Annals of the Sri Lanka Department of Agriculture. 2008. 10:223-230.

EVALUATION AND ADVANCEMENT OF MAINTAINER GENE POOL IN RICE FOR DEVELOPMENT OF IMPROVED HYBRIDS

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ABSTRACT

The magnitude of yield heterosis realized at farmer fields' in Sri Lanka and India is around 10 - 20 %, which is generally inconsistent and not economically attractive for the rice farmers to take up large scale adoption of the technology. For the heterosis of yield to be economically advantageous, a variety must have 25 % more yield than the best commercial variety. To increase the economic advantage of this technology for ready acceptance by the farmers and for large scale adoption, the magnitude of heterosis in rice hybrids has to be enhanced besides improving the grain quality. To further improve yield levels and grain quality in rice hybrids, the development and improvement of parental lines used is a pre-requisite. This experiment was conducted at the Directorate of Rice Research, Hyderabad, India during 2006/2007 in a half diallel fashion. The evaluation of 45 F_1s with parental lines was carried out during 2007 in a Complete Randomized Block Design with three replications. Observations were recorded for thirteen characters. The GCA/SCA variance for all the characters studied was less than one, indicating that they are predominantly governed by non-additive gene actions. From the General Combining Ability (GCA) effects, IR68897B was a superior general combiner. From the Specific Combining Ability (SCA) results, IR68897B x IR79156B was superior. The studies revealed that five crosses could be considered for selection of desirable maintainers from F_2 generation onwards.

KEYWORDS: Heterosis, Hybrids, Improvement, Maintainers, Rice and Yield.

INTRODUCTION

Prospects of increasing rice productivity by conventional methods at the present time are less encouraging as the genetic gains obtained have diminished with time. Among the available genetic options to enhance the rice productivity, development and large scale adoption of hybrid rice appears to be a practically feasible approach, as exemplified in China.

The magnitude of yield heterosis realized at farmer fields' in Sri Lanka and India is around 10-20 % (Sumanaratne, 2007) which is inconsistent and not economically attractive enough for the rice farmers to take up large scale adoption of the technology. For the heterosis to be economically advantageous, a variety must realize at least 25% more yield than the best commercial variety (Swaminathan *et al.*, 1972).

To increase the economic advantage of this technology for ready acceptance by the farmers and for large scale adoption, the magnitude of heterosis in rice hybrids has to be enhanced besides improving the grain quality. To further improve yield levels and grain quality in rice hybrids, the development and improvement of parental lines used is a pre-requisite. In any heterosis breeding programme, development and improvement of parental lines, particularly the female parental lines, plays a major role in the enhancement of heterosis and improvement of hybrids in terms of grain and eating quality.

At present, very few Cytoplasmic Male Sterile (CMS) lines with a narrow genetic base are being used for the development of hybrids in Sri Lanka and India (Sumanaratne, 2007). These CMS lines have certain defects such as low amylose content, (hence slight stickiness in the cooked rice from hybrids), undesirable smell of cooked rice on storage and low head rice recovery (Sumanaratne, 2007). To overcome these defects and to develop better combining CMS lines with higher out crossing ability through combining some of the desirable characters found in the current maintainer lines, there is an urgent need to initiate specific maintainer breeding programmes. Hence, to identify and develop a set of improved maintainer lines and subsequently CMS lines, a specific maintainer breeding programme was initiated.

MATERIALS AND METHODS

The experiment was conducted during *kharif* (wet) 2006 and *rabi* (dry) seasons of 2007 at the Directorate of Rice Research (DRR), Rajendranagar, Hyderabad. During the *kharif* season, superior maintainer lines from a maintainer collection available at the Directorate were selected and the crosses were made among the selected ten lines in a diallel (without reciprocals) fashion. The evaluation of F_1s with parental lines was carried out during the *rabi* season.

The experimental materials consisted of 50 maintainers, from which 10 maintainer lines were selected for crossing purpose and 45 F_1s were developed from selected 10 parental lines.

In order to have synchronization of flowering among the maintainer lines for the crossing programme, the 50 maintainers were sown on raised nursery beds on two different days at a two weeks interval at the DRR farm. Thirty days old seedlings of all the 50 lines, were transplanted in separate rows of 3 m length from the two sets. Each maintainer line was planted in two replications by adopting spacing of 20 cm between rows and 15 cm between plants within the rows. The recommended package of practices by the DRR was followed to raise the crop (DDR, http://www.drricar.org). The ten maintainer lines were selected considering the data and information of the maintainer lines available with the hybrid rice section at the DRR for certain specific traits (Table 1).

Table 1. Details of ten parental lines selected for crossing programme.

Maintainer line	*Source/Origin*	*Desirable character present*
IR58025B	IRRI, Philippines	Good combining ability
IR68897B	IRRI, Philippines	Better grain quality and good combining ability
CRMS32B	CRRI, Cuttack	Good grain quality and good combining ability
APMS6B	ANGRAU, Maruteru	Good grain quality and good plant type
PMS17B	PAU, Kapurthala	Good plant type and good grain quality
DRR2B	DRR, Hyderabad	Good grain quality
IR79128B	IRRI, Philippines	Good panicle exertion
IR79128B	IRRI, Philippines	Higher out crossing
IR67684B	IRRI, Philippines	Basmati type of grains
IR69628B	IRRI, Philippines	*Japonica* type

For making the crosses, the female plants were potted in plastic buckets and their spikelets were clipped at appropriate stage, anthers were removed and the clipped spikelets were covered with butter paper bags in the afternoon. At the time of anthesis (from 9.00 am to 11.00 am) the next day, panicles from the male parents were collected in glass beakers containing water. The glass beakers with panicles were placed in a pollination chamber for 15 minutes to facilitate proper opening of spikelets and pollen shedding. The female plants were shifted to the pollination room and dusted with pollen by tapping male parents' panicles over female parents' panicles and were covered with butter paper bags. After the pollination, the pots were labeled properly and shifted to the net house. After 30 days, crossed panicles were harvested and F_1 seeds were carefully collected. The seeds of ten parental lines were sown directly on raised nursery beds while the 45 F_1s were kept in petri dishes separately. After germination F_1s were transferred to the raised nursery beds. Thirty days old seedlings of all the genotypes were transplanted in separate rows of 1.5 m length in 3 replications by adopting spacing of 20 cm between rows and 15 cm between plants within the rows. Recommended package of practices by the DRR was adopted to raise a healthy crop (DDR, http://www.drricar.org).

Fifteen important characters in maintainer lines were recorded on randomly tagged 5 plants excluding border plants. The mean values were utilized for statistical analysis with the soft ware package of Windostat Genetics and Plant Breeding (http://members.fortunecity. com/indostat).

RESULTS AND DISCUSSION

There were significant differences between the genotypes of all the eleven quantitative characters studied indicating that there are differences between parents and F_1 hybrids. The parents and crosses were significant for all the eleven characters studied. The parents verses crosses were significant for most of the characters studied except 1000-seed weight and grain Length (L) / Breadth (B) ratio. The ratio of General Combining Ability (GCA) / Specific Combining Ability (SCA) was less than one for all the characters studied. Broad sense heritability of above 80 % was recorded by all the characters except panicle exertion. Narrow sense heritability of above 20 % was recorded by days to 50 % flowering, 1000-seed weight and grain L/B ratio (Table 2).

In the qualitative characters, the effects of spikelet opening in parental lines and direct crosses between two groups were not significantly different. Although the variances among the two groups were different, the effects on stiffness of culms in the selfed and crossed progenies were significantly different, and the variances of the two groups were also significantly different. The effects on leaf senescence in parental lines and F_1 hybrids were not significantly different. The variances of the two groups were also not statistically different and the effects on phenotypic acceptability for the crossed F_1s and selfed F_1s as well as the variance between parental lines and F_1 hybrids were significantly different.

The mean performance of a cross ($\bar{X}F_1$) between two parental lines could be presented as:

$$\bar{X}F_1 = GCAP_1 + GCAP_2 + SCAP_1P_2$$

The $GCAP_1$ and $GCAP_2$ is the General Combining Ability of two parents respectively and the cross of P_1 x P_2 is expected to have a performance equal to the sum ($GCAP_1$ + $GCAP_2$) of General Combining Ability of their parents. The actual performance of the cross, however, may be different from this sum by an amount equal to what is termed as Specific Combining Ability (Chahal and Gosal 2003). The good combiners are expected to give good segregants in further generations for selection of desirable type of maintainer lines.

The actual value of a pure line for hybrid breeding lies in its importance (combining ability) in hybrid combinations with other pure lines. General Combining Ability represents the average performance of a line in hybrid combinations while the Specific Combining Ability is the deviations in the performance of a cross over the values expected from the GCA of its two parents.

Table 2. Specific Combining Ability effects of different characters studied in the selected rice populations.

Combination	*Flowering 50%*	*Plant height (cm)*	*Panicle exertion rate (%)*	*Stigma exertion rate (%)*	*Panicle length (cm)*	*Filled grain rate (%)*	*Yield plant^{-1} (g)*	*1000 Seed weight (g)*	*Grains L/B ratio*
IR58025B/IR58025B	1.03	-11.98**	1.29	1.40	-2.87**	-1.34	-12.11**	-1.50*	0.19*
IR68897B/IR68897B	11.98**	10.21**	9.94**	27.11**	-1.47*	11.78**	-15.82**	-2.10**	0.02
CRMS32B/CRMS32B	3.14**	-1.97	9.04**	0.30	-1.44*	-1.84	-1.67	-2.06**	-0.14
APMS6B/APMS6B	5.92**	-2.12	2.75	34.40**	-1.83**	-6.73*	-12.65**	-2.59**	-0.12
PMS17B/PMS17B	6.53**	4.41	2.20	18.31**	-1.08	-4.64	-5.49	0.58	-0.04
DRR2B/DRR2B	-5.64**	-4.59	1.57	-5.20	-3.74**	23.55**	2.68	2.35**	-0.01
IR79128B/IR79128B	-2.25*	-6.80**	-1.35	-12.33*	-0.99	2.63	1.19	1.36*	0.07
IR79156B/IR79156B	9.70**	-2.83	4.68	10.90*	-0.94-	3.30	-6.40*	0.68	0.23**
IR67684B/IR67684B	5.31**	-12.13**	3.13	-19.62**	2.55**	3.65	-6.05*	-1.29	0.21**
IR69628B/ IR69628B	0.92	-1.48	1.09	-8.19	-1.48*	8.20**	-1.15	1.35*	0.01
IR58025B/IR68897B	-1.83	-3.17	-2.65	5.09	0.68	5.82	14.11**	2.27**	0.08
IR58025B/CRMS32B	-5.08**	-0.04	-5.52*	-31.75**	-1.60*	9.67**	7.88*	1.99**	0.07
IR58025B/APMS6B	-0.86	1.61	-5.83*	-18.20**	0.65	3.55	-0.56	1.67*	-0.02
I R58025B/PMS17B	-3.89**	-2.67	14.96**	14.84*	-0.32	3.38	-2.23	-0.79	0.32**
IR58025B/DRR2B	20.53**	6.75**	8.68**	16.20**	3.13**	-7.54*	-8.17*	-4.76	-0.04
IR58025B/IR79128B	-4.78**	14.45**	3.62	6.60	2.50**	-4.22	3.19	0.17	-0.19*
IR58025B/IR79156B	-4.30**	2.60	15.70**	5.32	1.68*	4.86	8.93**	1.39	0.05
IR58025B/IR67684B	-1.00	8.18**	-5.62*	-2.34	0.04	-1.19	0.74	1.47*	-0.43**
IR58025B/IR69628B	-0.86	-3.76	-25.88**	1.44	-1.04	-11.75**	0.32	-0.42	-0.22*
IR68897B/CRMS32B	3.39**	3.84	-5.49*	-23.19**	1.18	-3.55	-6.81	-0.18	0.01
IR68897B/APMS6B	-1.05	0.05	0.73	5.75	-1.04	6.78	11.75**	-0.96	0.01
IR68897B/PMS17B	4.92**	-7.59**	-3.32	-38.27**	-0.28	11.80**	0.15	-0.63	-0.22*
Continued									
IR68897B/DRR2B	-12.00**	-24.44**	-29.76**	-39.74**	-3.82**	-63.09**	-20.32**	-0.09	0.03
IR68897B/IR79128B	-4.64**	-11.28**	-0.02	11.62	-0.68	10.53**	11.60**	1.93**	0.22*
IR68897B/IR79156B	-7.16**	2.54	1.46	12.74*	1.66*	14.95**	16.18**	0.69	-0.13

IR68897B/IR67684B	-1.53	10.79**	5.85*	19.25**	2.32**	-2.14	-2.85	-0.93	0.13
IR68897B/IR69628B	-4.05**	8.82**	13.32**	-7.47	2.91**	-4.66	7.84*	1.54*	-0.16
CRMS32B/APMS6B	5.03**	5.94*	-5.20	13.45*	1.81**	-12.28**	-6.91*	0.69	0.09
CRMS32B/PMS17B	1.34	4.97	3.55	-4.68	1.44*	-1.06	11.39**	-0.34	-0.02
CRMS32B/DRR2B	-15.91**	-6.01*	4.64	11.62	-1.01	1.12	-8.01*	-0.14	-0.04
CRMS32B/IR79128B	9.78**	-1.82	-6.52*	20.59**	-0.60	7.31*	-11.82**	-1.55*	-0.12
CRMS32B/IR79156B	-2.75**	5.34*	0.29	-4.17	1.74*	8.50*	7.82*	0.88	-0.01
CRMS32B/IR67684B	-3.78**	-2.42	-1.12	18.94**	-0.06	-1.19	6.72*	1.69*	0.13
CRMS32B/IR69628B	1.70	-5.86*	-2.72	-1.41	-0.01	-4.95	3.08	1.06	0.18
APMS6B/PMS17B	-5.78**	10.58**	0.71	-3.10	0.89	4.57	5.68	0.51	-0.07
APMS6B/DRR2B	6.64**	4.37	-3.84	1.13	3.82**	3.28	7.38*	1.28	0.08
APMS6B/IR79128B	-7.33**	-2.54	4.57	2.00	-2.31**	1.13	4.47	0.44	0.08
APMS6B/IR79156B	-2.53*	-3.62	-1.58	-24.59**	-0.06	8.22*	7.08*	0.26	-0.17
APMS6B/IR67684B	-3.89**	0.33	2.67	-38.88**	-0.04	1.66	0.05	0.41	0.23**
APMS6B/IR69628B	-2.08*	-12.48**	2.27	-6.37	0.48	-3.46	-3.66	0.88	0.01
PMS17B/DRR2B	-4.39**	-3.24	-2.62	6.07	0.07	1.90	-6.32	-1.39	-0.10
PMS17B/IR79128B	2.64**	-8.91**	-6.88*	-10.03	0.55	-10.58**	-1.83	0.17	0.08
PMS17B/IR79156B	0.78	6.14*	-2.90	2.79	0.96	11.61**	5.91	0.46	-0.07
PMS17B/IR67684B	-3.91**	3.22	-4.90	12.20**	0.35	-8.28*	1.18	1.38	0.28**
PMS17B/IR69628B	-4.78**	-11.32**	-3.01	-16.46**	-1.50*	-4.07	-2.93	-0.52	-0.13
DRR2B/IR79128B	9.06**	9.81**	-1.35	-2.00	1.17	8.50*	11.53**	0.60	0.16
DRR2B/IR79156B	-9.47**	-12.01**	-5.77*	-16.68**	-1.99**	-3.28	-4.83	1.10	0.20*
DRR2B/IR67684B	10.50**	15.41**	12.52**	19.06**	5.24**	5.50	20.35**	0.31	-0.11
DRR2B/IR69628B	6.31**	18.54**	14.35**	14.74*	0.86	6.51	3.03	-1.62*	-0.16
Continued									
IR79128B/IR79156B	0.89	10.76**	4.93	-12.22**	-1.52*	-24.42**	-14.00**	-3.18**	-0.32**
IR79128B/IR67684B	-1.80	-6.13*	3.49	0.79	-1.42*	15.96**	-8.73**	-0.30	-0.11
IR79128B/IR69628B	0.67	9.26**	0.86	7.30	4.30**	-9.47*	3.22	-1.00	0.64**
IR79156B/IR67684B	-0.66	-5.48*	-19.63**	0.31	0.82	-30.06**	-5.52	-1.17	-0.48**
IR79156B/IR69628B	5.81**	-0.62	-1.87	14.69*	-0.89	3.02	-8.77**	-1.80*	0.44**
IR67684B/IR69628B	-4.55**	0.36	0.49	9.93	-2.16**	12.43**	0.17	-0.82	0.05
SE (Sij)	1.02	2.61	2.72	6.00	0.08	3.50	3.23	0.74	0.09

CD 5% (±)	2.02	5.18	5.39	11.90	1.36	6.94	6.40	1.46	0.19
SE (Sij-Sik)	1.50	3.84	4.00	8.83	1.01	5.15	4.74	1.08	0.14
SE (Sij-Skl)	1.43	3.66	3.81	8.45	0.96	4.91	4.52	1.03	13.13
h^2 Narrow Sense	0.20	0.16	0.02	0.08	0.16	0.10	0.16	0.23	0.26
h^2 Broad Sense	0.98	0.92	0.09	0.88	0.89	0.93	0.88	0.80	0.80
GCA/SCA Ratio	0.13	0.11	0.01	0.05	0.11	0.06	0.11	0.20	0.25

* Significance at 0.05 probability level.

** Significance at 0.01 probability level.

The differences in GCA of lines are due to additive genetic variance and additive x additive type of epistasis whereas SCA is a reflection of non additive genetic variations. Inbreeding and crossing is the only approach to exploit variances for both GCA and SCA in the base population. Therefore, selection of both General as Specific Combining Ability is essential for judicious use of available genetic variation in any hybrid programme (Chahal and Gosal 2003).

According to results of the this investigation (Table 2), the GCA/SCA variance for the all characters studied were less than one indicating that they are predominantly governed by non-additive gene actions. However, grain length and breadth ratio and days to 50 % flowering show the least magnitude of the predominance of non-additive gene actions while panicle exertion rate, stigma exertion rate showed the highest magnitude of the non-additive gene actions. From the General Combining Ability effects, IR68897B was a good general combiner. From the Specific Combining Ability results, IR68897B x IR79156B was a good combiner. According to the overall studies based on Specific Combining Ability, heterosis and heterobeltiosis, the following five crosses *viz.* IR58025Bx IR79156B, IR68897BxIR79156B, IR68897BxIR69628B, APMS6Bx PMS17B and DRR2BxIR67684B could be given consideration for selection of desirable maintainers from F_2 generation onwards.

CONCLUSIONS

The study provided information as well as material to the development of maintainer gene pool in rice for improved hybrids. Therefore it is worthwhile to continue the process by growing F_2 populations and further segregating generations and selecting the desirable segregants in each generation and advancing them until F_6 generation when stabilized new maintainer lines can be obtained. The maintainer lines need to be further converted into CMS lines through backcrossing programme to develop CMS lines with desirable characteristics.

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