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## Assessment of genetic variability, correlation and path association for yield and yield components in aromatic non-basmati rice

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### Abstract

Twenty eight genotypes were grown in a randomized complete block design with three replications for two kharif seasons (2015-2016). The analysis of variance revealed that mean squares due to genotypes for all the sixteen quantitative characters were significant indicating presence of genetic variability. Coefficient of variability (CV) was highest in harvest index followed by number of productive tillers per plant. The estimates of GCV and PCV value for number of panicle, harvest index, spikelet density, showed higher differences which indicated the greater role of environmental factor influencing the expression of this character. High to moderate estimates of heritability accompanied with high to moderate genetic advance for number filled grain, days to 50% flowering, grain yield per plant indicated the predominance of additive gene action for the expression of these characters. Grain yield per plant was found to be positively and significantly correlated with agronomical traits at both genotypic and phenotypic levels indicating the importance of these characters for yield improvement. Phenotypic and genotypic path co-efficient revealed that greater emphasis during selection of characters should be given on number of panicle/plant, primary branch, number of filled grain/panicle and test weight for improvement of grain yield.

**Keywords:** Aromatic rice, genetic variability, heritability, character association, yield, yield components

### Introduction

Rice is staple food crop for more than half of the world's human population. Aromatic rice constitutes a small and special group of rice that is regarded as best in quality. The aromatic rice praised for its unique quality, a nature's gift to Indian sub-continent. In India, aromatic rice is popularly known as Basmati rice which is usually grown in north western Indian states like Punjab, Haryana, Himachal Pradesh, Jammu and Kashmir and parts of Uttar Pradesh. The areas for basmati production are limited due to specific eco-geographic conditions. Aromatic rice occupies a prime position in Indian culture; not only because of their high quality, but that they have been considered auspicious. India has had immense wealth of non-Basmati aromatic rices. But a lot has already been lost as an aftermath of the green revolution where major emphasis was on yield rather than quality (Sing and Sing, 1998) [32]. The aromatic rice is preferred over non-aromatic rice due to special occasions and for export, and thus they command a higher market price.

To improve the productivity of these landraces in comparison to high yielding variety of rices, our primary consideration should be to bring about genetic improvement of the crop and development of scientific breeding programme based upon the available genetic variability. Knowledge on the genetic architecture of genotypes is necessary to formulate efficient breeding methodology. The systematic breeding programme involves the steps like creating genetic variability practicing selection and utilization of selected genotypes to evolve promising varieties. The heritable variation is masked by non-heritable variation which creates difficulty in existing selection. Hence it become very much essential to split total variation in to heritable and non heritable component which may enable breeder to plan a second breeding programme. Direct selection based on crop yields is often a paradox in breeding programmes because yield is a complex polygenically inherited character, influenced by its component traits. Yield enhancement is the major breeding objective in rice breeding programmes and knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative characters like yield and its components is essential for effective genetic improvement. A critical analysis of the genetic variability parameters, namely, Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), heritability and genetic advance for different traits of economic importance is a major pre-requisite for any plant breeder to work with crop improvement programmes.

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Further, information on correlation co-efficients between grain yield and its component characters is essential for yield improvement, since grain yield in rice is a complex entity and is highly influenced by several component characters. Studies on path co-efficient also provide useful information regarding the direct and indirect effects of different yield component characters on grain yield and thus aid in the identification of effective selection criteria for effective yield improvement.

### Materials and Methods

The present investigation was carried out during two consecutive *kharif* (warm wet) seasons at the Agriculture Farm of Palli Siksha Bhavana (Institute of Agriculture), Visva-Bharati, Sriniketan for estimating genetic variability present in a pool of twenty eight genotypes of aromatic rices. The experimental materials consisted of twenty eight diverse genotypes of aromatic non-basmati rice (Table-1). The origins

of these genotypes were in different eco-geographical region of eastern India. These were collected from different research stations and institutions belonging to West Bengal and Bihar. The farm is situated at 23°29' N latitude and 87°42' E longitudes with an average altitude of 58.9 meter above mean sea level under sub-humid, subtropical, lateritic belt of West Bengal. The seedlings were transplanted in the main field 35 days after sowing. Before transplanting, the land was prepared following proper agronomic practices. All the genotypes were grown in a Randomized Complete Block Design (RCBD) with 3 replications during the two growing seasons. The experimental plot of each genotype consisted of 5 rows of 1.5 meter length keeping plant-to-plant and row-to-row spacing of 15 cm and 20 cm apart. All recommended package of practices were followed during the crop season for raising a healthy crop.

**Table 1:** List of genotypes of twenty eight aromatic rice

Serial Number	Name of Genotypes	Serial Number	Name of Genotypes
1	124(17)10	15	Subhasita
2	33(9)17	16	Sheeta bhog
3	Chinakamini	17	Bahadurbhog
4	Dehradoongandeshari	18	Seetasail
5	Danaguri	19	Manipuri Black Rice
6	Dudhaswar	20	Tulsimukul
7	Gobindabhog	21	88(8)3
8	Kalikasha	22	BM 1
9	Kaminibhog	23	BM4
10	Krishnabhog	24	BM 7
11	Radhunipagal	25	BM 34
12	Rajendrasubhasini	26	BM 35
13	Radhatilak	27	Keralasundori
14	Shantibhog	28	Gopalbhog

The observations were recorded in all the two seasons on the following different quantitative characters in the field. Data on various quantitative characters viz., days to 50% flowering, plant height, flag leaf length, flag leaf width, flag leaf area, number of effective tillers per hill, panicle length, number of primary branches, number of secondary branches, number of spikelets per panicle, number of filled grains per panicle, test weight, biological yield per plant, harvest index and grain yield were recorded on 5 randomly selected competitive plants from the 3 rows except 2 border rows. Data on days to 50% flowering was recorded on whole plot basis.

The total variations among genotypes for different characters were tested for significance by 'F' test using analysis of variance technique, to find out the 'F' values from the table (Fisher and Yates, 1953) the mean square values were tested, against the error mean squares. Phenotypic ( $\sigma^2_p$ ) and genotypic variance ( $\sigma^2_g$ ), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) were estimated using standard procedure (Singh and Chaudhary, 1995) [31]. Heritability was calculated according to Singh and Chaudhary 1995 [31], Genetic advance was estimated by the formula described by Allard (1960) [2], Correlation coefficient was calculated by the formula suggested by Johnson *et al.* (1955) [13] and Al. Jibouri *et al.* (1958) [1]. Path co-efficient analysis was carried out according to Dewey and Lu (1959) [8].

### Results and Discussion

The analysis of variance of twenty eight genotypes pooled over two seasons with respect to sixteen quantitative

characters which are presented in Table 2. The mean squares due to seasons for all the above characters except test weight, biological yield per plant and harvest index were highly significant indicating the role of seasons for expression of the characters. The mean squares due to genotypes for all the above characters were highly significant which indicated genetic variability among the experimental materials. The significant mean square due to genotypes  $\times$  season interaction for all the above characters indicated differential performance of the genotypes with the change in growing environment. From the values of coefficient of variation, it was observed that variability was highest in harvest index followed by number of panicle per plant, biological yield per plant, grain yield per plant and flag leaf area., Considerable amount of variability for harvest index per panicle (Kole *et al.*, 2008) [15], number of panicle per plant (Sarvan *et al.*, 2015) [35], biological yield per plant (Chourasia *et al.*, 2012) [6], grain yield per plant (Pratap *et al.*, 2012) [23], flag leaf area (Krishnamurthy *et al.*, 2012) [18], have been reported earlier.

The mean performances of twenty eight genotypes for sixteen characters are given in Table 3. Considering the performance of the genotypes for important characters including grain yield, the genotypes viz., Danaguri, Dudheshwar, Kalikasha, Monipuri black rice, Subhasita, Shanti bhog, Kerala sundari, Bahadurbhog, Seetasail, BM-7, Gopalbhog, 88(8)3, and 33(9)17 were promising. However, before drawing any definite conclusion repetition of the experiment under different crop growing condition is needed.

The estimation of phenotypic coefficient variation (Table 4.) ranged from 8.24% in panicle length to 44.38% in harvest index, where as for genotypic coefficient of variation it was

6.90% in panicle length to 38.77% in grain yield. The estimates of genotypic and phenotypic coefficient of variation (GCV and PCV) were high (>20%) for grain yield, harvest index, number of spikelet per panicle, number of filled grains per panicle, test weight, biological yield per plant, spikelet density, number of panicle per plant, flag leaf area, moderate (10-20%) for plant height, flag leaf length, flag leaf width, and low (<10%) for days to 50% flowering, panicle length, and primary branch. Similar results for high GCV and PCV for grain yield per plant (Koli *et al.*, 2012; Pratap *et al.*, 2012) [17, 23] for number of spikelet per panicle (Sravan *et al.*, 2015) [35] number of filled grain per panicle per plant (Patil and Sarawagi, 2005) [5] 1000 grain yield number of panicle / plant (Kole *et al.*, 2008; Sravan *et al.*, 2015) [15, 35], flag leaf area (Krishnamurthy *et al.*, 2012; Pratap *et al.*, 2012) [18, 23], biological yield per plant and low GCV and PCV for days to 50% flowering (Bhaskar *et al.*, 2006; Kole *et al.*, 2008) [4, 15] were reported earlier. The estimates of GCV and PCV value for number of panicle, harvest index, spikelet density, showed higher differences which indicated the greater role of environmental factor influencing the expression of this character. Very low differences was observed for days to 50% flowering, plant height indicating low sensitivity to environment and consequently greater role for genetic factors influencing the expression of these characters. Similar results for days to 50% flowering and plant height have been reported by Kole *et al.* 2008 [16].

The estimates of heritability in broad sense (Table 4) were very high for days to 50% flowering (98.70%), number of filled grain/panicle (90%), grain yield (86.40%), and number of spikelet per panicle (86%). Similar results for high heritability for 50% flowering (Vanisree *et al.*, 2013) [36], plant height, grain yield per plant (Reddy *et al.*, 2013) [25], number of spikelet per panicle (Singh *et al.*, 2011) [33] reported earlier. Heritability in broad sense were moderate for flag leaf length, flag leaf width, flag leaf area, panicle length, secondary branch and test weight. Similar result for test weight (Sadhukhan *et al.*, 2000) [28] reported earlier. The estimates of heritability were low for number of panicle per plant, primary branch, harvest index, spikelet density which indicated higher influence of environment for the expression of these characters. Low heritability for number of panicle per, plant reported by Mishu *et al.* 2015 [20]

The estimates of (Table 4) genetic advance as per cent mean were high for biological per plant, 1000 grain weight, number of filled grain/panicle, flag leaf area, spikelet density, grain yield, number of spikelet per panicle. High genetic advance for biological yield (Chourasia *et al.*, 2012) [6], grain yield (Kole *et al.*, 2008; Reddy *et al.*, 2013) [15, 25], test weight (Singh *et al.*, 2011; Koli *et al.*, 2012) [33, 17], number of filled grain/panicle (Singh *et al.*, 2011) [33] reported earlier. The value genetic advance for harvest index, secondary branch, numbers of panicle/plant, plant height, flag leaf length, flag leaf width were moderate. Same results for plant height (Sanghera *et al.*, 2013) [29] reported earlier. The estimates of genetic advance were low for days to 50% flowering, Panicle length, and primary branch.

According to Jhonson *et al.* (1955) [13] and heritability used in conjunction with genetic advance provides better information for selecting the best individuals then the heritability alone. High to moderate estimates of heritability accompanied with high to moderate genetic advance for number filled grain/panicle, days to 50% flowering, grain yield indicated the

predominance of additive gene action for the expression of these characters (Jhonson *et al.*, 1955) [13]. Hence selection of these characters would be effective in this population.

A perusal of the Table 4, wherein the results of PCV, GCV, heritability and genetic advance have been furnished, revealed that selection for number of spikelet per panicle, number of filled grain/panicle, test weight, biological yield would be effective for improvement of grain yield in this population.

Complete knowledge on interrelationship of plant character like grain yield with other characters of paramount importance to the breeder for making improvement in complex quantitative character like grain yield for which direct selection is not much effective. Hence association analysis was undertaken to determine the direction of selection and number of characters to be considered in improving grain yield. In the present investigation, an attempt has been made to estimate the phenotypic and genotypic correlation in all character combination with the objects to get information about the nature extent and direction of selection pressure to achieve practical and usable results. The estimates of genotypic and phenotypic correlation coefficient have been presented in Table 5. Grain yield per plant was found to be positively and significantly correlated with harvest index, flag leaf area, flag leaf area, plant height, biological yield per plant, number of filled grain per panicle, test weight, flag leaf length, days to 50% flowering, primary branch, at both genotypic and phenotypic levels indicating the importance of these characters for yield improvement. Similar correlation of grain yield with harvest index (Krishnamurthy *et al.*, 2012) [18], biological yield per plant (Pratap *et al.*, 2012) [23], number of filled grain per panicle (Ratna *et al.*, 2015) [24], 1000 grain weight (Mishu *et al.*, 2015) [20], Days to 50% flowering (Singh *et al.*, 2006) [34], Flag leaf width (Mazari *et al.*, 2007) [19], Plant height (Kole *et al.*, 2008) [16] reported earlier.

While selecting characters having direct bearing on grain yield, their associations with other characters are to be considered simultaneously as this will indirectly affected yield. Positive and significant correlation at both phenotypic and genotypic level were observed in case of days to 50% flowering with plant height, number of filled grain/panicle, biological yield per plant and grain yield. Plant height with flag leaf length, primary branch, number of spikelet per panicle, spikelet density, grain yield; flag leaf length with flag leaf area, test weight, grain yield; flag leaf width with flag leaf area, test weight, biological yield per plant, Flag leaf area with yield; primary branch with secondary branch, number of spikelet per panicle, grain yield; secondary branch with number of spikelet per panicle and spikelet density; number of spikelet with spikelet density; number of filled grain per panicle with harvest index, spikelet density, grain yield; test weight with biological yield per panicle, grain yield; harvest index with grain yield. Significant negative correlation in this experiment were observed for grain yield with number of panicle/plant at genotypic level indicating negative influence of these characters in increasing grain yield. Plant height with number of panicle per plant; flag leaf length with number of panicle per plant; flag leaf width with number of panicle per plant; number of panicle with primary branch, secondary branch, number of spikelet per panicle, spikelet density showed significantly negative correlation at both genotypic and phenotypic level.

**Table 2:** Analysis of variance for sixteen quantitative character in aromatic rice

Source	d.f	Mean sum of square															
		50% flowering	Plant height (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Flag leaf area (cm <sup>2</sup> )	No. of panicle	Panicle length	Primary branch	Secondary Branch	No. of spikelet/panicle	Spikelet density	No. of filled grain/panicle	Test weight	Biological yield /plant	Harvest index	Grain yield (g)
Season	1	3207**	1511.5**	348.76**	0.05*	194.90**	89.21**	21.07**	34.30**	57.70*	2763.25**	1.27*	1644.75**	6.48	90.66	20.8	4.16**
Replication	2	6.38	32.75	0.28	0.01	1.19	0.95	0.73	0.12	7.22	182.88	0.19	107.25	4.4	26.05	75.13	3.12
S × R	2	5.38	59.5	33.03	0.03	56.72	0.36	1.07	1.02	13.21	14.5	0.02	54.31	3.45	31.36	31.54	8.03
Genotypes	27	691.88**	3939.55**	211.09**	0.19**	592.98**	26.15**	24.34**	4.91*	232.30**	6856.75**	9.96**	9044.08**	218.44**	569.04**	785.96**	148.36**
G × S	27	31.27**	53.54**	57.71**	0.03**	112.61**	4.62**	5.29**	1.78**	32.40**	1059.34**	1.22*	488.86**	3.64*	102.30*	146.41*	9.69**
Error	108	1.48	17.02	10.37	0.01	20.94	3.12	1.36	0.35	11.29	157.72	0.23	159.3	2.19	59.38	78.14	4.67

\*, \*\*: Significant at P=0.05 and 0.01, respectively

**Table 3:** Mean performance of twenty eight genotypes for sixteen quantitative characters in aromatic rice

	50% flowering	Plant height(cm)	Flag leaf length(cm)	Flag leaf width(cm)	Flag leaf area(cm <sup>2</sup> )	No. of panicle/plant	Panicle length(cm)	Primary branch	Secondary Branch	No. of spikelet/panicle	spikelet density	No. of filled grain/ panicle	Test weight (g)	Biological yield/plant	Harvest index	Grain yield(g)
124(17)10	112.17	131.51	25.67	0.99	23.10	11.90	26.48	8.73	21.12	110.57	4.16	66.17	12.70	40.00	17.61	6.97
33(9)17	116.83	94.77	21.34	0.80	14.35	16.40	20.27	6.59	9.73	54.33	2.68	40.80	14.15	33.97	23.08	7.75
Chinakamini	119.33	143.01	28.88	1.20	29.85	6.72	24.27	10.39	36.25	178.34	7.33	148.70	14.03	42.33	25.14	10.58
Dehradoongandeshari	111.67	134.97	34.79	1.12	35.41	9.70	24.52	10.80	27.07	128.41	5.23	96.41	17.56	40.50	23.32	9.16
Danaguri	121.50	140.89	38.93	1.12	37.10	11.04	28.14	10.03	24.74	128.04	4.55	107.15	15.99	43.67	36.35	14.79
Dudhaswar	118.50	148.89	29.90	1.15	30.88	8.13	23.13	9.55	27.62	131.16	5.69	110.39	17.11	47.00	29.37	13.76
Gobindabhog	116.83	137.39	25.23	0.89	19.44	9.37	25.38	9.83	30.26	165.89	6.55	126.87	8.86	39.50	29.42	11.11
Kalikasha	106.83	148.02	25.41	1.01	21.83	11.01	26.69	11.00	37.29	186.56	7.04	159.60	10.64	45.00	34.52	14.84
Kaminibhog	113.83	158.24	26.62	1.12	25.87	7.33	26.36	10.41	33.89	183.23	6.95	154.30	10.28	42.67	27.78	11.72
Krishnabhog	110.67	166.21	26.53	0.94	22.40	8.40	29.73	9.34	29.49	155.31	5.20	116.44	9.88	37.00	24.23	8.92
Radhunipagal	116.67	151.62	26.34	1.03	23.54	7.97	26.05	9.84	29.30	150.13	5.75	128.41	9.45	36.50	30.63	10.95
Rajendrasubhasini	109.17	93.72	30.98	1.11	29.66	9.07	24.33	8.90	22.68	95.25	3.92	43.90	14.42	34.83	6.43	2.23
Radhatilak	116.17	143.23	28.15	1.08	26.11	9.40	27.34	10.77	36.40	193.70	7.09	154.72	11.21	41.17	29.61	12.28
Shantibhog	118.17	166.10	48.88	1.56	66.35	7.79	25.50	9.91	28.78	134.35	5.28	109.36	33.73	42.67	48.18	20.05
Subhasita	112.17	145.46	29.36	1.24	32.27	8.93	23.39	10.05	30.59	151.71	6.47	129.57	16.20	44.00	32.89	13.73
Sheeta bhog	118.83	134.55	32.11	0.98	27.00	9.97	26.10	9.37	28.95	153.01	5.87	122.11	11.85	40.00	27.41	10.89
Bahadurbhog	121.67	152.67	29.25	1.21	26.83	7.27	25.87	10.69	38.18	225.17	8.74	173.34	10.20	33.67	45.16	13.91
Seetasail	122.33	152.53	29.15	1.29	28.30	7.60	24.42	10.10	30.04	152.43	6.22	130.16	16.49	48.67	41.94	19.22
Manipuri Black Rice	125.33	161.69	39.17	1.49	43.81	6.63	24.50	9.93	19.79	119.78	4.88	97.45	24.47	60.00	31.34	18.65
Tulsimukul	122.33	159.53	27.23	1.12	22.94	8.53	24.43	9.31	28.92	154.51	6.32	133.38	9.06	37.83	34.53	12.82
88(8)3	115.83	100.30	21.08	1.06	16.97	11.50	25.51	8.29	16.81	96.27	3.77	76.91	13.07	40.17	28.06	11.27
BM 1	98.17	98.15	29.86	1.13	29.12	8.26	27.43	9.33	23.22	118.48	4.29	53.08	20.70	34.17	12.94	4.43
BM4	96.67	100.90	32.95	1.00	27.82	9.71	27.32	9.71	27.42	137.54	5.01	49.69	14.67	39.17	11.92	4.48
BM 7	91.67	128.55	28.11	1.27	31.42	10.40	28.41	9.74	29.70	133.76	4.72	97.11	18.58	32.20	62.92	18.53
BM 34	93.17	97.43	29.90	1.07	24.00	8.59	27.23	9.38	25.65	125.91	4.62	44.22	18.27	31.83	37.29	11.96
BM 35	90.33	96.27	32.45	1.04	23.36	7.03	27.53	8.78	25.18	135.29	4.89	57.03	16.65	27.00	39.97	10.32
Keralasundori	112.67	130.41	33.96	1.49	37.98	9.47	24.16	9.98	28.30	141.93	5.87	122.81	20.28	70.33	34.88	22.05
Gopalbhog	136.17	183.74	40.24	1.32	39.68	6.03	28.90	10.56	24.59	146.94	5.09	122.82	30.01	66.00	30.61	19.87
RANGE(min)	90.33	93.72	21.08	0.80	14.35	6.63	20.27	6.59	9.73	54.33	2.68	40.80	8.86	27.00	6.43	2.23

RANGE(max)	136.17	183.74	48.88	1.56	66.35	16.40	29.73	11.00	38.18	225.17	8.74	173.34	33.73	70.33	62.92	22.05
GM	113.06	135.74	30.45	1.14	29.19	9.08	25.84	9.69	27.57	142.43	5.51	106.18	15.73	41.85	30.63	12.40
CV	1.08	3.04	10.53	9.24	15.67	19.47	4.51	6.12	12.19	8.82	8.70	11.89	9.41	18.41	28.86	17.42
SE	0.70	2.38	1.86	0.06	2.64	1.02	0.67	0.34	1.94	7.25	5.10	7.29	1.25	0.85	4.45	0.28
CD at 5%	1.40	4.76	3.72	0.12	5.28	2.04	1.35	0.68	3.88	14.50	10.21	14.57	2.50	1.71	8.90	0.55
CD at 1 %	1.84	6.24	4.87	0.16	6.92	2.67	1.76	0.90	5.08	19.00	13.37	19.09	3.27	2.24	11.66	0.72

**Table 4:** Phenotypic and genotypic coefficients of variability, heritability and genetic advance for sixteen quantitative characters in aromatic rice

	Grand mean	Range		coefficient of variation %		Heritability (%)	Genetic advance	Genetic advance as percent of mean
		Min	Max	GCV	PCV			
50% flowering	113.06	90.33	136.17	9.28	9.34	98.70	21.47	18.99
Plant height	135.74	93.72	183.74	18.75	18.99	97.40	51.75	38.12
Flag leaf length	30.45	21.08	48.88	16.61	19.69	71.10	8.78	28.84
Flag leaf width	1.14	0.80	1.56	14.18	16.93	70.20	0.28	24.62
Flag leaf area	29.19	14.35	66.35	30.65	34.43	79.30	16.41	56.21
No. of panicle	9.08	6.03	16.40	20.87	28.55	53.50	2.85	31.40
Panicle length	25.84	20.27	29.73	6.90	8.24	70.00	3.07	11.88
Primary branch	9.69	6.59	11.00	7.45	9.64	59.70	1.15	11.87
Secondary Branch	27.57	9.73	38.18	20.94	24.23	74.70	10.28	37.29
No. of spikelet/panicle	142.43	54.33	225.17	21.82	23.54	86.00	59.37	41.68
spikelet density	30.63	6.43	62.92	33.71	44.38	57.70	16.16	52.76
No. of filled grain/panicle	106.18	40.80	173.34	35.56	37.50	90.00	73.78	69.49
Test weight	12.40	2.23	22.05	38.77	42.50	83.20	9.03	72.81
Biological yield /plant	15.73	8.86	33.73	38.03	39.18	94.20	11.97	76.08
Harvest index	41.85	27.00	70.33	21.07	27.98	56.70	13.68	32.69
Grain yield	5.51	2.68	8.74	21.93	23.59	86.40	2.31	41.95

**Table 5:** Genotypic (G) and Phenotypic (P) correlation coefficient for sixteen quantitative characters in Aromatic Rice

		Plant height	Flag leaf length	Flag leaf width	Flag leaf area	No of panicle/plant	Panicle length	Primary branch	Secondary Branch	No of spikelet/panicle	Spikelet density	No of filled grain/panicle	Test weight	Biological yield /plant	Harvest index	Grain yield
50% flowering	G	0.701**	0.243	0.274	0.270	-0.172	-0.305	0.268	0.05	0.224	0.309	0.572**	0.110	0.667**	-0.013	0.424*
	P	0.683**	0.196	0.228	0.235	-0.125	-0.250	0.210	0.043	0.208	0.287	0.541**	0.105	0.491**	-0.002	0.391**
Plant height	G		0.394*	0.463*	0.458*	-0.533**	0.150	0.764**	0.525	0.604**	0.589**	0.805	0.154	0.555**	0.396*	0.626**
	P		0.328	0.407*	0.417*	-0.393*	0.127	0.589**	0.446*	0.553**	0.541**	0.761	0.149	0.430	0.293	0.568**
Flag leaf length	G			0.87	0.979**	-0.477*	0.146	0.438*	-0.024	-0.062	-0.076	-0.010	0.942**	0.600	0.251	0.558**
	P			0.665**	0.933**	-0.284	0.122	0.306	0.012	-0.046	-0.070	-0.019	0.779**	0.371	0.161	0.413*
Flag leaf width	G				0.907**	-0.669**	-0.112	0.473*	0.096	0.029	0.107	0.231	0.808**	0.708**	0.553**	0.817**
	P				0.843**	-0.422*	-0.076	0.282	0.081	0.025	0.077	0.192	0.653**	0.441*	0.346	0.64**
Flag leaf area	G					-0.427*	-0.022	0.369	0.022	-0.088	-0.051	0.091	0.920	0.581**	0.347	0.622**
	P					-0.276	0.004	0.253	0.041	-0.067	-0.051	0.078	0.796**	0.381*	0.241	0.513**
No of panicle	G						-0.352	-0.815**	-0.624**	-0.635**	-0.591**	-0.436	-0.313	-0.284	-0.293	-0.386*
	P						-0.176	-0.383*	-0.403*	-0.435*	-0.418*	-0.309	-0.233	-0.114	-0.138	-0.183
Panicle length	G							0.341	0.255	0.267	0.014	0.033	0.066	-0.175	0.205	0.004
	P							0.184	0.197	0.263	-0.035	0.057	0.049	-0.091	0.163	0.068
Primary	G								0.885**	0.869**	0.840	0.850	0.118	0.401*	0.423*	0.498**

branch	P								0.707**	0.691**	0.684**	0.652	0.093	0.260	0.247	0.378*
Secondary branch	G									0.963**	0.944**	0.808	-0.309	-0.017	0.348	0.209
	P									0.869**	0.846**	0.701	-0.252	-0.008	0.277	0.212
No of spikelet/panicle	G										0.966**	0.886	-0.334	0.056	0.384*	0.270
	P										0.951**	0.852	-0.300	0.001	0.344	0.274
Spikelet density	G											0.911**	-0.341	0.129	0.350	0.297
	P											0.866**	-0.307	0.048	0.309	0.278
No of filled grain/panicle	G												-0.262	0.343	0.429**	0.501**
	P												-0.238	0.222	0.407**	0.502**
Test weight	G													0.512**	0.255	0.508**
	P													0.387*	0.186	0.451*
Biological yield/plant	G														0.190	0.708**
	P														-0.196	0.478**
Harvest index	G															0.832**
	P															0.734**

\*\*\*: Significant at P=0.05 and 0.01, respectively

**Table 6:** Phenotypic path coefficient analysis of nine characters on grain yield

	50% flowering	Plant height	Flag leaf area	No of panicle/plant	Panicle length	Primary branch	Secondary Branch	No of filled grain/panicle	Test weight	Correlation with seed yield
50% flowering	-0.2240	0.0910	-0.0250	-0.0230	0.0030	-0.0410	-0.0040	0.5300	0.0850	0.3920**
Plant height	-0.1530	0.1320	-0.0440	-0.0730	-0.0010	-0.1160	-0.0450	0.7460	0.1210	0.5670**
Flag leaf area	-0.0530	0.0550	-0.1050	-0.0510	0.0000	-0.0500	-0.0040	0.0770	0.6430	0.5120**
No of panicle/plant	0.0280	-0.0520	0.0290	0.1850	0.0020	0.0750	0.0410	-0.3030	-0.1880	-0.1830
Panicle length	0.0560	0.0170	0.0000	-0.0330	-0.0110	-0.0360	-0.0200	0.0560	0.0400	0.0690
Primary branch	-0.0470	0.0780	-0.0270	-0.0710	-0.0020	-0.1960	-0.0710	0.6390	0.0750	0.3780**
Secondary Branch	-0.0100	0.0590	-0.0040	-0.0750	-0.0020	-0.1390	-0.1010	0.6870	-0.2040	0.2110
No of filled grain	-0.1210	0.1010	-0.0080	-0.0570	-0.0010	-0.1280	-0.0710	0.9800	-0.1930	0.5020**
Test weight	-0.0240	0.0200	-0.0830	-0.0430	-0.0010	-0.0180	0.0250	-0.2330	0.8090	0.4520*

Residual=0.339

\*, \*\*: Significant at P=0.05 and 0.01, respectively, Bold figure indicate direct effects

**Table 7:** Genotypic path coefficient analysis of nine characters on grain yield

	50% flowering	Plant height	Flag leaf area	No of panicle/plant	Panicle length	Primary branch	Secondary Branch	No of filled grain/panicle	Test weight	Correlation with grain yield
50% flowering	0.3310	0.4660	-0.3050	-0.1910	0.1500	0.6490	0.0020	-0.8050	0.1260	0.4230*
Plant height	0.2320	0.6650	-0.5160	-0.5940	-0.0740	1.8520	0.0170	-1.1330	0.1760	0.6250**
Flag leaf area	0.0890	0.3050	-1.1270	-0.4760	0.0110	0.8940	0.0010	-0.1280	1.0530	0.6220**
No of panicle/plant	-0.0570	-0.3550	0.4810	1.1140	0.1730	-1.9770	-0.0200	0.6130	-0.3580	-0.3860*
Panicle length	-0.1010	0.1000	0.0250	-0.3920	-0.4920	0.8260	0.0080	-0.0460	0.0750	0.0030
Primary branch	0.0890	0.5080	-0.4160	-0.9080	-0.1680	2.4250	0.0290	-1.1960	0.1350	0.4980*
Secondary Branch	0.0170	0.3490	-0.0250	-0.6950	-0.1250	2.1450	0.0320	-1.1360	-0.3540	0.2080
No of filled grain	0.1890	0.5350	-0.1020	-0.4850	-0.0160	2.0600	0.0260	-1.4070	-0.2990	0.5010**
Test weight	0.0360	0.1020	-1.0370	-0.3490	-0.0320	0.2850	-0.0100	0.3680	1.1440	0.5070**

Residual= 0.4851

\*, \*\*: Significant at P=0.05 and 0.01, respectively, Bold figure indicate direct effects

Such type of negative association may arise primarily from developmentally induced relationship. The developing structures of the plant compete for a common factor, possibly limited nutrient supply and if one structure is more favoured than the other for any reason, a negative correlation may arise in between them. Component compensation of parents allows on opportunity to have reasonable compromise and balance between one or two components resulting high yield. The optimal genetic level for each component would differ depending on the type of the environment encountered. Pleiotropy and / or linkage may also be genetic reasons for this type of negative association. The pleiotropic that affect both characters in the desire direction will be strongly acted upon by selection and rapidly brought towards fixation. The results of correlation coefficient implied that days to 50% flowering, number of filled grain per panicle, biological yield per plant, harvest index, test weight, may be considered for selection for yield improvement in the population of aromatic rice under study.

Path coefficient is standardized partial regression coefficient, which splits the correlation coefficients into the measures of direct and indirect contributions of independent variables on dependent variables. In the present investigation, considering grain yield as effect of nine characters as causes, phenotypic and genotypic correlation coefficients were partitioned by using the method of path analysis has been presented in Table 6 and Table 7 respectively. In the present investigation it has been observed that the characters like number of filled grain per panicle and primary branch had negative direct effect on grain yield, but these characters had positive indirect effect via other important characters indicating that a restricted selection method is to be imposed so that emphasis should be given on those characters (having positive indirect effect) for overall improvement of grain yield. Phenotypic and genotypic path analysis revealed that greater emphasis during selection of characters should be given on number of panicle/plant, primary branch, number of filled grain/panicle and test weight for improvement of grain yield. Similar results related to positive direct effect on grain yield per plant of number of filled grain per panicle (Nagle *et al.*, 2014; Devi *et al.*, 2017)<sup>[21, 7]</sup>, test weight (Dilruba *et al.*, 2014; Devi *et al.*, 2017)<sup>[9, 7]</sup>, number of panicle (Devi *et al.*, 2017)<sup>[7]</sup>, days to 50% flowering (Kole *et al.*, 2008)<sup>[16]</sup> reported earlier. The residual effect in phenotypic path coefficient (0.339) and genotypic path coefficient (0.485) indicated that the nine characters included in this study explain moderate percentage of variation in grain yield in this population. So, some other factors, which have not been considered here, need to be included in this analysis to account fully for the variation in grain yield. The result of path analysis indicating that selection for tall plant height, late flowering with restricted panicle number, high number of primary branch, number of filled grain and test weight are important which will helps to improve grain yield in the population under study.

### Conclusion

From the study of variability, correlation and path coefficient analysis it may be concluded that plant height, days to 50% flowering, number of field grain per panicle, test weight, primary branches are the most promising characters for yield improvement. So selection of these characters will be much more helpful for breeding programme of yield improvement and make elite genotype. The conclusions drawn from the present investigation are based on a particular location, which may have wide implications. The experiment need to be

conducted in different locations under different agronomic practices before drawing any definite conclusion.

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