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Heritability, genetic advance and correlation studies of cross pollination in CMS lines of rice influenced with floral traitst

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Abstract
Heritably is the most important feature of a trait that is directly affected the selection for improvement and selection is the basic tool of any crop improvement program. At the genetic level variability is the necessity of the selection. The variability in floral traits of CMS lines is very useful particularly for breeding CMS lines with high out crossing potential in rice. This experiment is an attempt that has been made to study floral variability and association among floral traits. Ten cyto-sterile lines and their maintainers, possessing "Wild Abortive" (WA) type of stable cytoplasm were studied for Heritability, Genetic advance and Correlation among floral traits influencing out crossing in rice. Significant positive correlation were observed between stigma breath with anther breadth & anther size; percentage of stigma exsertion with stigma length, angle of opened florets and style length; angle of opened florets with style length; stigma length with anther length; duration of opening of floret with percentage of stigma exsertion, angle of opened florets, filament length and filament length after elongation; stigma breadth with stigma surface, anther breadth and anther size; anther breadth with anther size and filament length; filament length with filament length after elongation. Characters such as blooming, angleof florets, stigma exertion, stigma breadth, stigma surface, style length, anther breadth and filament showed high broad sense heritability attached with medium genetic advance were useful trait for genetic improvement.

Keywords: Correlation, Cyto-sterile Line, Genetic Advance (GA), Heritability

Introduction
Rice grown as worldwide but Asian countries are having biggest part of the area as well as production of the world. It is also a world fame cereal crop that belongs to the sub-family Oryzoidae of family Poaceae, genus Oryza and tribe Hordae. The cultivated rice is an annual grass with round, hollow, green and jointed culms, flat leaves, fibrous root system and terminal inflorescence which are referred as panicle composed of spikelets. The flower is autogamous which consists of six stamens (exceptional) unlike three in other cereals (Prakash *et al.*, 2018) [16]. The edible seed is monocotyledonous called as caryopsis have lemma and pelea. It has one third part of the food for total population of the world. It's also grown as worldwide but most part covered in Asian countries. The success of any breeding programme depends on quantum of genetic variability present in the available genetic stocks (Basavaraja *et al.*, 2013) [2]. Many traits are observed in rice which have high heritability and vast genetic variability. The floral biology of CMS lines is an important mechanism for out-crossing and seed setting in hybrid seed production. Information regarding correlation among the floral traits, heritability and genetic advance is essential for effective selection. A Major problem of low seed set in hybrid seed production plots due to its very low out crossing of the CMS lines in rice crop. A line (cytoplasmic male sterile) with excessive out crossing potential will certainly be economize that affect the cost of hybrid seed production. Virmani, (1996) [24] reported that the male sterility is the most important floral traits that influencing out crossing in rice. Male fertile plant shows very little influence, if out crossing due to self-pollinating nature of rice flower. Though, male sterile plants, extent of out crossing is promoted orinfluenced by its other floral traits which are stigma size and exsertion, duration of floret opening, pollen density per unit area, anther size, duration of spikelet blooming and filament

length, etc. have been reported by Virmani (1994) [24].

Materials and Methods
Ten cyto-sterile lines and their maintainers, possessing "Wild Abortive" (WA) type of cytoplasm, collected DRR (Directorate of rice research), Rajendra Nagar, Hyderabad and NDUAT, Kumarganj, Faizabad (U.P.), constituted the materials for present studies. The cyto-sterile lines and their maintainers were grown in tow Kharif Sessions (2009 and 2010) in Randomized Block Design with three replications in three meter rows and twenty centimeters apart. Plant to plant desistance within the rows was fifteen centimeters. Cyto-sterile (A) and Maintainers lines (B) were transplanted in 4:2 ratios, respectively. Recommended agronomic practices were implemented to grow a good and healthy crop. Duration of opening of florets (mm), angle of opened florets (degree), percentage of stigma exsertion, and percentage of panicle exsertion, anther length (mm), anther breadth (mm), anther size (mm), fragment length (mm), filament length after elongation(mm), stigma length(mm), stigma surface and style length were recorded. Heritability estimates was worked out with the help of its formula that suggested by lush (1949) and Burton and De Vance (1953) and Genetic Advance as suggested by Lush (1949) and Johnson, Robinson and Comstock (1995a). Correlation analysis was performed as has been given by Panse and Sukhatme (1954).

Heritability (Broad sense): $H_B^2 = \frac{Vg}{Vp}$

Where,
H_B^2= Heritability in broad sense
Vg = Genotypic variance;
Vp = Phenotypic variance;

Expected genetic advance (GA):

GA% = K x Vp x H_B^2 x 100

Where, K = 2.06 at 5% selection intensity for trait
Vp = Phenotypic variance for trait
Broad Sense heritability of the trait and Genetic advance as % of mean is calculated by,

GA% = K x $\sqrt{Vp}$ x H_B^2 x 100

Pearson's correlation coefficients were computed to evaluate the relationship among the observed variables and the data analyzed using Unweighted Paired Group Method based Centroids (UPGMC).

Results and Discussion
The presence of genetic variability is essential requirement for the selection of an superior genotype during crop improvement programme. Therefore, assessment of extent of variation present in the genetic material is important to estimate the magnitude of improvement that can be achieved in breeding material for numerous characters (Singh and Verma, 2018) [19]. Ten cyto-sterile lines having 'WA'cytoplasm and respective maintainers were used for thirteen floral traits *viz;* duration of blooming, angle of opened florets, percentage of panicle exsertion, percentage of stigma exsertion, stigma length (mm), stigma breadth (mm), stigma surface (mm^2), style length (mm), anther length (mm), anther breadth (mm),anther size (mm^2), filament length(mm), filament length after elongation (mm) for different variability parameters such as mean, range, variance and coefficient of variation. Analysis of variance showed highly significant difference for all ten traits that indicating the presence of high variability for selection. Some important floral traits *viz;* angle of opened florets, percentage of stigma exsertion, percentage of panicle exsertion and duration of opening of florets, directly influencing out crossing substantially were predominant in cyto-sterile lines PMS2A/B, PMS6A/B, PMS7A/B, IR58025A/B and IR62829A/B. On the studies variability, cyto-sterile line IR62829A/B showedthe best values for the traits of stigma (stigma length, stigma exsertion percentage, and stigma surface) followed by PMS2A/B, PMS10A/B and PMS3A/B. The most outstanding line IR58025A exhibited poor performance for stigma traits as compared to other cytosterile lines. However, it possessed prominent anther traits. For anther characteristics (anther length, anther breadth, anther size, filament length, filament length after elongation) cyto-sterile line PMS3A/B, PMS10A/B, PMS2A/B, IR62829A/B and NMS 1A/B were having floral traits contributing substantially to out crossing (Table1).
Correlation studies among all floral traits revealed interesting results. Stigma breadth was observed positively correlated with anther breadth and anther size at genotypic as well as phenotypic level (Table 2) among the cyto-sterile lines. In cyto-sterile line percentage of stigma exsertion was positively correlated with stigma length (0.498 and 0.442), angle of opened florets (0.437 and 0.295) and style length (0.179 and 0.226) at genotypic as well as phenotypic level respectively. Similar results were made by Patil and Sarawgi (2005) [15], Khan *et al.* (2009) [8] and Singh (2012, 2014) [18, 19]. Another significant negative correlation was observed between percentage of panicle exsertion with stigma breadth, anther breadth and anther size at both genotypic and phenotypic levels. Angle of opened florets was significantly and positively correlated with style length (0.666) at only genotypic level, whereas another positive correlation was also be observed with stigma length (0.148 and 0.129) and anther length (0.440 and 0.183). Duration of opening of florets was positively correlated at both genotypic as well as phenotypic level with percentage of stigma exsertion (0.170) and (0.104), angle of opened florets (0.057 and 0.080), filament length (0.285 and 0.058) and filament length after elongation (0.542 and 0.375), respectively, whereas another negative significant correlation was observed with stigma surface (0.795) at phenotypic level. Stigma breadth was positively and significantly correlated with stigma surface, anther breadth and anther size at genotypic level, this result indicated that stigma breadth was much more influenced by environment. Another correlation coefficient in case of anther breadth was significant and positively correlated with anther size (0.959 and 0.946) at genotypic and phenotypic level and it was also founded positive and significant correlation with filament length (0.690) at genotypic level only. Another interesting correlation was observed between filament length and filament length after elongation, which was positive at genotypic as well as phenotypic level but significant at genotypic level only. These findings are in general agreement with the results of Chaudhary and Motiramani, (2003) [4]; Khedikar *et al*. (2004) [9]; and Jaiswal *et al*. (2007) [5].
In general higher estimates of heritability were observed in A-lines than their respective B- lines for at the time of opening of florets, opened floret' sangle, stigma breadth percentage,

stigma surface, style length, anther breadth and filament length (Table 3). Higher estimates of heritability indicate preponderance of additive gene action as suggested by Subramaniam and Rathinam, (1984) [22]. Higher percentage of heritability was recorded for exserted stigma, spikelet length, anther length, stigma length by Virmani and Athwal, (1973) [27] and Singh (1995) [21]. Sahoo *et al.* (1997) [17] observed heritability over 90% for the characters like duration of floret opening, angle of opened florets, percentage of exserted stigma, spikelet length, anther length, stigma length, etc. These findings support the present observations. Present findings contradict the observation made by Virmani and Athwal (1973) [27] in percentage of exserted stigma, stigma length who observed high heritability. Highest values (50.04%) of genetic advance observed for blooming of florets followed by stigma exsertion, stigma breadth and stigma surface. In general heritability estimates was high for these characters, but to arrive a reliable conclusion that the high estimates of heritability must be accompanied by the high genetic advance (Johnson *et al.* 1955a) [6]. Mahalingam *et al*. (2013) [11] also observed and reported that the high heritability joined with high genetic advance as percent of mean for five floral traits *viz.*, stigma length, style breadth, stigma exsertion rate, anther length, and glume opening angle**.** It may be suggested on the basis of present study style length, anther breadth and filament length showed high broad sense heritability coupled with medium genetic advance and most of these having high genotypic coefficient of variation, may be advocated for selection as traits with high outcrossing potential.

It was calculated that there is presence of floral variability for different out crossing influencing traits among the ten cyto-sterile lines and their maintainers studied during the course of present investigation. Floret's opening time and opened floret's angle are two important traits influence out crossing were positive correlated and can be improved together. In general stigma and anther floral traits were negatively correlated but within stigma/ anther floral parts, they were positively correlated, indicating that male and female organs should be improved separately. On the basis of overall analysis, IR62829A was best followed by PMS10A, PMS2A and IR58025A for having out crossing influencing traits. In general cyto-sterile have better floral traits than there maintainers influencing out crossing.

Conclusion

On the findings of the present study we concluded here that the heritability and correlations between different floral traits founded significantly that affected by their genetic consequences. Some observations founded positively correlated such as stigma breadth with anther breadth and anther size at genotypic as well as phenotypic level among the cyto-sterile lines. This study would be helpful for future in hybrid seed production technology to develop new parental lines for hybridization.

Table 1: Based on the per se performance and variability studies, it was found that following were the outstanding cyto-sterile and maintainers lines with respect to each trait contributing to outcrossing.

A. Duration of floret opening (min) -	Names of Line	Range
A-lines -	PMS2A, PMS6A, PMS7A, IR58025A	(61.67-146.67)
B-lines -	PMS6B, NMS2B, IR58025B, IR62829B	(47.50-84.17)
B. Angle of Opened florets (0˚) -		
A-lines -	PMS7A, IR62829A, NMS 1A, PMS6A	(22.89-32.45)
B-lines -	PMS7B, IR62829B, NMS1B, PMS3B	(19.67-27.67)
C. Percentage of Panicle Excretion (%)		
A- lines -	NMS1A, IR58025A, IR62829A, PMS2A (58.45-69.01)	
B-lines -	PMS6B, NMS1B, PMS7B, PMS8B	(77.90-100.0)
D. Stigma Characters		
(i) Percentage of Excreted Stigma (%)		
A- lines -	PMS6A, PMS8A, IR62829A, NMS1A	(7.88-66.71)
B-lines -	PMS8B, IR62829B, PMS10B, PMS6B	(29.45-75.19)
(ii) Stigma Length (mm)		
A- lines -	IR62829A, NMS1A, PMS8A, PMS10A	(1.19-1.97)
B-lines -	IR62829B,NMS1B, PMS8B, PMS10B	(1.19-2.02)
(iii) Stigma Breadth (mm)		
A- lines -	NMS2A,PMS10A, PMS3A, PMS8A	(0.36-0.63)
B-lines -	NMS2B, PMS10B,PMS3B, PMS8B	
(iv) Stigma Surface (mm^2)		
A- lines -	IR62829A, NMS2A,PMS3A,PMS10A	(0.47-0.80)
B-lines -	NMS2B, PMS10B,PMS3B, PMS8B	(0.45-0.94)
(v) Stigma Length (mm)		
A- lines -	PMS7A,PMS2A, PMS3A,PMS10A,	(0.82-1.23)
B-lines -	PMS7B, PMS2B,PMS3B, PMS10B	(0.85-1.23)
E Anthers characters		
(i) Anther Length (mm)		
A- lines -	PMS7A,PMS10A, NMS1A, PMS3A	(1.72-2.04)
B-lines -	IR62829B, PMS7B,PMS10B, NMS1B	(1.72-2.19)
(ii) Anther Breadth (mm)		
A- lines -	NMS2A,IR62829A, PMS10A, PMS3A	(0.23-0.44)
B-lines -	NMS2B, IR62829B,PMS2B, PMS10B	(0.29-0.55)
(iii) Anther Size (mm^2)		

A- lines -	NMS2A,PMS10A, PMS3A,NMS1A	(0.42-0.89)
B-lines -	IR62829B, NMS2B, PMS10B,PMS2B,	(0.54-1.13)
(iv) Filament Length (mm)		
A- lines -	PMS10A,PMS6A, NMS2A, IR8025A	(0.79-1.33)
B-lines -	PMS3B,IR62829B, PMS10B,PMS2B	(1.17-1.53)
(v) Filament Length after elongation (mm)		
A- lines -	PMS10A,PMS6A, IR8025A,PMS3A,	(6.75-8.47)
B-lines -	PMS10B, PMS6B,IR8025B, PMS3B	(6.76-8.50)

Table 2: Estimation of genotypic and phenotypic correlation coefficient among various floral traits in ten cyto-sterile lines of rice

Characters		2	3	4	5	6	7	8	9	10	11	12	13
1. Duration of opening of florets	G	0.170	-0.105	0.057	-0.502	-0.391	-0.795**	0.348	-0.380	-0.082	-0.020	0.285	0.542
	P	0.104	-0.133	0.080	-0.376	-0.334	-0.596	0.140	-0.307	0.054	-0.067	0.058	0.375
2. Percentage of stigma exsertion	G		-0.901**	0.437	0.498	-0.984**	0.455	0.179	-0.445	-0.845**	-0.905**	-0.353	-0.182
	P		-0.784**	0.295	0.442	-0.812**	0.338	0.226	-0.264	-0.698*	-0.634*	-0.225	-0.137
3. Percentage of panicle exsertion	G			-0.195	-0.291	0.816**	0.376	-0.383	0.256	0.918**	0.911**	0.344	0.002
	P			-0.183	-0.261	0.702**	0.344	-0.226	0.114	0.581	0.562	0.245	-0.069
4. Angle of opened florets	G				0.148	-0.397	-0.246	0.666*	0.440	-0.298	-0.175	-0.178	-0.252
	P				0.129	-0.265	-0.161	0.367	0.183	-0.271	-0.199	0.037	-0.230
5. Stigma length	G					-0.265	0.572	0.010	-0.222	-0.050	-0.126	-0.262	-0.437
	P					-0.270	0.551	0.028	-0.168	0.096	0.015	-0.165	-0.338
6. Stigma breadth	G						0.632*	-0.342	0.400	0.916**	0.955**	0.434	0.124
	P						0.579	-0.269	0.325	0.431	0.512	0.264	-0.039
7. Stigma surface	G							-0.163	0.291	0.689*	0.701*	0.035	-0.203
	P							-0.120	0.123	0.451	0.446	0.055	-0.281
8. Style length	G								0.733	-0.020	0.138	0.004	0.283
	P								0.372	-0.106	-0.005	-0.165	0.052
9. Anther length	G									0.208	0.477	0.258	-0.009
	P									0.191	0.493	0.142	0.131
10. Anther breadth	G										0.959**	0.690*	0.312
	P										0.946**	0.412	0.334
11. Anther size	G											0.677*	0.274
	P											0.423	0.327
12. Filament length	G												0.988**
	P												0.535

2. %age of stigma exsertion 3. % age of panicle exsertion 4. Angle of opened florets 5. Stigma length 6. Stigma breadth7.Stigma surface 8. Style length 9. Anther length 10. Anther breadth 11. Anther size 12. Filament length 13.Filament length after elongation G = Genotypic, P= Phenotypic * and ** Significant at 5% and 1% probability level.

Table 3: Heritability and Genetic advance of thirteen floral traits in cyto-sterile lines and their and their maintainers.

Parameters/ Traits	Heritability (h^2) (%)		G.A.		G.A.(% of mean)	
	A	B	A	B	A	B
1. Duration of opening of florets(min)	71.20	57.00	46.33	15.62	50.04	24.21
2. Angle of opened florets(O°)	70.90	66.30	4.63	3.79	18.33	16.41
3. Percentage of stigma exsertion	91.70	84.10	22.41	17.22	44.01	32.33
4. Percentage of panicle exsertion	88.20	92.30	9.18	17.34	14.20	19.25
5. Stigma length(mm)	86.10	86.40	0.42	0.45	29.57	31.47
6. Stigma breadth (mm)	78.30	50.10	0.14	0.16	32.56	32.65
7.Stigma surface (mm^2)	72.10	65.90	0.20	0.23	32.78	37.09
8. Style length(mm)	62.30	60.10	0.21	0.19	20.78	18.45
9. Anther length(mm)	44.50	60.80	0.12	0.21	6.35	10.77
10. Anther breadth (mm)	81.40	80.40	0.07	0.15	21.21	34.88
11. Anther size(mm^2)	51.30	81.70	0.15	0.34	23.80	40.47
12. Filament length(mm)	44.00	34.90	0.19	0.19	17.92	14.84
13. Filament length after elongation	51.90	52.30	0.70	0.73	9.07	9.32

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