant Breeding. 2022;13(3):959-66.
29. Bhargavi B, Suneetha Y, Violina JAK, Ratnam TV, Srinivas T. Genetic variability and trait associations for quality traits in high protein landraces of rice. Scientist. 2022:861-72.
30. Maurya RK, Dwivedi D, Khan N, Giri S, Dixit S. Genetic variability studies for qualitative and quantitative traits in rice (*Oryza sativa* L.). The Pharma Innovation Journal. 2022;11(5):1140-3.
31. Bhargavi M, Shanthi P, Reddy V, Mohan Reddy D, Ravindra Reddy B. Estimates of genetic variability, heritability and genetic advance for grain yield and other yield attributing traits in rice (Oryza sativa L.). The Pharma Innovation Journal. 2021;10(5):507-11.
32. Singh RK. Genetic Variability in Aromatic Rice. 2022;13(02):80-4.
33. Singh V, Snehi S, Singh P. Genetic variability, trait association studies for quality trait in short grain aromatic rice (*Oryza sativa* L.). The Pharma Innovation Journal. 2022;11(6).
34. Mahesh G, Ramesh T, Narendar Reddy S, Meena A, Rathod S, Fiyaz R, et al. Genetic variability, heritability, genetic advance and path coefficients for grain

protein content, quality traits and grain yield in rice (Oryza sativa L.) germplasm lines. The Pharma Innovation Journal. 2022;11(3):1836-9.

35. Dinkar AK, Kumar RR, Kumar M, Singh S. Genetic variability, correlation and path analysis for selection in elite breeding materials of Aromatic rice (*Oryza sativa* L.). The Pharma Innovation Journal. 2023.
36. Kumar R, Manhar A, Salam J, Netam R, Singh D, Nag S, et al. Genetic variability studies for qualitative traits in rice germplasm (*Oryza sativa* L.) of Bastar region. The Pharma Innovation Journal. 2022;11(2).
37. Tripathi A, Kumar S, Singh MK, Kumar A, Karnwal MK. Phenotypic assessment of rice (*Oryza sativa* L.) genotypes for genetic variability and varietal diversity under direct seeded condition. Journal of Applied Natural Science. 2017;9(1):6-9.
38. Yano K, Morinaka Y, Wang F, Huang P, Takehara S, Hirai T, et al. GWAS with principal component analysis identifies a gene comprehensively controlling rice architecture. Proceedings of the National Academy of Sciences. 2019;116(42):21262-7.
39. Gunasekaran A, Seshadri G, Ramasamy S, Muthurajan R, Karuppasamy KS. Identification of Newer Stable Genetic Sources for High Grain Number per Panicle and Understanding the Gene Action for Important Panicle Traits in Rice. Plants. 2023;12(2):250.
40. Donde R, Mohapatra S, Baksh SY, Padhy B, Mukherjee M, Roy S, et al. Identification of QTLs for high grain yield and component traits in new plant types of rice. PLoS One. 2020;15(7):e0227785.
41. Kujur VK, Abhinav Sao M, Tiwari A. Genetic variability, heritability and association analyses for yield and related characters in rice germplasm (*Oryza sativa* L.). The Pharma Innovation Journal. 2023;12(4):2236 - 40.
42. Govindaraj P, Vinod K, Arumugachamy S, Maheswaran M. Analysing genetic control of cooked grain traits and gelatinization temperature in a double haploid population of rice by quantitative trait loci mapping. Euphytica. 2009;166:165-76.
43. Pushpa R, Sassikumar D, Iyyanar K, Suresh R, Manimaran R. Study of physicochemical, cooking and nutritional properties of promising rice varieties of Tamil Nadu. Electronic Journal of Plant Breeding. 2019;10(3):1071-8.

44. Naik MVK, Pillai MA, Saravanan S. Assessment of Physicochemical Properties and Cooking Quality of Promising Rice Varieties. International Journal of Bio-resource Stress Management. 2023;14(Mar, 3):353-61.
45. Tian R, Jiang G-H, Shen L-H, Wang L-Q, He Y-Q. Mapping quantitative trait loci underlying the cooking and eating quality of rice using a DH population. Molecular Breeding. 2005;15:117-24.
46. Yadav R, Khatkar B, Yadav B. Morphological, physicochemical and cooking properties of some Indian rice (*Oryza sativa* L.) cultivars. Journal of Agricultural Technology. 2007;3(2):203-10.
47. Thomas R, Wan-Nadiah W, Bhat R. Physiochemical properties, proximate composition, and cooking qualities of locally grown and imported rice varieties marketed in Penang, Malaysia. International Food Research Journal. 2013;20(3).
48. Mohapatra D, Bal S. Cooking quality and instrumental textural attributes of cooked rice for different milling fractions. Journal of food engineering. 2006;73(3):253-9.
49. Ge X, Xing Y, Xu C, He Y. QTL analysis of cooked rice grain elongation, volume expansion, and water absorption using a recombinant inbred population. Plant Breeding. 2005;124(2):121-6.
50. Malini N, Sundaram T, Ramakrishnan SH. Interrelations among grain quality characters in rice. Electronic Journal of Plant Breeding. 2011;2(3):397-9.
51. Nirmaladevi G, Padmavathi G, Kota S, Babu V. Genetic variability, heritability and correlation coefficients of grain quality characters in rice (*Oryza sativa* L.). SABRAO journal of Breeding Genetics. 2015;47(4):424-33.