Research Article

GENE ACTION AND FERTILITY RESTORATION BEHAVIOUR OF THE TROPICAL JAPONICA/INDICA, JAPONICA/INDICA AND INDICA DERIVED RESTORERS' CROSSES USING CMS BREEDING SYSTEM IN RICE (*Oryza sativa* L.)

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Abstract- To study the gene action and fertility restoration behavior of tropical japonica/indica and indica derived advanced breeding lines, seven testers comprised of new plant type *i.e.*, NPT 2-2-694-1, NPT 9, NPT 80-1 and elite testers *i.e.*, ET 1-12, ET 1-13, TOX 981-11-2-3 and R 1244-1246-1-605-1 along with three CMS lines *i.e.*, APMS 6 A, CRMS 31 A and IR 79156 A and their generated 21 F1 crosses were evaluated for yield and yield attributing traits in a randomized complete block design during (RCBD) wet season 2010. The phenotypic quantitative recorded data was undertaken as per L x T analysis. Under the genetic analysis found all the traits was registered the preponderance of positive non-additive gene action whereas, negative for flag leaf length. All the seven testers exhibited either minor or additive cytoplasmic gene action which influenced the fertility restoration behavior of different combinations of the same pollen parent. The probability of the potential restorer combination (47.76%) was more followed by partial restorers (28.57%), potential maintainers (19.04%) and partial maintainer (4%). Probability of high x high allelic reaction was more in potential restorer combinations (70.00%) followed by partial restorers (16.67%), potential maintainers (0%) and partial maintainer (0.0%). The additive x additive reaction was found for the fertility restoration in 70% restorer combination.
Key words- *Rice (Oryza sativa L.), Genetic behaviour, Gene action, Fertility restoration*

Introduction

Cytoplasmic male sterility (CMS) and nuclear –controlled fertility restoration are wide-spread plant reproductive features that provide useful tools to exploit heterosis in crops [1]. The nature of gene action plays important role on the expression of the fertility restoration behaviour of the restorer in different cross combinations. The fertility restoration, GCA, SCA effects and per se performance of the genetic material decide the true exploitation of potentiality of the heterotic combinations to exploit in practical level. High yield of F1 hybrids depends largely upon high pollen or spikelet fertility which is determined by the mode of genes prevalent in the restorer lines of the hybrids [2,3]. The knowledge of the genetic control of male fertility restoration is also useful to transfer fertility restoring genes to promising breeding lines and undertake improved restorer breeding programme. The fertility restorer alleles (Rfs) are always tightly evolved with cytoplasmic male sterility (CMS) during plant evolution. Research of Rfs inheritance is the precondition for breeders to develop elite restorer lines [4-6]. For studying the inheritance of the fertility of the restorers, in general, the main three indexes (percent of fertile pollen, bagged seed setting and open seed setting) are often used as the evaluation criteria to evaluate fertility restoration. Of these, the percentage of fertile pollen is thought as most reliable criteria for evaluating plant fertility [7]. Grain yield is a complex character dependent upon the contribution of various characters affecting directly or indirectly. The existence of total genetic variability and magnitude under improvement to a large extent would dictate the choice of breeding methodology. Therefore, the allelic status and the nature of gene action play important role for the expression of the trait of interest *viz.*,

the nature of pollen as well as spikelets fertility controlled. There is necessity to determine the genetic behaviour of fertility restoration of the WA source with different fertility restoration of different genetic backgrounds so that true interpretation of various gene actions on fertility restoration behaviour could be clarified for development of parent's restorer combinations. Therefore, the present study was undertaken with a view to understand the nature of gene action and fertility restoration behaviour of the advanced breeding lines from different genetic background with the widely used WA-CMS line.

Materials and Methods
Plant materials
The breeding material comprised three CMS lines *viz.*, APMS 6 A, CRMS 31A and IR 79156 A; seven testers *i.e.* three new plant type tropical japonica/indica derived advanced breeding lines *viz.* NPT 2-2-694-1, NPT 9 and NPT 80-1; two elite semi-dwarf japonica/indica advanced breeding lines *i.e.* ET 1-12 and ET 1-13; other two advanced breeding lines *i.e.* TOX 981-11-2-3 from West African Rice Development Association (WARDA-IRRI, Philippines) and R 1244-1246-1-605-1 from IGKV, Raipur and their twenty-one crosses.

Phenotyping
To study the nature of gene action and fertility restoration behavior of the restorers, the crosses were attempted in L x T mating design, the parentages and their crosses were evaluated in randomized complete block design (RCBD) during kharif 2009 and kharif 2010 at the Research and Instructional Farm, IGKV, Raipur.

Gene action and Fertility Restoration Behaviour of the Tropical Japonica/Indica, Japonica/Indica and Indica derived Restorers crosses using CMS Breeding system in Rice (*Oryza sativa* L)

Table-1 *Analysis of variance for line x tester analysis*

Source of Variance	Degree of freedom	Days to 50 % flowering	Flag leaf length (cm)	Flag leaf width (cm)	Flag leaf area (cm²)	Plant height (cm)	Productive tillers per plant	Pollen fertility (%)	Sterile spikelet per Panicle	Fertile spikelet per Panicle	Spikelets per panicle	Spikelets fertility (%)	Panicle length (cm)	1000 Seed weight (g)	Grain yield per plant (g)	Head rice recovery (%)
Replication	1	3.562	2.382	0.074	0.021	0.980	2.295	0.409	1.715	2.436	0.097	4.941*	0.156	0.001	1.580	2.852
Treatments	30	87.744**	52.574**	7.683**	6.864**	4.384**	42.309**	555.564**	670.050**	941.149**	1148.665**	875.688**	10.894**	23.795**	508.442**	367.462**
Parents	9	57.654**	49.766**	7.587**	8.664**	3.988**	64.090**	847.652**	570.018**	397.834**	2583.857**	154.354**	9.779**	17.822**	271.868**	443.910**
Hybrids	20	90.456**	49.818**	7.632**	6.297**	4.596**	34.179**	446.325**	739.189**	1207.539**	553.913**	1191.257**	11.878**	27.230**	613.723**	346.650**
Parent vs. hybrids	1	304.307**	132.958**	9.567**	2.024**	3.712	8.886**	111.570**	187.541**	503.186**	126.964**	1056.319**	1.257	8.854**	531.980**	95.673**
Lines	2	0.654	0.233	2.159	3.604	1.348	3.208	2.153	1.550	2.930	0.359	1.689	3.348	0.613	0.155	3.354
Testers	6	6.135**	0.864	2.747	5.550	1.042	0.564	1.702	1.832	4.469*	1.507	2.330	1.739	2.378**	1.536	0.760
Line x Tester	12	36.098**	56.453**	4.654**	2.398**	4.387**	31.354**	336.648**	566.639**	540.580**	509.152**	811.482**	8.155**	19.807**	570.155**	297.964**
Error	31	1.635	0.023	0.023	58.181	168.07	0.41	4.824	23.51	23.04	13.43	1.83	2.24	1.58	0.658	0.80
Genetic components																
σ2gca		4.94	-0.07	0	12.54	5.67	0.13	36.01	280.62	865.36	66.9	43.86	0.53	0.77	3.45	3.28
σ2sca		28.69	39.86	0.04	40.68	284.66	6.29	809.58	6647.87	6216.96	3411.12	740.39	8.02	14.86	187.29	119.31
σ2gca/ σ2sca		0.172	-1.756	0	0.308	0.019	0.02	0.044	0.042	0.139	0.019	0.059	0.066	0.052	0.018	0.027

* & **, significant at p ≤ 0.05 l and 0.01, respectively

The characterization was taken under for fifteen major traits including grain yield per plant. All the genotypes were evaluated at phenotypic level and categorized on the basis of fertility restoration as per Virmani *et al*., 1997 [8].

Pollen fertility evaluation
The spikelets fertility also influenced by pollen fertility. Pollen fertility study was conducted using IKI 1% stain. Anthers were collected from F1 and their respective pollen parent separately from five randomly chosen spikelets (top to middle), preserved in 70% alcohol and pollen grains were treezed out of the anther on glass slide. The fertile and sterile pollen grains were counted in five microscopic fields under a compound light microscope. The pollen fertility was calculated as the ratio between the number of fertile (round and darkly stained) and sterile pollen grain (yellow, shriveled, partially stained or unstained) in the microscopic field. The ratio of filled grains to the total number of spikelets was expressed as seed setting rate [9].

Result and Analysis
Biometrical analysis
The field and lab evaluated quantitative characters were analysed as per estimate proposed by Kempthorne, 1957 for the estimation of genetic components *viz*., GCA and SCA variance, GCA and SCA effect and gene action [10].

Results
The analysis of variance due to treatments, parents, hybrids, line x testers exhibited highly significant for all the fifteen traits *i.e.* days to 50% percent flowering, flag leaf length (cm), flag leaf width (cm), flag leaf area (cm²), pollen fertility (%), plant height (cm), productive tillers per plant, panicle length (cm), filled spikelets per panicle, sterile spikelets per panicle, spikelets per panicle, spikelets fertility (%), 1000-seed weight (g), grain yield per plant (g) and head rice recovery (%) whereas, parents vs. hybrids was significant for all the traits except plant height and panicle length. However, testers were found significant for days to 50% flowering, fertile spikelets per panicle and 1000-seed weight. The variance due to line APMS 6 A, CRMS 31 A and IR 79156 A was not significant for any of the trait which might be due to less number of lines included [Table-1].

Important biometrical traits and their gene action in the performing respective crosses
In the per se performance as per sca and gca effect of their respective crosses, top five crosses the trait days to 50% flowering crosses registered the three over-dominance *i.e.* CRMS 31 A/ET 1-12, IR 79156 A/ET 1-12, APMS 6 A/NPT 2-2-694-1; one epistatic *i.e.* APMS 6 A/ET 1-12 and one incomplete dominance gene action *i.e.* CRMS 31 A/ET 1-12 [Table-2]. In the per se performance as per sca and gca effect of their respective crosses, top five crosses the trait flag leaf area crosses registered the two over-dominance *i.e.* IR 79156 A/ET 1-13, APMS 6 A/NPT 2-2-694-1; two epistatic *i.e.* IR 79156 A/ET 1-12, APMS 6 A/ET 1-12 and

one dominance gene action *i.e.* CRMS 31 A/ET 1-12 [Table-2]. In the per se performance as per sca and gca effect of their respective crosses, top five crosses the trait plant height (dwarfness) crosses registered the three over-dominance *i.e.* APMS 6 A/TOX 981-11-2-3, CRMS 31 A/ET 1-13, IR 79156 A/ET 1-12 and two epistatic *i.e.* CRMS 31 A/ET 1-12, APMS 6 A/ET 1-13 [Table-2]. In the per se performance as per sca and gca effect of their respective crosses, top five crosses the trait plant height crosses registered the three over-dominance *i.e.* IR 79156 A/ET 1-12, APMS 6 A/TOX 981-11-2-3, CRMS 31 A/ET 1-13; two epistatic *i.e.* APMS 6 A/ET 1-13 and CRMS 31 A/ET 1-12 [Table-2]. In the per se performance as per sca and gca effect of their respective crosses, top five crosses the trait productive tillers per plant crosses registered the two over-dominance *i.e.* CRMS 31 A/R 1244-1246-1-605-1, APMS 6 A/TOX 981-11-2-3; two epistatic *i.e.* IR 79156 A/NPT 80-1, IR 79156 A/TOX 981-11-2-3 and one dominance gene action *i.e.* IR 79156 A/NPT 9 [Table-2]. In the per se performance as per sca and gca of their respective crosses, top five crosses the trait spikelets per panicle crosses registered all epistatic gene action *i.e.* CRMS 31 A/ET 1-12, CRMS 31 A/ET 1-13, CRMS 31 A/TOX 981-11-2-3, CRMS 31 A/R 1244-1246-1-605-1 and IR 79156 A/NPT 80-1 [Table-2]. In the per se performance as per sca and gca effect of their respective crosses, top five crosses the trait panicle length, the crosses registered the two over-dominance *i.e.* CRMS 31 A/ TOX 981-11-2-3, IR 79156 A /ET 1-13; two epistatic *i.e.* CRMS 31 A/NPT 80-1, CRMS 31 A/ET 1-12 and one incomplete-dominance gene action *i.e.* APMS 6 A/ET 1-12 [Table-2]. In the per se performance as per sca and gca effect of their respective crosses, top five crosses the trait 1000-seed weight crosses registered the one over-dominance *i.e.* CRMS 31 A/NPT 9; one dominance *i.e.* IR 79156 A/NPT 80-1; one incomplete-dominance *i.e.* IR 79156 A/R 1244-1246-1-605-1 and two epistatic *i.e.* CRMS 31A/NPT 80-1, IR 79156 A/NPT 9 [Table-2]. In the per se performance as per sca and gca effect of their respective crosses, top five crosses the trait grain yield per plant crosses registered the one over-dominance *i.e.* APMS 6 A/TOX 981-11-2-3; one dominance gene action *i.e.* APMS 6 A/TOX 981-11-2-3 and three epistatic *i.e.* IR 79156 A/NPT 80-1, IR 79156 A/TOX 981-11-2-3, APMS 6 A/R 1244-1246-1-605-1 [Table-2]. In the per se performance as per sca and gca effect of their respective crosses, top five crosses the trait head rice recovery crosses registered the one over-dominance *i.e.* IR 79156 A/ NPT 2-2-694-1; one incomplete-dominance *i.e.* CRMS 31 A/ET 1-13 and three epistatic gene action *i.e.* CRMS 31 A/ET-1-12, CRMS 31 A/R 1244-1246-1-605-1, CRMS 31 A/TOX 981-11-2-3 [Table-2].

Identified restorer and maintainers
The cross combinations were categorized into four groups based on the phenotypic performance of pollen fertility (%) and spikelets fertility (%) *i.e.* potential restorer, partial restorer, potential maintainer and partial maintainer. Out of twenty one cross combinations, ten crosses recorded as potential restorers (47.61%) *i.e.* AMPS 6 A/ET 1-12, CRMS 31 A/NPT 9, CRMS 31 A/NPT 80-1, CRMS 31 A/ET 1-12, CRMS 31 A/TOX 981-11-2-3, CRMS 31 A/R 1244-1246-1-

Table-2 *Top five crosses with sca effects, per se performance and gca effects of parents for grain yield per plant and its components in rice*

Character/Cross	Mean performance	SCA effects	GCA effects Line	GCA effects Tester	GCA status
Days to 50% flowering(early)					
CRMS 31A x ET 1-13	74.50	-7.29**	0.62	-6.64**	H x L
CRMS 31A x ET 1-12	75.50	-2.95**	0.62	-9.98**	H x L
IR 79156A x ET 1-12	77.50	-16.44**	1.26	-9.98**	H x L
APMS 6A x ET 1-12	80.5	4.55**	-1.88	-9.98**	L x L
APMS 6A x NPT 2-2-694-1	80.50	-5.45**	-1.88	0.02	L x H
Flag leaf area (cm²)					
CRMS 31A x ET 1-12	84.45	8.88**	-6.73**	22.07**	L x H
IR 79156A x ET 1-12	74.77	-18.77**	4.77**	22.07**	H x H
IR 79156A x ET 1-13	72.03	11.02**	4.77**	1.15	H x H
APMS 6A x ET 1-12	71.07	-0.32	1.96	22.07**	H x H
APMS 6A x NPT 2-2-694-1	70.74	10.23**	1.96	2.08**	H x H
Plant height(dwarfness)					
APMS 6A x TOX 981-11-2-3	85.50	-20.24**	-8.77**	-3.25**	L x L
CRMS 31A x ET 1-13	95.10	-18.56**	0.74	-4.85**	H x L
IR 79156A x ET 1-12	110.65	-31.88**	8.03**	-5.23**	H x L
CRMS 31A x ET 1-12	113.45	0.17	0.74	-5.23**	H x L
APMS 6A x ET 1-13	114.25	10.11**	-8.77**	-4.85**	L x L
Productive tillers per plant					
CRMS 31A x R 1244-1246-1-605-1	14.91	2.73**	-0.89	0.01	L x L
IR 79156A x NPT 80-1	13.20	-2.04**	1.99	1.97**	H x H
IR 79156A x NPT 9	10.33	-0.59	1.99	-0.71	H x L
APMS 6A x TOX 981-11-2-3	10.15	2.73**	-1.10	0.12	L x H
IR 79156A x TOX 981-11-2-3	9.86	-2.35**	1.99	0.12	H x L
Spikelets per panicle					
CRMS 31A x ET 1-12	423.00	2.51**	6.17**	30.00**	H x H
CRMS 31A x NPT 80-1	402.50	-3.63**	6.17**	40.33**	H x H
IR 79156A x NPT 80-1	402.50	-2.07**	9.02**	40.33**	H x H
CRMS 31A x R 1244-1246-1-605-1	365.00	-15.39**	6.17**	17.33**	H x H
CRMS 31A x TOX 981-11-2-3	340.00	-15.39**	6.17**	20.17**	H x H
Panicle Length (cm)					
CRMS 31A x TOX 981-11-2-3	37.75	5.49**	2.38	1.64**	H x H
CRMS 31A x NPT 80-1	34.30	-0.90**	2.38	-4.47**	H x L
CRMS 31A x ET 1-12	32.87	-0.018	2.38	2.27**	H x H
IR 79156A x ET 1-13	30.12	3.149**	-0.86	0.40	L x H
APMS 6A x ET 1-12	29.73	0.75**	-1.53	2.27**	L x H
1000-seed weight (g)					
IR 79156A x NPT 80-1	34.30	6.06**	-0.61	6.10**	L x H
CRMS 31A x NPT 80-1	30.25	0.01	1.35	6.10**	H x H
CRMS 31A x NPT 9	26.44	3.62**	1.35	-0.83	H x L
IR 79156A x R 1244-1246-1-605-1	24.83	0.42	-0.61	3.21**	L x H
APMS 6A x NPT 9	24.25	3.08**	-0.74	-0.83	L x L
Grain yield per plant (g)					
IR 79156A x NPT 80-1	75.00	10.00**	6.05**	27.36**	H x H
CRMS 31A x NPT 80-1	74.46	12.33**	3.22	27.36**	H x H
APMS 6A x TOX 981-11-2-3	54.86	16.92**	-9.27**	15.62**	L x H
IR 79156A x TOX 981-11-2-3	54.76	1.50**	6.05**	15.62**	H x H
APMS 6A x R 1244-1246-1-605-1	44.45	15.61**	-9.27**	6.51**	L x H
Head rice recovery (%)					
CRMS 31A x R 1244-1246-1-605-1	54.58	-7.00	5.34**	4.11**	H x H
CRMS 31A x ET 1-12	54.21	12.91**	5.34**	-3.39**	H x L
CRMS 31A x ET 1-13	45.50	4.57**	5.34**	-3.77**	H x L
CRMS 31A x TOX 981-11-2-3	41.75	-7.00**	5.34**	4.02**	H x H
IR 79156A x NPT 2-2-694-1	40.85	10.42**	3.33**	8.37**	H x H

Table-3 *Restorers and Maintainers*

Reaction Lines	Potential Restorers	Partial Restorers	Potential Maintainers	Partial Maintainers
APMS 6 A	ET 1-12	NPT 80-1, TOX981-11-2-3, R 1244-1246-1-605-1	NPT 2-2-694-1, ET1-13	NPT 9
CRMS 31 A	NPT 9, NPT 80-1, ET 1-12, TOX 981-11-2-3, R 1244-1246-1-605-1	ET 1-13	NPT 2-2-964-1	-
IR 79156 A	NPT 2-2-694-1, NPT 80-1, TOX981-11-2-3, R 1244-1246-1-605-1	ET 1-12, ET 1-13	NPT 9	-

Table-4 *Gene action in potential restorer, partial restorers, potential maintainers and partial maintainer*

Cross Combination Potential restorers	Mean performance		SCA effects		GCA effects				GCA status	
					Female		Male			
	PF (%)	SF (%)	PF	SF	PF	SF	PF	SF	PF	SF
APMS 6 A/ET 1-12	93.50	71.43	27.25	16.17	-18.25	-15.42	25.35	11.52	L x H	L x H
CRMS 31 A/NPT 9	82.50	83.97	30.20	42.15	08.96	08.49	-15.81	-30.87	H x L	H x L
CRMS 31 A/ NPT 80-1	77.50	83.97	1.04	-3.63	08.96	08.49	08.35	19.96	H x H	H x H
CRMS 31 A/ET 1-12	94.50	81.67	1.04	2.51	08.96	08.49	25.35	11.52	H x H	H x H
CRMS 31 A/TOX 981-11-2-3	77.00	73.52	-5.80	-15.39	08.96	08.49	14.19	21.27	H x H	H x H
CRMS 31 A/R 1244-1246-1-605-1	96.50	84.24	-5.80	-15.39	08.96	08.49	18.02	20.67	H x H	H x H
IR 79156 A/NPT 2-2-694-1	92.50	78.45	52.25	43.30	09.28	06.93	-28.18	-30.93	H x L	H x L
IR 79156 A/NPT 80-1	77.50	83.97	-2.07	9.28	09.28	06.93	8.35	19.96	H x H	H x H
IR 79156 A/ TOX 981-11-2-3	88.50	88.79	05.88	01.44	09.28	06.93	14.19	21.27	H x H	H x H
IR 79156 A/R 1244-1246-1-605-1	82.50	77.04	05.88	01.44	09.28	06.93	18.02	20.67	H x H	H x H
Potential maintainers										
APMS 6 A/NPT 2-2-694-1	00.01	03.24	-12.57	-9.57	-18.25	-15.42	-28.18	-30.93	L x L	L x L
APMS 6 A/ET -1-13	00.01	01.35	-18.82	-30.81	-18.25	-15.42	-21.93	-11.62	L x L	L x L
CRMS 31 A/NPT 2-2-964-1	00.02	03.00	-39.68	-33.72	08.96	08.49	-28.18	-30.93	H x L	H x L
IR 79156 A/NPT 9	00.10	02.30	-42.62	-32.93	09.28	06.93	-15.81	-30.87	H x L	H x L
Partial maintainer										
APMS 6 A/NPT 9	37.25	3.65	12.41	-9.23	-18.25	-15.42	-15.81	-30.87	L x L	L x L
Partial restorers										
APMS 6 A/NPT 80-1	47.50	69.35	-1.75	5.70	-18.25	-15.42	08.35	19.96	L x H	L x H
APMS 6 A/TOX 981-11-2-3	55.00	79.96	-0.09	13.95	-18.25	-15.42	14.19	21.27	L x H	L x H
APMS 6 A/R 1244-1246-1-605-1	52.50	78.19	-6.42	13.79	-18.25	-15.42	18.02	20.67	L x H	L x H
CRMS 6 A/ET 1-13	49.00	68.18	02.82	12.16	08.96	08.49	-21.93	-11.62	H x L	H x L
IR 79156 A/ET 1-12	65.50	58.93	-39.69	-29.69	09.28	06.93	25.35	11.52	H x H	H x H
IR 79156 A/ET 1-13	62.50	73.12	16.00	18.65	09.28	06.93	-21.93	-11.62	H x L	H x L

605-1, IR 79156 A/NPT 2-2-694-1, IR 79156 A/NPT 80-1, IR 79156 A/TOX 981-11-2-3 and IR 79156 A/R 1244-1246-1-605-1; followed by six crosses partial restorers (28.57%) *i.e.* APMS 6 A/NPT 80-1, APMS 6 A/TOX 981-11-2-3, APMS 6 A/R 1244-1246-1-605-1, CRMS 31 A/ET 1-13, IR 79156 A/ET 1-12 and IR 79156 A/ET 1-13; four partial maintainers (19.04%) *i.e.* APMS 6 A/NPT 2-2, APMS 6 A/ET 1-13, CRMS 31 A/NPT 2-2-694-1 and IR 79156 A/NPT 9; and one partial maintainer (4%) *i.e.* APMS 6 A/NPT 9 [Table-3].

Allelic reaction in potential restorer combinations
The allelic reaction as per GCA effect for spikelets fertility percent was found high x high in eight (70%) among the potential restorer cross combinations *i.e.* APMS 6 A/ET 1-12, CRMS A/NPT 80-1, CRMS 31 A/ET 1-12, CRMS 31 A/TOX 981-11-2-3, CRMS 31 A/R 1244-1246-1-605-1, IR 79156 A/TOX 981-11-2-3, IR 79156 A/R 1244-1246-1-605-1, IR 79156 A/NPT 80-1; whereas, two (20%) allelic reaction was registered high x low *i.e.* in CRMS 31 A/NPT 9 and IR 79156 A/NPT 2-2-694-1 and with low x high in one (10%) cross combination *i.e.* APMS 6 A/ET 1-12 [Table-4].

Allelic reaction in partial restorer combinations
The allelic reaction as per GCA effects for pollen fertility and pollen fertility percent was recorded high x high in one (16.66%) cross combinations *i.e.* IR 79156 A/ET 1-12; whereas, high x low in two (33.33%) cross combinations *i.e.* CRMS 31 A/ET 1-13 and IR 79156 A/ET 1-13; low x high in three (50%) *i.e.* APMS 6 A/NPT 80-1, APMS 6 A/TOX 981-11-2-3 and APMS 6 A/R 1244-1246-1-605-1 [Table-4].

Allelic reaction in potential maintainer combinations
The allelic reaction as per GCA effects for pollen and spikelets fertility percent was recorded high x low in two (50%) cross combinations *i.e.* CRMS 31 A/NPT 2-2-694-1 and IR 79156 A/NPT 9; on the other hand low x low in two (50%) cross combinations *i.e.* APMS 6 A/NPT 2-2-694-1 and APMS 6 A/ET 1-13 [Table-4].

Allelic reaction in partial maintainer combination
A single cross combination exhibited as partial maintainer *i.e.* APMS 6 A/NPT 9 with low x low allelic reaction in pollen fertility and spikelets fertility per cent [Table-4].

Fertility restoration behavior of the pollen parents with different CMS line in different combinations
The tester NPT 2-2-694-1 was recorded potential restorer for IR 79156 A and potential maintainer for APMS 6 A and CRMS 31 A. The tester NPT 9 was found potential restorer for CRMS 31 A and potential maintainer for IR 79156A and partial maintainer for line APMS 6 A. The tester NPT 80-1 registered as potential restorers for CRMS 31 A and IR 79156 A and partial restorer for APMS 6 A. The tester ET 1-12 exhibited as potential restorer for APMS 6 A and CRMS 31 A line whereas, partial restorer for IR 79156 A. The tester ET 1-13 found as partial restorer for CRMS 31 A and IR 79156 A and partial maintainer for APMS 6 A. The tester TOX 981-11-2-3 had been found as potential restorer for CRMS 31 A and IR 79156 A whereas, partial restorer for APMS 6 A. The tester R 1244-1246-1-605-1 recognized as potential restorer for CRMS 31 A and IR 79156 A whereas, partial restorers for APMS 6 A [Table-3] and [Table-4].

Discussion
All the traits under study may be exhibited the preponderance of the non-additive gene action because the SCA variance was higher than the GCA variance. All the traits registered the role of positive non-additive gene action except flag leaf length [Table-1]. The present finding also supported by the earlier finding of Sao and Motiramani, 2006, Saidaiah *et al.*, 2010, Bagheri and Jelodar, 2011 [11-13]. The high and low GCA effect may be due to the additive and dominance gene action. The similar results have also been reported earlier by Singh and Sinha, 1988; Malarvizhi *et al.*, 2003; Saidaiah *et al.*, 2010; and Bagheri and Jelodar, 2011 [14-15]. The SCA effects as per se performance of top five crosses and the GCA effects of the respective parentages were evaluated for important nine traits. The allelic reactions were registered for high x high in 20 crosses (44.44%), high x low in 11 crosses (24.44%) low x high in 10 crosses (22.22%) and low x low in four crosses (8.89%) crosses [Table-3]. These results were also supported by the earlier findings of Singh and Sinha, 1988; Anadkumer and Subramanian, 1992; He *et al.*, 2006 [16]. The dominance, incomplete-dominance, over-dominance and epistatic type of gene action have been registered the materials used. The gene action predicted as per the sca and gca effects of the cross and their respective parentages [Fig-1], [Table-2], [Table-3]. The plant having dominant alleles of one of the two genes in homozygous or heterozygous condition but homozygous

recessive alleles of the other gene (R1-/r2r2 or r1r1/R2-) will behave partially sterile or partially fertile and vice-versa. The plants homozygous for the recessive alleles of both genes (r1r1/r2r2) will be completely sterile. The same pollen parent exhibited different type of fertility restoration behavior in different CMS line combinations have been found in the material under study. Such type of results was due to the minor gene with additive gene action with the cytoplasmic genes of different CMS line. The high and low reactions may be as per allelic status of the respective cross combinations. The result has been supported by the findings of Kumeri *et al*., 1998, Gannamani, 2001, and. Rosamma and Vijayakumar, 2005 [17-21]. The gene action and fertility restoration behavior of tropical japonica/indica and indica derived advanced breeding lines, seven testers comprised of new plant type *i.e.* NPT 2-2-694-1, NPT 9, NPT 80-1 and elite testers *i.e.* ET 1-12, ET 1-13, TOX 981-11-2-3 and R 1244-1246-1-605-1 along with three CMS lines *i.e.* APMS 6 A, CRMS 31 A and IR 79156 A and their generated 21 F1 crosses. All the seven testers exhibited either minor or additive cytoplasmic gene action which influenced the fertility restoration behavior of different combinations of the same pollen parent. The probability of the potential restorer combination (47.76%) was more followed by partial restorers (28.57%), potential maintainers (19.04%) and partial maintainer (4%). Probability of high x high allelic reaction was more in potential restorer combinations (70.00%) followed by partial restorers (16.67%), potential maintainers (0%) and partial maintainer (0.0%). The additive x additive reaction was found for the fertility restoration in 70% restorer combination. The gene action influenced the fertility status of the different cross combination by dominance, over-dominance, incomplete-dominance and epistatic interaction as per SCA effects influenced by the GCA effects of their respective parentages [Fig-1].

Application of research: As per the analysis of variance found all the fifteen traits registered the non-additive gene action but as per the GCA effect of the patents and their respective cross combination the SCA effects registered as the interaction for most of the restorer combinations.

Research Category: Genetics and Plant Breeding

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Author Contributions: All author equally contributed

Author statement: All authors read, reviewed, agree and approved the final manuscript

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.

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