Original Research Article

Genetic Variability of Floral and Agronomic Characteristics that Influence Outcrossing Rate Percentage of Cytoplasmic Male Sterile Rice

ABSTRACT

Developing high yielding hybrid rice varieties is much needed to ensure food security to meet the requirement of increasing population across the world. Cytoplasmic male genetic sterility system is a valuable technology for exploitation of heterosis and production of high yielding hybrid rice with better grain quality. Large scale commercial exploitation of hybrid vigour in rice largely depends on the availability of good CMS lines. A total of eighteen traits of five CMS lines of rice were evaluated to study the variability and correlation between floral and other yield contributing traits with outcrossing rate using Randomized Complete Block Design with three replications. High significant variation was observed among the genotypes for all the studied traits. High GCV and PCV coupled with high heritability and high genetic advance in percent of mean were observed for number of panicles per plant, filled grain, flag leaf breadth, stigma length and breadth, filament length and outcrossing rate which indicated the broad genetic base, less environmental influence and these traits are under control of additive gene action. character association and path analysis indicated that number of grain per panicle, filled grain per panicle, stigma length and breadth possessed both positive significant correlation and positive direct effects on outcrossing rate therefore, selection for the traits mentioned above will certainly bring in the improvement of outcrossing percentage of the lines, which in turn enhances the seed quantity of the hybrid.

Keywords: CMS, Outcrossing, Rice, Variability, Heritability

1. INTRODUCTION

Rice is one of the most ancient grain crops which is used as a staple food in most of the countries for containing high amount of carbohydrates, low fat and rich amount proteins, vitamins and minerals [1]. Daily we get 1329 kcal energy from rice that is about 60% of our total energy requirement. It's digestibility also high than other cereal crop (99.70%) [2]. Rice is a major source of dietary carbohydrate for more than half of the world's population [3]. In Bangladesh about 75% (11.2 million ha) of total cropped land is covered by rice and more than 60% man is engaged with it. Rice alone contributes around 10% of GDP in this country [4]. Thus the single crop rice has a multiple effect day to day daily life and economy [5]. A modest estimate suggests that the demand for rice in Bangladesh will increase by over 80% in the next 20 years to feed the growing population [6].

It is predicted that the population in the world will increase continually to 8 million in 2030. According to document from FAOSTAT 2015 [7], the annual loss of land for other uses is estimated to be about 10 to 35 million m^2/year, half of the coming from the crop land. Facing the challenges of population growth and cropland reduction, it is obvious that the only way to solve the problem is to improve the yield of cereal crops. Fortunately, the importance of rice to feed the population is recognized by united nations. The year 2004 was declared as the International year of rice, which reflects the importance of rice as a primary food source. It attracts a growing number of scientists around the world attempting to increase grain yield to keep pace with the demand of burgeoning world population

Large scale commercial exploitation of hybrid vigour in rice largely depends on the availability of good CMS lines and restorer lines. In recent times, cytoplasmic male sterility (CMS) technology has emerged as a promising approach for dramatic enhancement of productivity. In this system generally three lines are essential that is A, B and R lines. A line (CMS) is the cytoplasmic genetic male sterile line which is characterized by the absence of pollen grain, abortive anther and stable sterility. The economic feasibility of hybrid rice seed production largely depends on the availability of good CMS lines with desirable traits, the knowledge on the desirable traits of CMS lines is quite essential in enhancing seed yield of the potential rice hybrids. If parental lines of hybrids are locally adapted and adequate knowledge of agronomical and floral morphology of parental lines were gathered, it could lead self-sufficiently in F_1 seed production. So, the knowledge of agronomic and floral traits A lines is very much important. There is ample scope to study these characteristics influencing out crossing rate of component lines of hybrid rice under the local environment. It would help designing row ratio estimation for CMS multiplication and F_1 seed production and ultimately helps in building cost effective seed production package development. The promising CMS lines are now being studied for their combining ability and use in breeding programs. Hence, the present study is undertaken to evaluate the locally adoptable CMS lines for their traits to identify promising parental lines for developing heterotic hybrid rice. Therefore, this study was conducted to identify the most important characters for breeding programme by exploiting the genetic variation, heritability, and path analysis of outcrossing and related attributes of CMS lines of rice.

2. MATERIALS AND METHODS

The present investigation was carried out during *aman,* 20018-19 at the experimental field of Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Gazipur located at centre of Madhupur Tract (24º29 N latitude and 90º26 E longitude) having an altitude of 8.2m from the sea level. The climate of the experimental site is subtropical in nature characterized by heavy rainfall during the months from June to September and scanty in winter with gradual fall of temperature from the month of September. The experimental materials were collected from the Department of Genetics and Plant Breeding of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur. The experimental material comprised of five Cytoplasmic Male Sterile (A) lines those are IR 58A, IR 62A, IR 68888A, Gan 46A and BRRI 1A. The experiment was conducted in a completely randomized block design with three replications. Thirty days old seedlings were transplanted in each row by adopting inter and intra row spacing of 20 cm x 15cm. Fertilizer application and other cultural management practices were performed as per recommendation of Aman season. Standard crop management practice was done as and when necessary.

Five plants of each genotype in each replication were selected randomly to recording different parameters. The parameters were collected for the characters *i. e* Days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), number of tiller per hill, number of panicle per plant, number of grain per panicle, 1000 grain weight (gm), filled grain, flag leaf length (cm), flag leaf width (cm), anther length (µm), anther breadth (µm), stigma length (µm), stigma breath (µm), filament length (µm), pollen sterility (%), and outcrossing rate (%). Most of the traits were measured in the field except anther length, anther breadth, stigma length, stigma breath, filament length, and pollen sterility those were measured in laboratory. Anther length, anther breadth, stigma length, stigma breath and filament length was measured with microscope using ocular micrometer (level 1) before anthesis.
For statistical analysis, analysis of variance, estimation of mean, range, standard error, coefficient of variation, Estimation of phenotypic and genotypic correlations, Path coefficient analysis were considered. In order to test the significance of treatments critical difference was calculated [8]. Phenotypic and genotypic coefficients of variation (PCV and GCV) were analyzed according to [9] Heritability in broad sense and genetic advance were calculated according to methods specified by [10] and categorized according to [11]. Correlation coefficients were calculated for all quantitative character combinations at phenotypic, genotypic and environmental level by the formula set by [12]. Path coefficient analysis proposed by [13] and explained by [14] was used to analyze the direct and indirect impact of various traits to out crossing.

3. RESULTS AND DISCUSSION

3.1 Analysis of variance

The analysis of variance studied for 18 characters was furnished in Table 1a, 1b. The analysis of variance revealed significant differences for all the characters studied except panicle length and pollen sterility, Which indicated that wide range of variability present among the genotype. Previous studies also found significant variation for these traits [15].

Table 1a: Analysis of variance for different parameters of CMS (A) lines

Source of variation	**d.f**	**50% F**	**DMT**	**PH (cm)**	**PL (cm)**	**NT/H**	**NP/P**	**NG/P**	**TGW (gm)**	**Filled grain**
Replication	2	0.0	0.000	0.800	0.285	4.067	3.267	5.400	2.319	0.467
Genotype	4	33.0**	287.4**	146.267**	5.965NS	20.50*	49.833**	123.933**	30.47**	47.767**
Error	8	0.0	0.000	2.717	1.81	1.900	1.433	1.983	0.806	1.467

50% F = Days to 50% flowering, DMT = Days to maturity, PH = Plant height, PL = Panicle length, NT/H = Number of tiller per hill NP/P = Number of panicle per tiller, NG/P = Number of grain per panicle, TGW = Thousand grain weight

Table 1b: Analysis of variance for different parameters of CMS (A) lines

Source of variation	**d.f**	**FLL (cm)**	**FLW (cm)**	**AL (µm)**	**AB (µm)**	**SL (µm)**	**SB (µm)**	**FL (µm)**	**PS (%)**	**OCR (%)**
Replication	2	0.129	0.109	.9080	1.817	17.317	0.267	7.371	0.001	0.467
Genotype	4	62.16**	0.311*	298.25*	188.558**	13356.29**	1079.64**	41759.02**	1.5NS	21.5**
Error	8	0.308	0.027	25.350	2.983	15.192	6.142	16.614	0.001	0.800

FLL = Flag leaf length, FLW = flag leaf width, TW = Test weight, AL = Anther length ,AB = Anther breadth, SL= Stigma length, SB = Stigma breadth, FL = Filament length, PS = Pollen sterility ,OCR = Outcrossing rate

* = Significant at 5% level, ** = Significant 1% level, d.f = Degrees of freedom

3.2 Genetic parameters for different characters of tested centries

The estimates of mean, range, phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV), heritability (h^2) and genetic advance as per cent of mean (GAM) are presented in table 2.

Table 2: Mean, range, genetic variability, heritability (broad sense) and genetic advance as percent of mean for outcrossing and its component traits for five CMS lines of rice

Sl. No	Character	Mean	Range	Coefficient of variation		Heritibility (%)	GAM (%)
				PCV(%)	GCV(%)		
1	50% flowering	66.66	63-70	5.08	5.04	98.55	10.32
2	Days to maturity	82.93	73-96	11.98	11.97	99.89	24.65
3	Plant height (cm)	70.20	61.66-77.67	10.12	9.85	94.62	19.74
4	Panicle length (cm)	22.29	20.48-24.30	7.95	5.22	43.26	7.08
5	Number of tiller/hill	19.33	15.67-22.33	14.72	12.87	76.54	23.21
6	Number of panicle /plant	11.66	8.33-17.33	35.92	34.42	91.84	67.96
7	Number of grain/panicle	137.2	146.3-131.7	4.75	4.64	95.34	9.34
8	Thousand weight (gm)	17.97	13.47-22.30	18.19	17.49	92.46	34.65
9	Filled grain	17.86	14-22.33	52.25	49.93	91.32	98.30
10	Flag leaf length (cm)	24.47	20.52-32.51	18.48	18.35	98.52	37.52
11	Flag leaf breath(cm)	1.24	0.83-1.53	27.97	24.68	77.80	44.84
12	Anther length(μm)	395.86	384-407.33	2.71	2.40	78.46	4.39
13	Anther breath(μm)	74.36	66-83.16	10.82	10.57	95.39	21.27
14	Stigma length(μm)	257.83	190.6-365.5	25.90	25.86	99.65	53.18
15	Stigma breath (μm)	69.13	47.33-92.33	27.59	27.36	98.31	55.88
16	Filament length (μm)	518.69	413.1-667.5	22.75	22.74	99.88	46.81
17	Pollen sterility (%)	97.73	96-99	1.15	1.05	84.21	1.99
18	Out crossing rate %	19.43	17.96-21.27	39.14	37.37	85.03	32.24

PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation,

GAM = Genetic advance as percent of mean

3.3 Coefficient of variation (PCV, GCV)

Higher phenotypic co-efficient of variation, compared to genotypic co-efficient of variation were recorded for all the quantitative traits studied in the present investigation, indicating the influence of environment. Similar findings were reported earlier by Mamta Singh et al. (2007) [16]. However, high (>20%) phenotypic co-efficient of variation for number of panicles per plant, filled grains/panicle, flag leaf breadth, stigma length, stigma breadth, filament length and outcrossing rate in the present research was noted to be closely and essentially related with high genotypic co-efficient of variation, indicating the negligible influence of environment and existence of high genetic variability for these traits. Hence, selection on the basis of phenotype of these genotypes can be effective. Similar results were described earlier by Misra [17] and Hossain [18]. However, moderate (10-20%) genotypic and phenotypic coefficients of variation were recorded in the present study for days to maturity, plant height, thousand grain weight, flag leaf length, and anther breadth. These results are similar with the findings of Bornane [19] for thousand grain weight. In contrast, low (<10%) estimates of genotypic and phenotypic coefficients of variation were observed in the present study for days to 50% flowering, number of grain per panicle, anther length, and pollen sterility indicating low variability for these characters in the present experimental material and therefore, there is little scope for improvement of these traits. Similar findings were reported earlier by Satish [20] for plant height.

3.4 Heritability (broad sense) and Genetic Advance as Percent Mean (GAM)

Heritability estimates in broad sense (h2b) were relatively higher (>60%) for almost all the traits studied. Iftekharuddaula [5] stated similar result in hybrid rice. High heritability evaluations have been found to be helpful in making selection of superior genotypes on the basis of phenotypic performance. High heritability (>60%) coupled with high genetic advance as percent mean (>20%) was recorded for days to maturity, number of tillers per hill, number of panicles per plant, thousand grain weight, filled grains/panicle, flag leaf length, flag leaf breadth, anther breadth, stigma length and breadth, filament length and outcrossing rate indicating that the high heritability observed is due to additive gene effects and selection may be effective for these characters. Similar findings were observed by [22] for thousand grain weight, and [23] for outcrossing rate. On contrary, high heritability coupled with moderate genetic advance in percent of mean (10-20%) was observed for days to 50% flowering, and plant height indicating the role of both additive and non additive gene effects for controlling these characters. The results are similar with the reports of Seyoum [24]. Further, information on genetic variation along with heritability and genetic advance assessments has been informed to give a better idea about the efficiency of selection.

In the present study, high GCV and PCV coupled with high heritability and high genetic advance in percent of mean were observed for number of panicles per plant, filled grain, flag leaf breadth, stigma length and breadth, filament length and outcrossing rate indicating the preponderance of additive gene action and therefore, there is scope for improvement of the trait through selection. Similar results were given earlier by [25] and [26].

3.5 Mean Performance

BRR1 1A recorded for maximum days to 50% flowering (70) and minimum in Ghan 46 A (63) ; Ghan 46A recorded for maximum days to maturity (90) followed by BRRI 1A (89); highest plant height observed in IR 58A (75.67 cm) and minimum in BRRI 1A (61.67 cm) ; panicle length found maximum in Ghan 46 A (24.30 cm) followed by IR 62A (23.21 cm); BRRI 1A revealed maximum number of tiller per hill (22.33) and panicle per plant (17.33) followed by Ghan 46 A (21.33) and (14.67) respectively; number of grain per panicle found highest in IR 58A (146.3) but number of filled grain observed highest in IR 62A (22.33); thousand grain weight found maximum in Ghan 46A (22.30gm) followed by IR 58 A (18.56 gm); highest flag leaf length found in IR 58A (32.52 cm) followed by Ghan 46A (24.10 cm) and highest flag leaf width observed in Ghan 46A (1.533 cm) followed by IR 58A (1.467); Ghan 46A recorded for maximum anther length (444.0 um) followed by IR 58 A (407.3); maximum anther breadth recorded in IR 58A (93.17 um) followed by Ghan 46 A (92.50 um); BRRI 1A recorded for maximum stigma length (365.5um) and breadth (82.33um) followed by Ghan 46A (191.2 and 80.83) respectively; filament length observed highest in IR 62A (713.2 um) followed by Ghan 46 A (644.7 um); outcrossing rate found maximum in IR 58A (21.17) and minimum in BRRI 1A (17.96). Results revealed that out crossing rate varied significantly among the CMS lines (Table 3b) suggested out crossing rate appeared as less flexible over the genetic background of the CMS lines. [27] reported significant difference in out crossing potential among the CMS lines.

Table 3a: Mean performance of 5 CMS lines for 18 characters in rice (*Oryza sativa* L.)

CMS line	**50% F**	**DMT**	**PH (cm)**	**PL (cm)**	**NT/H**	**NP/T**	**NG/P**	**TGW**	**Filled grain**
Ghan46A	63 d	96 a	71.67 b	24.30 a	21.33 a	14.67 b	135.7 c	22.30 a	15.000 b
BRRI 1A	70 a	89 b	61.67 c	20.48 b	22.33 a	17.33 a	131.7 d	13.47 c	16.000 b
IR 68A	65 c	75 d	77.67 a	22.18 ab	18.67 b	9.000 c	131.7 d	17.00 b	14.000 b
IR 62A	64 d	73 e	64.33 c	23.21 a	18.67 b	9.000 c	141.0 b	18.55 b	22.33 a
IR 58A	69 b	79 c	75.67 a	22.29 ab	15.67 c	8.333 c	146.3 a	18.56 b	22.00 a
CV	.612	.3813	2.34	5.98	7.12	10.26	1.02	4.99	15.39
S.E	.235	.182	.95	.77	.79	.69	.81	.51	.69

50% F = Days to 50% flowering, DMT = Days to maturity, PH = Plant height, PL = Panicle length, NT/H = Number of tiller per hill NP/P = Number of panicle per tiller, NG/P = Number of grain per panicle, TW = Thousand grain weight

Table 3b: Mean performance of 5 CMS lines for 18 characters in rice (*Oryza sativa* L.)

CMS Line	**FLL(cm)**	**FLW(cm)**	**AL (µm)**	**AB (µm)**	**SL (µm)**	**SB (µm)**	**FL (µm)**	**PS**	**OCR**
Ghan46A	24.10 b	1.533 a	444.0 a	92.50 a	191.2 b	80.83 b	644.7 b	100.00 a	20.92 b
BRRI 1A	20.52 c	0.8333 b	405.3 c	66.00 c	365.5 a	82.33 a	443.3 c	97.00 b	21.27 a
IR 68A	23.27 b	1.433 a	418.0 b	91.83 b	197.2 c	62.50 d	354.7 d	95.00 c	18.77 c
IR 62A	23.32 b	0.9667 b	392.5 b	81.33 b	194.7 d	72.67 c	713.2 a	97.00 b	17.96 c
IR 58A	32.52 a	1.467 a	407.3 a	93.17 a	190.7 e	47.33 e	547.6 a	95.00 c	18.22 c
CV	2.24	13.18	1.2	2.32	2.25	3.5	.78	0.75	5.40
S.E	.32	.094	2.88	.99	2.25	1.43	2.35	1.34	0.60

FLL = Flag leaf length, FLW = flag leaf width, AL = Anther length, AB = Anther breadth, SL = Stigma length, SB= Stigma breadth, FL = Filament length, PF = Pollen sterility, OCR= Out crossing rate

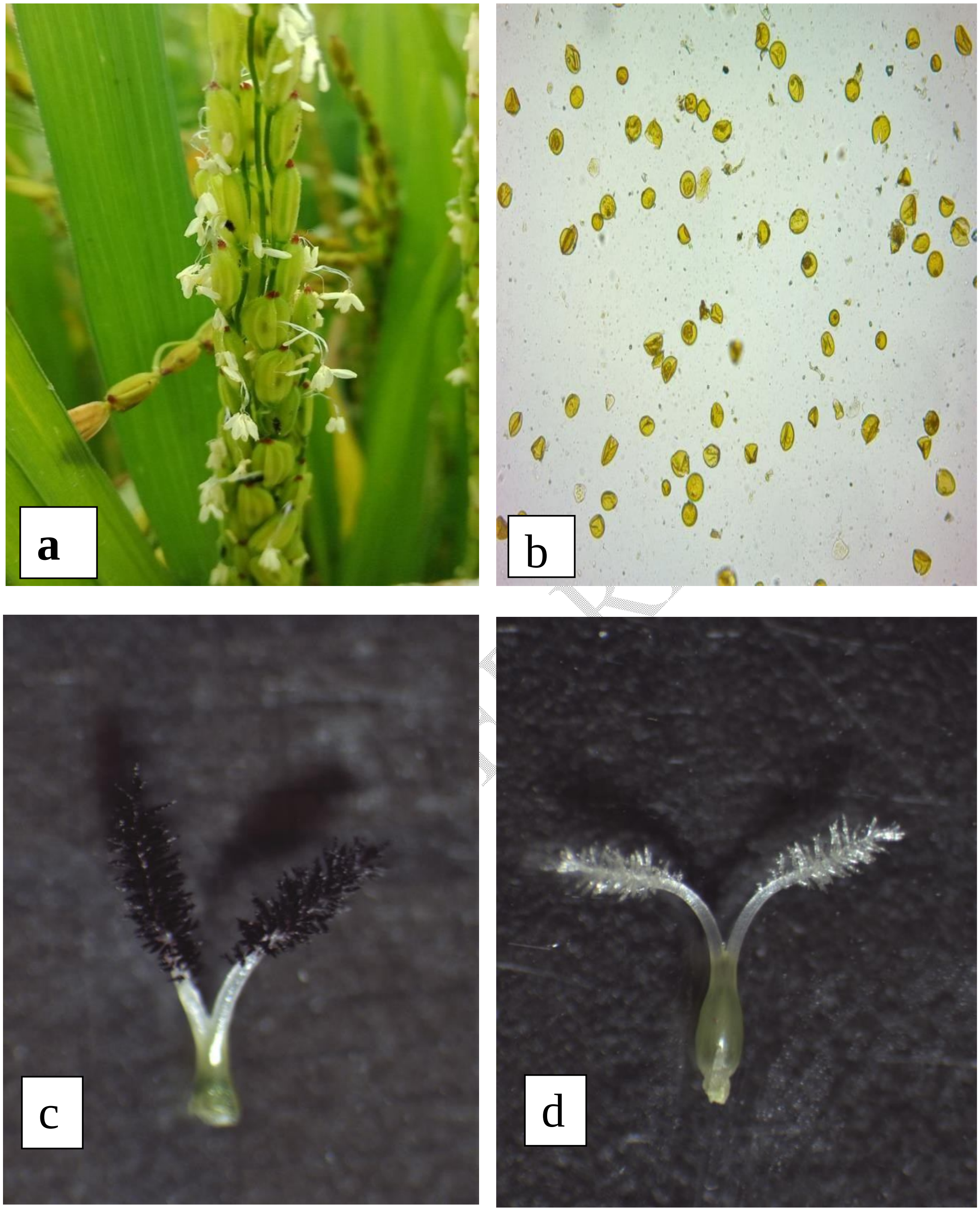

Fig 1: Different floral traits of CMS line; a) White color anther with filament, b) Sterile pollen, c) Black color stigma, d) White color stigma

Correlation and Coefficient

The phenotypic and genotypic correlation coefficients between outcrossing and other characters and inter relations among them were estimated and presented in Table 4a, 4b. In general, the results revealed that the genotypic correlations were higher than the phenotypic correlations for almost all the characters under study. Outcrossing ability of a CMS line is very important for seed setting. It is being influenced by several inter dependable traits. So, selection for outcrossing rate might not be effective unless influential traits would not be take into consideration. Character association studies revealed positive and significant association of outcrossing rate with number of grain per panicle, filled grain per panicle, stigma length and breadth both at genotypic and phenotypic levels, indicating that these traits were influenced by outcrossing rate. Similar results are reported by[29]. While this trait showed significant negative association anther length and anther breadth. Similar results are reported [30]. Plant height exposed positive association with panicle length, number of grain per panicle, thousand grain weight. This trait showed negetive association with number of tiller, number of panicle per plant and outcrossing rate at both genetypic and phenotypic levels respectively. Related findings were carried out by [31].

Table 4a : Phenotypic (above diagonal) and genotypic (below diagonal) correlations for floral and agronomical characters in CMS lines rice (*Oryza sativa* L.)

Character	**Days to 50% flowering**	**Days to maturity**	**Plant height**	**Panicle length**	**Number of tiller /hill**	**Number of panicle /plant**	**Number of grain /panicle**	**thousand grain weight**	**Filled grain**	**Out crossing rate**
Days to 50% flowering	-	.0371	-.0933	-.6588*	-.0863	.2228	-.0376	-.7312**	.0658	-.0156
Days to maturity	.0399	-	-.2003	.0994	-.6272	-.8153*	.3091**	.2270	.4832*	.1230
Plant height	-.1127	-.2005	-	.2576	-.4999	-.5363*	.1504	.3984	-.1938	-.4505
Panicle length	-1.068*	.1622	.3605	-	-.0256	-.1834	.1834	.6848**	.0328	.1897
Number of tiller/hill	-.0945	-.7199*	-.6594	-.2280	-	.8747**	-.7453**	-.1514	-.645*	-.2723
Number of panicle/tiller	.2280	-.8541**	-.609*	-.3615	.9324**	-	-.5731*	-.2540	-.533*	-.1642
Number of grain/panicle	-.0311	.3158	.1657	.4106	-.7868**	-.5854*	-	.3559	.872**	.775**
Test weight	-.7415	.2314**	.4306	1.22**	-.2328	-.2606	.4006	-	.0745	.1805
Filled grain	.0693	.5059	-.1822	.1481	-.6449*	-.5302*	.9119**	.1041	-	.877**
Outcrossing rate	-.0164	.1235	-.4604	.2063	-.3131	-.1629	.8078**	.1957	.914**	-

Table 4b- Phenotypic (above diagonal) and genotypic (below diagonal) correlations for floral and agronomical characters in CMS lines rice (*Oryza sativa* L.)

Character	Flag leaf length	Flag leaf width	Anther length	Anther breadth	Stigma length	Stigma breadth	Filament length	Outcrossing rate
Flag leaf length	-	.5171	-.5427*	.7546**	.7442**	.7276**	.7021**	-.4878
Flag leaf width	.6162	-	.3300	.7109*	-.5248	-.5829*	.5654*	-.1041
Anther length	-.6554*	.3015	-	-.1080	.5553*	.8490**	.8491**	-.6112
Anther breadth	.7753**	.9009*	-.1103	-	.5362*	-.4139	-.3894	-.1087
Stigma length	.7486**	-.6163	.6340*	.5426*	-	-.851**	.5631*	.7637*
Stigma breadth	-.7459**	-.6413*	.9319**	-.4159	-.8615**	-	.8869**	.6905**
Filament length	.7086**	.6302*	.9572**	-.4051	.5659*	.8961**	-	-.4072
Outcrossing rate	-.5643	-.1894	-.7562	-.0692	.9453**	.8454**	-.5107	-

3.6 Path Coefficient Analysis

As simple correlation does not provide the true contribution of the characters towards the yield, these genotypic correlations were partitioned into direct and indirect effects through path coefficient analysis [32]. Path coefficient analysis allows the separation of the direct effect and their indirect effects through other attributes by apportioning the correlations for better interpretation of cause-and-effect relationship. Path coefficient analysis was carried out using genotypic correlation, using outcrossing rate as a dependent variable. The results of path analysis revealed that panicle length, number of tiller per hill, number of grain per panicle, filled grain per panicle, thousand grain weight, flag leaf width, stigma breadth and filament length exhibited positive direct effects with outcrossing rate.

Critical analysis of results obtained from character association and path analysis indicated that number of grain per panicle, filled grain per panicle, stigma length and breadth possessed both positive significant correlation and positive direct effects on outcrossing rate. The results clearly indicated the true association of these traits with the outcrossing of these lines. Hence, that could be used in selective breeding program.

Table 5a: Direct and indirect effects (phenotypic) of agronomic and floral characters on yield in 5 CMS (A) lines of rice (*Oryza sativa*

Character	**Days to 50% flowering**	**Days to maturity**	**Plant height**	**Panicle length**	**Number of tiller /hill**	**Number of panicle /tiller**	**Number of grain /panicle**	**Thousand grain weight**	**Filled grain**
Days to 50% flowering	**.2618**	-.0062	.0451	-.1396	-.0273	.0100	.0143	-.2082	.0337
Days to maturity	.0104	**-.1544**	.0803	.0212	.2083	.0373	-.1454	.0650	-.2462
Plant height	-.0295	.0310	**-.4004**	.0471	-.1908	-.0266	.0763	.1209	-.0887
Panicle length	-.2796	-.0251	-.1443	**.1308**	-.0660	-.0158	.1890	.3452	.0721
Number of tiller/hill	-.0247	-.1112	.2604	-.0298	**.2893**	.0407	-.3623	.0654	-.3139
Number of panicle/tiller	.0597	.1319	.2439	-.0473	.2697	**.-0437**	-.2695	-.0732	-.2581
Number of grain/panicle	.0081	.0488	-.0664	.0537	-.2276	.0256	**.4604**	.1125	.4439
Thousand grain weight	-.1941	-.0357	-.1724	.1607	-.0673	-.0114	.1845	**.2808**	.0507
Filled grain	.0181	.0781	.0729	.0194	-.1866	-.0232	.4199	.0292	**.4867**
Outcrossing rate	**-.0164**	**-.1235**	**-.4607**	**.2063**	**.3131**	**.1629**	**.8078**	**.1957**	**.9146**

RESIDUE= 0.0234

Table 5b: Direct and indirect effects (phenotypic) of floral and agronomical characters on yield in 5 CMS lines of rice

Character	**Flag leaf length**	**Flag leaf width**	**Anther length**	**Anther breadth**	**Stigma length**	**Stigma breadth**	**Filament length**
Flag leaf length	**-.1463**	.1541	-.2015	-.1733	.1054	-1.1093	.8067
Flag leaf width	-.0902	**.2501**	-.0927	-.1427	.1224	-.9538	.7174
Anther length	-.0959	.0754	**-.3074**	-.1468	.0150	-1.3861	1.0896
Anther breadth	-.1134	.2253	-.0339	**-.1256**	.1359	-.6186	.4612
Stigma length	.1095	-.1541	.1949	.2315	**-.0737**	1.2814	-.6442
Stigma breadth	.1091	-.1604	.2865	.1994	-.0565	**1.4873**	-1.0201
Filament length	-.1037	.1576	-.2943	-.1310	.0551	-1.3328	**1.1384**
Outcrossing rate	**-.5643**	**-.1894**	**-.7562**	**-.0691**	**.9452**	**.8454**	**-.5106**

RESIDUE=.3914

4. Conclusion

The germplasm utilized in this study possessed useful variability and genetic parameter estimates for the studied traits that could be exploited for the rice genetic improvement program. The maximum outcrossing rate was found in IR 58A and minimum in BRRI 1A. Correlation and path analysis revealed that number of grain per panicle, filled grain per panicle, stigma length and breadth had positive significant correlation along with direct effect on outcrossing. Hence, it can be concluded that selection for the traits mentioned above will certainly bring in the improvement of outcrossing percentage of the lines, which in turn enhances the seed quantity of the hybrid and thus making hybrid seed production more economical and profitable to the seed industry and ultimately to the farming community.

COMPLIANCE WITH ETHICAL STANDARDS

Conflict of interest: The authors declare that they have no conflict of interest.

References

[1] Hossain, M. S., Ivy, N. A., Raihan, M. S., Kayesh, E., &Maniruzzaman, S. (2020). Genetic Variability, Correlation and Path Analysis of Floral, Yield and its Component Traits of Maintainer Lines of Rice (Oryza sativa L.). *Bangladesh Rice Journal*, *24*(1), 1-9.

[2] Shozib, Habibul & Jahan, Saima & Sultan, Zakir & Alam, Samsul & Amin, Rifat & Hasan, Mahedi & Siddiquee, Muhammad. (2018). Nutritional Properties of Some BRRI HYV Rice in Bangladesh. Journal of Vitamins and Minerals. 07. 10.4172/2376-1318.1000174.

[3] Babu, V. R., Shreya. K., Kuldeep Singh Dangi, Usharani, G. and Nagesh, P. 2013. Genetic variability studies for qualitative and quantitative traits in popular rice (O*ryza sativa L.*) hybrids of India. *International Journal of Scientific and Research Publications*, 2(6):

[4] Yearbook of Agricultural Statistics-2017 July 2016 Bangladesh Bureau of Statistics (BBS) Statistics and Informatics Division (SID) Ministry of Planning Government of the People's Republic of Bangladesh www.bbs.gov.bd.

[5] Iftekharuddula, K.M.,Akhtar, K.,Hassan, M.S., Fatema, K. and Badshah, A.2011. Genetic divergence, character association and selection criteria in irrigated rice.J. Biol. Sci., 2(4):243-246. *International Rice Research Notes*, *23*(2), 1-1.

[6] Zaman, F. U., Abraham, M. J., Mahendru, A., Natarajan, U. S., & Mohammad, F. (1998).

[7] FAOSTAT. 2015. World's crop production. Food and agricultural organization.

[8] Fisher, R. A., & Yates, F. (1963).Statistical tables for biological, agriculturaland medical research.*Statisticaltablesforbiological,agriculturalandmedicalresearch.*,(6thed).

[9] Burton,G.W.(1952,August).Qualitativeinheritanceingrasses.Vol.1.In *Proceedingsofthe 6th International Grassland Congress, Pennsylvania State College* (pp. 17-23).

[10] Allard, R W. 1960. Principles of Plant Breeding. John Willy and Sons, Inc., New York

[11] Johnson, H W, H F Robinson and R E Comstock. 1955. Estimation of genetic and environmental variability in soybean. *Agronomy Journal,* 47:314-318.

[12] Miller, P.A., Williams, J. C., Robinson, H.F., & Comstock, R.E. (1958). Estimate of genotypic and environmental variances and co-variance in upland cotton and the implication selection. Agronomy Journal, 50, 126 131.

[13] Wright, S. 1921. Correlation and causation.*Journal of Agricultural Research*, 20: 257-287.

[14] Dewey DR, KH Lu. A correlation and path coefficient analysis of components of crested wheat grass and seed production. Agronomy Journal.1956;51:515–7.

[15] Yaqoob, M., Anjum, R., Hussain, M., & Shah, M. J. (2012). Genetic diversity analysis and character association in some Chinese hybrid rice under dry conditions. *Pakistan Journal of Agricultural Research*, *25*(4).

[16] Mamta Singh, K Kumar and R P Singh. 2007. Study of co-efficient of variation, heritability and genetic advance in hybrid rice. *Oryza*, 44 (1): 160-162.

[17] Mishra, L K and R K Verma. 2002. Genetic variability for quality and yield traits in non segregating populations of rice (*Oryza sativa* L.). *Plant Archives,* 2(2): 251-256

[18] Hossain, Md & Maniruzzaman, Sheikh & Ivy, Nat & Sharif Raihan, Mohammad & Akter, Anowara & Hossain, Md. (2022). Assessment of Genetic Diversity, Correlation and Principal Component Analysis of Restorer Lines of Hybrid Rice. International Journal Of Advance Research And Innovative Ideas In Education. Volume 8. 1359-1374.

[19] Bornare, S. S., Mittra, S. K., & Mehta, A. K. (2014).Genetic variability, correlation and path analysisoffloral, yieldand itscomponenttraitsincmsandrestorerlinesofrice(Oryza sativa L.).*Bangladesh Journal of Botany*, *43*(1), 45-52.

[20] Satish, Y, K V S Ramaiah, S R Reddy and T C M Naidu. 2003. Genetic variability, heritability and Genetic advance in scented rice (*Oryza sativa* L.). *The Andhra Agricultural Journal*, 50 (1&2): 24-26.

[21] Cochran,W. G.(1950).*Experimentaldesign*.JohnWiley&Sons. Developing Pusa 5A, a stable indica CMS line with high outcrossing potential.

[22] Adilakshmi, D and M Girijarani. 2012. Variability, character association and path analysis in rice under submergence. *Crop Research*, 44(1 & 2): 146-151.

[23] Madhavilatha, L, M ReddiSekhar, Y Suneetha and T Srinivas. 2005. Genetic variability, correlation and path analysis for yield and quality traits in rice (*Oryza sativa L.*). *Research on Crops*, 6 (3): 527-534.

[24] Seyoum, M, S Alamerew, and K Bantte. 2012. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). *Journal of plant sciences*, *7*(1):13-22.

[25] Mohana Krishna, D, D M Reddy, K H P Reddy and P Sudhakar. 2009. Character association and interrelationship of yield and quality attributes in rice (*Oryza sativa* L.). *The Andhra Agricultural Journal*, 56(3): 298-301.

[26] Hossain, M. S., Ali, M. A., Khan, M. A. I., &Maniruzzaman, S. (2020). Prevalence and Transmission of Fusariummoniliforme: A Seed Borne Pathogen of Rice. *Bangladesh Rice Journal*, *24*(1), 11-19.

[27] Hashim S, Ding P, Ismail MF, Ramli A. Floral traits and flowering behaviors of Malaysian rice cytoplasmic male sterile and maintainer lines and its relationship with out-crossing performance. Aust. J. Crop Sci. 2021;15:180–186

{28] Sheeba, A., Vivekanandan, P., & Ibrahim, S. M. (2006). Genetic variability for floral traits influencing outcrossing in the CMS lines of rice. *Indian Journal of Agricultural Research*, *40*(4), 272-276.

[29] Singh, B., & Singh, R. (1998). Genetic variability in floral traits of 10 cytosterile lines of rice (Oryza sativa L.). *International Rice Research Notes*, *23*(3), 1-1.

[30] Hasan, J. M., Kulsum, U. M., Majumder, R. R., &Sarker, U. (2020). Genotypic variability for grain quality attributes in restorer lines of hybrid rice. *Genetika*, *52*(3), 973-989.

[31] Bidhan, R., Hossain, M., Hossain, F. and Roy, B. (2001), Genetic variability in yield components of rice (Oryza sativa L.). Environ. and Ecol., 19(1): 168-189.

[32] Maniruzzaman, S., Rahman, M. A., Hasan, M., Rasul, M. G., Molla, A. H., Khatun, H., &Akter, S. (2022). Genetic Mapping to Detect Stringent QTLs Using 1k-RiCASNP Genotyping Platform from the New Landrace Associated with Salt Tolerance at the Seedling Stage in Rice. *Plants*, *11*(11), 1409.