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Morphological and Quality Characterization of Aromatic Rice Genotypes for Mid Hill Parts of Nepal

Prakash Kumal[1], Ujjawal Kumar Singh Kushwaha[2]* and Nav Raj Adhikari[1]
[1]Department of Plant Breeding, Institute of Agriculture and Animal Science, Tribhuvan University, Kritipur, Kathmandu, Nepal
[2]National Plant Breeding and Genetics Research Centre, Nepal Agricultural Research Council, Khumaltar, Lalitpur, Nepal
**Corresponding Author Email : kushujjwal@gmail.com*

Abstract

A field experiment was conducted to characterize 12 aromatic rice genotypes in a randomized complete block design with 3 replications at National Plant Breeding and Genetics Research Centre, Nepal Agricultural Research Council (NARC), Khumaltar Lalitpur Nepal from May 2019 to February 2020. We found the mean sum of squares due to genotypes were highly significant for all the traits except tillers/hill suggesting existence of considerable amount of variability. Genotypic coefficient of variation (GCV) ranged from 1.73% for days to maturity to 32.48% for sterile grain number, while the phenotypic coefficient of variation (PCV) ranged from 1.97% for days to maturity to 46.49% for grain yield per plant. Thus PCV was higher than GCV indicating the apparent variation is not only due to genotypes but also due to the influence of environment which helped to maximize their expression at phenotypic level. High estimates of heritability and genetic advance were obtained for length, length/breadth ratio of milled grain, plant height, kernel elongation ratio and cooking time which indicates that the heritability is due to additive gene effects and thus selection may be effective. Similarly, the result of correlation and path analysis revealed that days to maturity, tillers/hill had significant positive correlation with grain yield per plant which indicated direct selection for these traits will be rewarding for yield improvement. Sugandha-3 was found the best genotype in terms of both quality and yield attributing traits followed by Gudgudo, Jhinuwa Masino and Sugandha-1.

Key words : *variability, heritability, genetic advance, correlation, rice characterization.*

Introduction

Rice is the main staple food crop for >3.5 billion people in the world (1). It is a very ?exible crop which is grown all over the world but >90% of world rice is grown in Asia only (2,3). This crop is widely grown in tropical and subtropical regions and belongs to the tribe Oryzeae under the family Gramineae (4).

Rice is the principal staple food crops followed by maize and wheat in Nepal. It ranks first position in terms of area, and production and contributes nearly 15% to the agricultural gross domestic product (AGDP) and almost 5% to gross domestic product (GDP) of the country[5]. Rice is cultivated in about 1.46 million hectares with an annual production of 5.56 million tones and productivity of 3.8 ton/ha in Nepal (5).

Rice is mainly consumed as whole grains form and it accounts >40% of the total calories of Nepalese people which invokes quality considerations are much more important than the total yield (6). Although production, harvesting and post harvesting operations are the factors which determine the overall quality of milled rice, still cultivars remains the most important determinant of market and end use qualities. Rice has specific quality based on different geographical region and consumers demand also change with the specific quality traits of milled rice (7). Though many components contribute to rice quality, the most important are cooking and eating qualities. The physical and chemical characteristics of starch are primarily involve in these parameters. The important roles that play in the constituents of cooking and eating quality are amylose content, gelatinization temperature, and gel consistency (8). According to (9) the key selection criteria highly prioritized by farmers and consumers of rice is only grain quality and therefore farmer select rice that are best for consumption as well as for production and sale.

Nearly 2300 rice landraces are reported in Nepal which are cultivated from 60 to 3,050 m altitude, thus it is one of the center of origin of rice genetic resources (10). Nepal is also the key place for the origin of aromatic rice varieties but very few farmers grow these varieties although they have higher demand in the market. Aromatic varieties are most appreciated by consumers and fetch higher market price than non-aromatic rice varieties in the world market. Most of the aromatic landraces have to characterize for their ultimate use either in breeding purposes or as a variety. This study aimed to characterize 12 aromatic rice genotypes based on their morphology and quality traits.

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Materials and Methods

The present research work was conducted at National Plant Breeding and Genetics Research Center, Nepal Agricultural Research Council (NARC), Khumaltar, Lalitpur, Nepal from May 2019 to February 2020. Twelve aromatic rice genotypes were selected and 26 days old seedlings transplanted in the field in randomized complete block design (RCBD) with three replications (Table-1).

Cultural practices : Low land irrigated field was selected with a net plot size of 3m x 1.5m with both row to row and plant to plant spacing of 20cm x 15cm. Fertilizer N:P_2O_5:K_2O were applied @80:30:30 kg/ha. The entire dose of phosphorous and potassium along with half dose of nitrogen was applied as basal dose at the time of final puddling. The remaining dose of nitrogen was applied in two splits, first at the time of beginning of tillering and second at nearly heading stage. Agronomical practices adopted were similar for all the treatments.

Data collection : Rice morphological and agronomic data were taken in different growth stage by adopting the standard evaluation system (11). Five random plants from each of the plot was taken for recording data on agro-morphological and yield characters. The paddy samples was milled in rice sheller for further analysis. In this research work, observations on various agro-morphological and quality traits were recorded to fulfill the objectives of the study.

Statistical analysis : Data entry and processing were carried out by using Microsoft Office Excel 2010 software. Analysis of variance was calculated by using R Studio and estimation of genetic parameters was computed by using Microsoft Office Excel 2010. Correlation was computed using SPSS-16. Principle component analysis and clustering were done by using MINITAB. Likewise significance of correlation coefficient was done as proposed by Kothari (12). The phenotypic and genotypic variances were computed according to Ghimire and Mahat (13). Broad sense heritability was calculated using formula suggested by (14). The genetic advance value were estimated and categorized them as high, medium and low (15). Coefficient of genotypic and phenotypic variation were categorized as proposed by (16).

Results and Discussion

Analysis of variance : The analysis of variance for yield attributing and quality traits of 12 aromatic rice genotypes are presented in Table-2. The mean sum of squares due to genotypes were found highly significant for all the characters except tillers/hill. This clearly indicates that variability does exist in all the genotypes for all the traits. This study resembles with the study of (17, 18), found significant differences among the genotypes with respect to all the traits. The significant variability among grain yield observed is supported by the findings of (19, 20, 21).

Mean performance : Results revealed that high degree of variability was present in the breeding lines for all the characters under study. Mean performance for different quantitative and quality characters under present study is presented in Table-3 and 4.

Genetic parameters : The genetic parameters genotypic variance, phenotypic variance, environmental variance, broad sense heritability (H), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), genetic advance (GA) and genetic advance of percentage of mean GAM) is presented in Table-5.

The highest value of PCV coupled with GCV was recorded in grain yield (46.49%-27.79%) followed by sterile grain number (41.57%-32.48%), straw yield (31.62%-22.47%), tillers/hill (26.44%-11.14%), L/B ratio of cooked kernel (24.77%-23.10%) and plant height (20.14%-19.54).

The values of PCV were higher than GCV, indicating the apparent variation is not only due to genotypes but also due to the influence of environment. The high magnitude of genotypic coefficient of variation revealed the high genetic variability present in the material studied. In the present investigation, the phenotypic coefficient of variation was recorded higher than genotypic coefficient of variation and was in accordance with the findings of (16, 22). Similar result was reported by (19) who found high magnitude of genotypic coefficient of variation for grain yield. The high magnitude of GCV and PCV for the above traits suggested the presence of high degree of variability and so better scope for the improvement through simple selection.

Heritability and genetic advance as percentage of mean : In the present investigation, heritability in broad sense and genetic advance were calculated for 19 yield attributing and quality characters under study and are presented in Table-5. High estimate of heritability was found for all characters except for panicle length (48.1%), tillers/hill (17.9%), fertile grain number (32%), straw yield (50.4%)), grain yield (35.7%), harvest index (31.5%), breadth of milled grain (36.4%) and breadth of cooked kernel (51.5%). The highest heritability was estimated for water uptake ratio (99.1%) followed by length of milled grain (95.1%), L/B of milled grain (94.4%), plant height (94.2%), length of cooked kernel (92.4%). This finding is in agreement with (19, 23). Highest value of heritability indicated that it was predominantly governed by additive gene effect. Such traits can be improved by doing mass selection and adapting several other breeding strategies

Table-1 : List of aromatic rice genotypes used for the study purposes.

S.N.	Treatment	Genotypes	Parents
1.	T_1	Sugandha-1	Local selection
2.	T_2	Sugandha-3	Local selection
3.	T_3	NR11042-B-B-B1-B-13	Gudgudo/Himali
4.	T_4	Aanga	Local selection
5.	T_5	IR67017	IRRI
6.	T_6	Pokhreli masino	Local selection
7.	T_7	Gudgudo	Local selection
8.	T_8	Hansaraj	Local selection
9.	T_9	CNTRL-85033	ABD
10.	T_{10}	Basmati-370	Local selection
11.	T_{11}	Jhinuwa masino	Local selection
12.	T_{12}	IR775-39-80-2-2-2	IRRI

Table-2 : Analysis of variance of 18 yield attributing and quality traits from 12 aromatic rice genotypes.

Traits	Source of variation	Mean sum of square		
		Genotypes	Replication	Error
	Degree of Freedom	11	2	22
1.	Days to Maturity (DM)	25.05**	2.52	2.25
2.	Plant height (PH)	2090.00***	79.69	41.96
3.	Panicle length (PL)	12.19**	4.72	3.22
4.	Tillers/hill	16.50	9.42	9.26
5.	Fertile grain number	9116.8*	563.7	3777.1
6.	Sterile grain number	17393.2*	6055.5	5967.5
7.	Straw yield	0.51**	0.10	0.126
8.	Grain yield/plant	15.64*	0.893	5.86
9.	Harvest Index	0.015*	0.0039	0.006
10.	Length of milled grain (mm)	2.88***	0.01227	0.048
11.	Breadth of milled grain(mm)	0.012*	0.0080528	0.0044
12.	L/B of milled grain	0.97***	0.069	0.019
13.	Length of cooked kernel	5.25***	0.5989	0.1394
14.	Breadth of cooked kernel	0.232**	0.002544	0.0557
15.	L/B of cooked kernel	1.74***	0.099	0.083
16.	Kernel elongation ratio	0.079***	0.010148	0.0044
17.	Cooking time (min)	8.39***	0.0824	0.7499
18.	Water uptake ratio	0.069***	0.000016	0.0002

*, ** and *** Significant at 5%, 1% and 0.1% probability level.

based on progeny selection. High heritability with low genetic advance as percentage of mean was observed for and days to maturity (77.1-3.14). This indicates non-additive (dominance and epistasis) gene action and the genotype by environment interaction play a significant role in the expression of the trait. These findings are in agreement with findings of (24, 25). Very low heritability and genetic advance for tillers/hill (17.9-9.72) observed may be due to non-additive gene action and great influence of the environment on the trait. These findings were supported by (26).

Correlation and path analysis : In correlation analysis, panicle length (0.82), fertile grain number (1.12) and tillers/hill (0.70) had positive and highly significant correlation with grain yield per plant. It indicates strong correlation of these traits with grain yield and selection of these traits will be useful in improving grain yield. Positive correlation of panicle length on grain yield was also reported by (27). Similarly, (28) also reported positive correlation of tillers/hill and panicle length on the rice yield which is supportive to the present findings.

From the path analysis result, it is clear that days to maturity, tillers/hill, harvest index, kernel elongation ratio and length of milled grain had very positive direct effect on grain yield. The high positive direct effect has been reported for tillers/hill (29). Days to maturity had direct positive effect with grain yield was in accordance (30, 31). The genotypic correlation between number of days to maturity and tillers/hill on grain yield per plant was positive (0.41 and 0.70). This positive relationship between the

Table-3 : Mean performance of aromatic rice genotypes selected under study.

S.N.	Genotypes	DM	PH	PL	T/H	FGN	SGN	SY/P	GY/P	HI
1.	Sugandha-1	157^{b}	171^{a}	24.6^{a}	11.53^{c}	484.33^{ab}	248.33^{bc}	1.75^{ab}	6.88^{b}	0.78^{ab}
2.	Sugandha-3	157^{b}	149.8^{bc}	26.5^{a}	10.66^{c}	471.33^{abc}	232.33^{bcd}	1.53^{b}	12.75^{a}	0.88^{a}
3.	NR11042-B-B-B1-B-13	157^{b}	156.6^{b}	26.06^{a}	$12.06b^{c}$	426.33^{abc}	302.0^{ab}	1.49^{b}	5.66^{b}	0.76^{ab}
4.	Aanga	161^{a}	100.5^{e}	23.4^{ab}	13.80^{abc}	398.66^{abcd}	241.33^{bcd}	1.61^{b}	6.47^{b}	0.78^{ab}
5.	IR67017	162^{a}	141.7^{c}	20.5^{b}	17.60^{a}	499.66^{a}	161.66^{cd}	2.30^{a}	6.98^{b}	0.72^{bc}
6.	Pokhreli masino	162^{a}	158.4^{b}	24.8^{a}	11.93^{bc}	474.00^{abc}	116.0^{d}	1.16^{bc}	6.07^{b}	0.83^{ab}
7.	Gudgudo	155^{b}	143.8^{c}	24.5^{a}	11.66^{c}	312.33^{d}	189.0^{bcd}	0.86^{c}	5.53^{b}	0.86^{a}
8.	Hansa raj	162^{a}	151.8^{bc}	20.6^{b}	16.93^{ab}	419.00^{abc}	173.33^{bcd}	2.31^{a}	4.04^{b}	0.61^{c}
9.	CNTRL-85033	162^{a}	102.3^{e}	23.2^{ab}	10.66^{c}	389.00^{bcd}	413.0^{a}	1.31^{bc}	4.92^{b}	0.77^{ab}
10.	Basmati-370	157^{b}	101.8^{e}	25.6^{a}	12.40^{abc}	370.66^{cd}	263.33^{bc}	1.72^{ab}	6.46^{b}	0.78^{ab}
11.	Jhinuwa masino	155^{b}	98.5^{e}	25.6^{a}	14.06^{abc}	469.00^{abc}	268.33^{bc}	1.54^{b}	7.95^{b}	0.82^{ab}
12.	IR775-39-80-2-2-2	156^{b}	127.3^{d}	26^{a}	11.60^{c}	410.00^{abcd}	245.0^{bcd}	1.55^{b}	4.18^{b}	0.72^{bc}
	Grand Mean	158.63	133.65	24.31	12.91	427.02	237.8	1.59	6.49	0.78
	LSD	2.54	10.96	3.04	5.2	104.06	130.8	0.6	4.09	0.136
	SEM	0.86	3.73	1.03	1.77	73.46	48.18	0.024	0.18	0.072
	CD 5%	2.54	10.96	3.04	5.15	215.45	141.33	0.02	0.54	0.21
	CV (%)	0.94	4.84	4.84	23.82	14.39	32.48	22.25	37.27	10.32

Table-4 : Mean performance of aromatic rice genotypes selected under study.

S.N.	Genotypes	LMG	BMG	L/BMG	LCK	WCK	L/BCK	KER	CT	WUR	Scent (Aroma)
1.	Sugandha-1	7.1^{c}	1.67^{cd}	4.25^{b}	7.78^{def}	2.80^{ab}	2.78^{ef}	1.09^{efg}	10.38^{de}	2.40^{d}	4
2.	Sugandha-3	8.2^{a}	1.74^{abcd}	4.73^{a}	8.12^{cde}	2.54^{bcd}	3.20^{cde}	0.98^{g}	9.36^{e}	2.36^{e}	4
3.	NR11042-B-B-B1-B-13	4.8^{h}	1.63^{d}	2.96^{f}	7.17^{f}	2.24^{d}	3.22^{cde}	1.47^{a}	13.01^{bc}	2.55^{a}	4
4.	Aanga	$6.3d^{e}$	1.71^{bcd}	3.72^{d}	7.55^{ef}	2.80^{ab}	2.71^{ef}	$1.18cd^{e}$	11.60^{cd}	2.35^{e}	1
5.	IR67017	7.3^{c}	1.74^{abcd}	4.21^{b}	11.19^{a}	2.32^{cd}	4.82^{a}	1.52^{a}	13.06^{bc}	2.54^{ab}	1
6.	Pokhreli masino	6.7^{d}	1.69^{bcd}	3.96^{c}	8.30^{cd}	2.44^{bcd}	3.43^{cd}	1.23^{cd}	10.37^{de}	2.52^{b}	2
7.	Gudgudo	5.9^{fg}	1.67^{cd}	3.54^{de}	6.26^{g}	2.62^{bcd}	2.40^{fg}	1.06^{fg}	10.32^{de}	2.01^{g}	2
8.	Hansa raj	5.5^{g}	1.85^{a}	2.98^{f}	6.51^{g}	3.18^{a}	2.04^{g}	1.17^{de}	13.90^{ab}	2.34^{e}	1
9.	CNTRL-85033	6.1^{ef}	1.81^{ab}	3.41^{e}	7.70^{def}	2.70^{bc}	2.90^{def}	1.24^{bcd}	14.76^{a}	2.25^{f}	1
10.	Basmati-370	7.3^{c}	1.77^{abc}	4.14^{bc}	9.46^{b}	2.23^{d}	4.24^{b}	1.29^{bc}	10.48^{de}	2.25^{f}	3
11.	Jhinuwa masino	6.1^{ef}	1.76^{abc}	3.50^{de}	8.36^{cd}	2.36^{bcd}	3.54^{c}	1.35^{b}	12.04^{c}	2.44^{c}	4
12.	IR775-39-80-2-2-2	7.8^{b}	1.72^{bcd}	4.54^{a}	8.77^{c}	2.64^{bcd}	3.33^{cd}	1.12^{ef}	12.52^{bc}	2.46^{c}	1
	Grand Mean	6.63	1.73	3.83	8.1	2.57	3.22	1.23	8.56	2.37	
	LSD	0.37	0.11	0.23	0.63	0.39	0.49	0.11	1.46	0.025	
	SEM	0.12	0.038	0.079	0.21	0.13	0.16	0.038	0.5	0.008	
	CD 5%	0.37	0.11	0.23	0.63	0.39	0.49	0.11	1.46	0.02	
	CV (%)	3.31	3.86	3.59	4.6	9.17	8.99	5.4	7.32	0.62	

(DM = Days to Maturity, PH = Plant Height, PL = Panicle Length, T/H =Tillers per Hill, FGN = Fertile Grain Number, SGN = Sterile Grain Number, SY/P = Straw Yield per Plant, GY/P = Grain Yield per Plant, HI = Harvest Index, LMG = Length of Milled Grain, BMG = Breadth of Milled Grain , L/BMG = Length Breadth ratio of Milled Grain, LCK = Length of Cooked Kernel, WCK = Breadth of Cooked Kernel, L/BCK = Length Breadth ratio of Cooked Kernel, KER = Kernel Elongation Ratio, CT = Cooking Time, WUR = Water Uptake Ratio, 1 = absence of aroma, 2 = slight aroma, 3 = moderate aroma, 4 = strong aroma).

characters shows that plant direct selection can be done on the basis of phenotypic value of the trait. Direct effect of plant height on grain yield per plant was found negative (-0.36). The genotypic correlation coefficient between two traits was also negative (-0.308). The negative value indicates that the direct selection would not be useful for the improvement of grain yield (32). (33) found that length of milled grain had direct positive effect on grain yield which is contradictory with the present study.

Multivariate Analysis

Principle component analysis : In the present investigation, PCA was performed for 18 yield attributing and quality contributing traits in 12 aromatic rice genotypes presented in Table-8 and 9. Out of 18 traits, only five principal components (PCs) exhibited more than 1.33 Eigen value, and showed about 87.1% cumulative variability among the traits studied. So, these 5 PCs were

Table-5 : Genetic parameters of yield and quality attributing traits of 12 aromatic rice genotypes.

Traits	GCV	PCV	H	GA	GAM
Days to maturity	1.73	1.97	0.771	4.98	3.14
Plant Height (cm)	19.54	20.14	0.942	52.24	39.08
Panicle Length (cm	7.11	10.25	0.481	2.47	10.16
Tillers/hill	11.14	26.30	0.179	1.25	9.72
Fertile Grain No.	9.87	17.45	0.320	49.18	11.51
Sterile Grain No	32.48	41.57	0.389	79.34	33.36
Straw Yield	22.47	31.62	0.504	0.525	32.89
Grain Yield	27.79	46.49	0.357	2.22	34.22
Harvest Index(HI)	7.00	12.47	0.315	0.06	8.11
Length of milled grain (mm)	14.654	15.024	0.951	1.953	29.445
Breadth of milled grain(mm)	2.920	4.843	0.364	0.063	3.627
L/B of milled grain	14.770	15.202	0.944	1.132	29.561
Length of cooked kernel	16.127	16.773	0.924	2.587	31.943
Breadth of cooked kernel	10.446	13.168	0.515	0.359	13.957
L/B of cooked kernel	23.101	24.773	0.870	1.429	44.377
Kernel elongation ratio	12.854	13.942	0.850	0.300	24.411
Cooking time (min)	13.503	15.363	0.773	2.890	24.450
Water uptake ratio	6.405	6.435	0.991	0.312	13.132

Table-6 : Correlation analysis (phenotypic above diagonal and genotypic below diagonal) of 18 yield attributing and quality traits of 12 aromatic rice genotypes.

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1.	1	0.05	-0.66**	0.31	0.31	-0.15	0.37*	-0.14	-0.29	-0.08	0.23	-0.13	0.17	0.31	0	0.23	0.40*	0.24
2.	0.21	1	-0.03	-0.008	0.28	-0.39*	0.11	-0.06	-0.03	-0.02	-0.32	0.07	-0.19	0.15	-0.21	-0.16	0.22	0.24
3.	0.55	0.55	1	-0.50**	-0.24	0.28	-0.46**	0.18	0.38*	0.22	-0.12	0.39	-0.14	-0.33*	0.02	-0.3	-0.44**	-0.01
4.	0.64*	-0.05	0.46	1	0.15	-0.35*	0.52**	-0.36	-0.62**	-0.08	0.18	-0.12	0.19	0.21	0.05	0.33*	0.28	0.18
5.	-0.82**	-0.7	0.26	-0.35	1	-0.26	0.34*	0.37*	0.07	0.24	-0.14	0.29	0.35	-0.02	0.24	0.17	0.09	0.59**
6.	-0.67*	0.97**	0.48	0.01	0.47**	1	-0.15	0.07	0.2	-0.13	0.22	-0.2	-0.11	-0.12	-0.02	0.04	0.35*	-0.12
7.	0.58**	-0.24	0.46*	-0.38	-0.60*	0.12	1	-0.08	-0.63**	0.13	0.34*	0.03	0.34*	0.17	0.19	0.24	0.28	0.35*
8.	-0.12	0.16	0.60*	-0.04	0.08	0.64**	-0.19	1	0.72**	0.34*	-0.22	0.41*	0.19	-0.18	0.2	-0.11	-0.48**	0.03
9.	0.03	0.90**	0.63**	-0.16	0.47*	-0.35	-0.49	0.09	1	0.13	-0.39	0.25	-0.04	-0.35*	0.09	-0.19	-0.51**	-0.17
10.	0.32	-0.84**	0.45	-0.13	0.60*	0.05	-0.44	-0.90**	-0.31	1	0.11	0.95**	0.58**	-0.11	0.43*	-0.37	-0.44**	0.08
11.	0.49	0.70*	-0.06	0.69*	0.24	-0.5	0.29	-0.41	-0.84**	0.07	1	0.18	0.04	0.22	-0.02	-0.1	0.32	-0.13
12.	0.03	-0.90**	0.13	0.66*	0.01	0.5	0.27	0.32	0.43	0.45	0.48	1	0.56**	-0.15	0.41*	-0.34	-0.53**	0.11
13.	-0.22	-0.24	-0.15	-0.21	0.05	-0.24	-0.16	-0.28	-0.14	0.3	0.4	-0.04	1	-0.41*	0.89**	0.51**	-0.02	0.47
14.	-0.25	0.63*	1.12**	-0.23	0.4	0.14	0.51	0.65*	-0.31	0.57	-0.11	-0.75**	0.64*	1	0.76**	-0.41	0.19	-0.23
15.	0.54	-0.66*	1.27**	0.70**	-0.74**	-0.34	0.88**	-0.49	0.51	-0.1	0.46	0.95**	0.73**	0.46	1	0.58**	-0.08	0.43**
16.	-1.35**	0.1	0.25	-0.78**	0.82**	1.02**	0.22	-0.96**	0.39	-0.11	-0.60*	0.06	-0.26	-0.66*	0.01	1	0.43**	0.52**
17.	-0.06	-0.018	0.45	-0.61*	0.05	-0.08	-0.05	-0.03	-0.54	0.07	-0.2	0.16	-0.2	-0.17	-0.27	0.24	1	0.19
18.	0	-0.79**	0.61*	0.15	-0.16	0.41	0.41	-0.75**	-0.09	0.61*	-0.2	0.17	0.35	0.03	0.25	0.53	0.27	1

(*, ** and *** Significant at 5%, 1% and 0.1 % probability level, 1. Days to maturity, 2. Plant height.cm, 3. Panicle length (cm), 4. Tillers/hill, 5. Fertile grain number, 6.Sterile grain number, 7.straw yield/plant (gm.), 8. Harvest index, 9. Length of milled grain (mm), 10. Width of milled grain (mm), 11.L.B of milled grain, 12. Length of cooked kernel (mm), 13.Breadth of cooked kernel (mm), 14. L.B ratio of cooked kernel, 15.kernel elongation ratio, 16. Cooking time (min), 17. Water uptake ratio).

given due importance for further explanation. The PC-1 showed 29.6% while, PC-2, PC-3, PC-4 and PC-5 exhibited 25.0%, 14.0%, 11.1 and 7.2% variability respectively among the accessions for the traits under study. The first PC accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible.

Scree plot explained the percentage of variation associated with each principal component obtained by drawing a graph between eigen values and principal component numbers. First 5 components explained 87.1% variation and eigen value >1. The PC-1 showed 29.6% variability with eigen value 5.33 which then declined gradually. From the graph, it is clear that the maximum variation was observed in PC-1.

Cluster analysis : Cluster analysis among 12 rice genotypes was studied. The clustering pattern of all the genotypes has been presented in Table-8. The 12 entries were grouped into 5 clusters. The highest number of genotypes appeared in Cluster II, which contained 4 genotypes followed by Cluster I (3 genotypes) and Cluster

Table-7 : Direct effects (bold) and indirect effects of yield attributing and quality traits on grain yield of 12 aromatic rice genotypes.

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1.	1.23	0	0.7	0.14	0.04	-0.02	0.26	-1.14	-1.25	-0.62	1.59	-0.51	-0.3	-0.14	1.26	-0.12	-0.05
2.	0	-0.36	0.05	-0.004	0.13	-0.1	0.03	-0.09	-0.44	0.56	-0.58	0.6	-0.14	0.8	-0.87	0.06	-0.05
3.	0.18	-0.008	-0.88	-0.3	0.02	0.04	-0.5	1.72	3.02	0.99	-3.14	0.33	0.53	-0.25	-1.31	0.15	-0.003
4.	-0.15	-0.002	1.19	1.02	0.16	-0.11	0.82	-1.25	-4.54	-0.9	3.95	-1.55	-0.08	-1.8	4.42	-0.15	-0.96
5.	-0.03	0.06	-0.08	0.12	0.29	-0.04	0.41	0.39	5.48	-0.14	-3	-1.95	0.27	-2.21	1.97	0.02	-0.23
6.	0.03	-0.08	-0.22	-0.14	-0.07	0.16	-0.14	-0.27	-2.93	-0.05	1.87	0.49	0.01	0.55	0.61	-0.11	-0.04
7.	-0.09	0.007	0.69	0.28	0.18	-0.03	0.64	-1.52	1.74	-0.68	-0.14	-1.5	-0.24	-1.26	2.17	-0.1	-0.1
8.	0.15	-0.007	-0.9	-0.16	-0.06	-0.02	-0.58	1.69	4.85	0.64	-3.62	0.31	0.52	-0.23	-2.37	0.22	0.07
9.	0.02	-0.004	-0.2	-0.07	0.12	-0.03	0.08	0.61	13.37	-0.03	-7.88	-1.89	0.14	-1.84	-1.78	0.11	-0.02
10.	-0.04	-0.07	0.85	0.19	0.04	0.009	0.43	-1.06	0.42	-1.02	0.97	0.5	-0.53	0.17	0.4	-0.14	0.04
11.	0.04	0.01	-0.34	-0.11	0.11	-0.03	0	0.76	13.21	0.12	-7.98	-1.75	0.21	-1.79	-1.94	0.14	-0.02
12.	-0.03	-0.02	0.09	0.11	0.19	-0.02	0.32	-0.17	8.45	-0.17	-4.66	-2.99	0.59	-3.76	2.44	-0.002	-0.1
13.	-0.08	0.02	0.54	0.02	-0.09	-0.003	0.17	-1.01	-2.17	-0.61	1.94	-2.03	-0.88	3.2	-3.52	-0.06	0.07
14.	-0.008	-0.02	-0.05	0.1	0.16	-0.02	0.21	0.1	6.38	0.04	-3.7	-2.9	0.72	-3.87	3.25	0.01	-0.1
15.	-0.05	-0.02	0.23	0.19	0.11	0.02	0.28	-0.8	-4.75	-0.08	3.08	-1.45	0.62	-2.51	5.01	-0.12	-0.12
16.	-0.12	-0.03	0.58	0.14	-0.03	0.08	0.29	-1.63	-6.62	-0.66	4.83	-0.03	-0.23	0.19	2.76	-0.23	-0.04
17.	-0.06	0.03	-0.01	0.09	0.31	-0.03	0.31	-0.59	1.23	0.19	-0.95	-1.43	0.31	-1.8	2.77	-0.04	-0.21

(*, ** and *** Significant at 5%, 1% and 0.1 % probability level, 1. Days to maturity, 2. Plant height.cm, 3. Panicle length (cm), 4. Tillers/hill, 5. Fertile grain number, 6.Sterile grain number, 7.straw yield/plant (gm.), 8. Harvest index, 9. Length of milled grain (mm), 10. Width of milled grain (mm), 11.L.B of milled grain, 12. Length of cooked kernel (mm), 13.Breadth of cooked kernel (mm), 14. L.B ratio of cooked kernel, 15.kernel elongation ratio, 16. Cooking time (min), 17. Water uptake ratio)

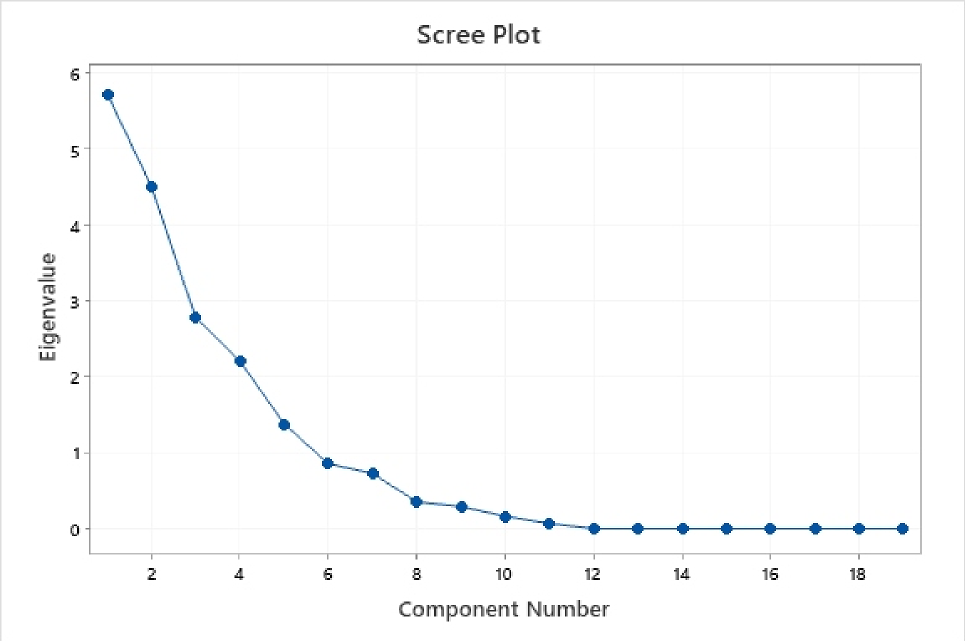

Fig.-1 : Scree plot showing eigen value and component number.

III (3 genotypes), Cluster IV and V (1 genotypes each). This pattern of group constellations described the existence of significant amount of variability among the studied genotypes. The inter- and intra-cluster distances among ten clusters were computed and are given in Table-9. The intra cluster distance was found to be 0.00 (same for all cluster).

The highest inter cluster distance was found between Cluster 5 and Cluster3 (277.529) followed by Cluster5 and Cluster4 (240.517). The lowest inter-cluster distance was found between cluster2 and Cluster1 (78.679). The inter-cluster distances in the present study were higher than the intra cluster distance in all cases reflecting wider diversity among the breeding lines of the distant group.

Conclusions

The characters under study had high estimate of genetic advance as percent of mean were governed by additive genes, and selection for them will be beneficial. The rice genotypes used in the study revealed significant variability for most of the morphological traits. Among the genotypes, high coefficients of variation were observed for most of the

Table-8 : Clustering patterns of 12 aromatic rice genotypes.

Cluster no.	No. of germplasm	Name of rice germplasm
I	3	Sugandha-1, Sugandha-3, Jhinuwa masino
II	4	NR11042-B-B-B1-B-13, IR775-39-80-2-2-2, Aanga, Basmati-370
III	3	Pokhreli masino, IR67017, Hansaraj
IV	1	Gudgudo
V	1	CNTRL-85033

Table-9 : Estimates of intra (diagonal and bold) and inter cluster distances among five clusters.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	0.000	78.679	112.913	167.574	172.667
Cluster 2		0.000	129.092	106.791	163.447
Cluster 3			0.000	157.151	277.529
Cluster 4				0.000	240.517
Cluster 5					0.000

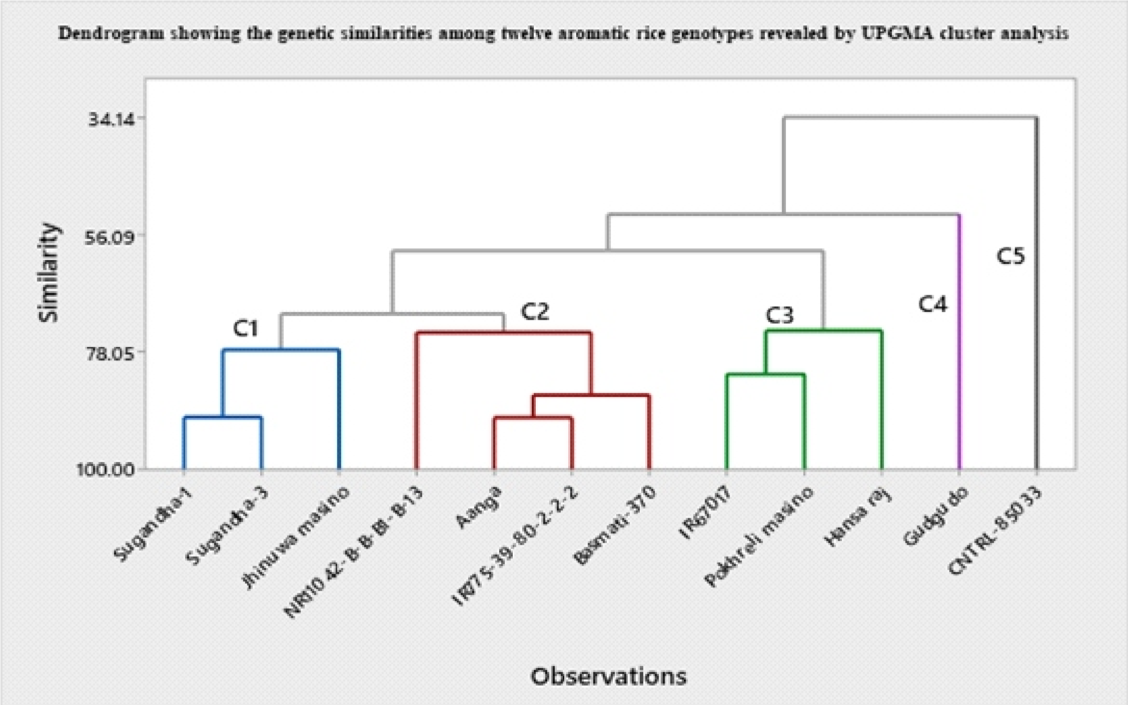

Fig.-2 : Dendogram of 12 aromatic rice genotypes constructed from 18 yield attributing and quality traits.

characters studied, indicating the existence of sufficient variability. Selection criteria based on correlation analysis revealed positive and highly significant correlation of grain yield per plant with panicle length (0.82), fertile grain number (1.12) and tillers/hill (0.70) which would be quite useful for further improvement. Therefore, it reveals the fact that the direct selection for characters viz. panicle length (0.82), fertile grain number (1.12) and tillers/hill (0.70) will be very effective for increasing the grain yield; hence they should be given consideration in the selection criteria. Component matrix revealed that the PC-1, PC-3 and PC4 was mostly related to cooking, yield and growth characters. So, a good breeding program can be initiated by selecting the genotypes from PC-1, PC-2 and PC-3 for quality aspect and yield related traits. Cluster analysis divided the 12 genotypes of rice into five clusters where the cluster II constituted of 4 genotypes, forming the largest cluster. Considering the importance of genetic distance and relative contribution of characters towards total divergence, the present study indicated that parental lines selected from cluster III (Pokhreli masino, IR67017, Hansaraj) and Cluster V (CNTRL-85033) could be used in crossing programs to achieve desired segregates.

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Author contributions

N.R. Adhikari and U.K.S. Kushwaha conceptualized the experiment and P. Kumal conducted the field and lab experiments. P. Kumal prepared the manuscript and U.K.S. Kushwaha edited the manuscript to the final version.

Ethical approval

This experiment does not involve any animals or living beings. Ethical approval was obtained for conducting the experiment from NARC.

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