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Evaluation of aerobic hybrid analysis of combining ability in three line hybrids in Rice (*oryza sativa* l.) under aerobic conditions

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Information on the availability of genetic variability and mode of gene action are critically important for choosing effective breeding methods that result in appreciable improvement in performance under drought stress. An investigation in rice (*Oryza sativa* L.) was carried out subjecting six 'lines' and 15 'testers' crossed in a Line x Tester mating design and the 90 hybrids along with 21 parents were tested for gene action, combining ability for 19 traits under aerobic condition. Three 'lines' *viz*., IR79128A (L_1), IR79156A (L_2) and IR70369A (L_4) and three 'testers' *viz*., IR7925A-428-2-1-1R (T_{11}), KMP -148 (T_{12}) and BI-33 (T_{15}) were identified as the best general combiners. The genotype IR70369A is suggested for conversion to cytoplasmic male sterility with suitable male sterile source. The parents MAS -26, IR 7925A-428-2-1-1R and KMP-105 are recommended for testing their restorability with suitable cytoplasmic male sterile source.

Key words: Additive genetic variance (σ^2A), dominance genetic variance (σ^2D), general combining ability variance/effects, specific combining ability variance/effects, aerobic rice.

INTRODUCTION

Rice is the staple food for over 70% of Asians, the majority of whom are living below the poverty line. More than 90% of the world's rice is produced and consumed in Asia (Barker et al., 1999) and rice production must be increased by an estimated 56% over the next 30 years to keep up with population growth and income-induced demand for food in most Asian countries where about 75% of total rice production comes from irrigated lowlands (Maclean et al., 2002).

Almost 25% of the world's rice is grown under rainfed lowlands and frequently affected by uneven rainfall distribution. Another 13% of the rice area under cultivation is always subjected to water stress during the growing season (Bouman et al., 2007). Food security in Asia and the increasing scarcity of fresh water resources for agriculture in many areas are stimulating the development of aerobic rice production system (Tuong et al., 2005).

Aerobic rice is high-yielding rice grown under non-flooded conditions in non-puddled and unsaturated (aerobic) soil. It is responsive to high inputs, can be rainfed or irrigated and tolerates occasional flooding (Maclean et al., 2002). The water use of aerobic rice was about 60% less than that of flooded rice and total water

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productivity was 1.6 to 1.9 times higher (Vijayakumar et al., 2006).

To formulate an efficient breeding program for developing drought tolerant varieties, it is essential to understand the mode of inheritance, the magnitude of gene effects and their mode of action (Farshadfar et al., 2008). Due to their quantitative nature, drought related traits cannot be studied in a simpler way. Specialized biometrical techniques are required to work out the type of genetic variability associated with the traits. These biometrical techniques are dependent on different mating designs such as diallel, line x tester, North Carolina design and generation mean analysis for the estimation of type of genetic variability.

In breeding high yielding varieties of crop plants, the breeders are often faced with the problems of selecting parents and crosses. Combining ability analysis is one of the powerful tools available to estimate the combining ability effects and aids in selecting the desirable parents and crosses for the exploitation of heterosis. The Line x Tester analysis provides information about general combining ability (*gca*) of parents and specific combining ability (*sca*) effects of crosses and is helpful in estimating various types of gene actions. Zhang et al. (2002) studied the heterosis and combining ability of hybrid rice. The genetic improvement of rice for aerobic environments has not been understood well and major efforts in this front are lacking.

Significant yield advantage gained through the adoption and spread of hybrid rice technology had helped China to add about 350 million tonnes of extra rice to its food basket during 1976-1998 and enabled it to divert some of their rice areas to other commercial crops. Hybrid rice technology had also shown increased yield, farmer profitability and better adaptability to stress environments such as water scarce and aerobic conditions. Considering all these issues the main objective of this study is to develop rice hybrids with high yield potential for aerobic conditions to overcome the existing water crisis in India. For this breeding strategies based on selection of hybrids require expected level of heterosis as well as the specific combining ability is the foremost.

MATERIALS AND METHODS

Site description

The present investigation was carried out in the Research farm of the Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai, Tamil Nadu, India during 2009-2011.

A set of 21 parents comprising of six 'A' lines and corresponding 'B' lines, eight 'R' lines and seven aerobic varieties were used for the study. The commercially cultivated hybrid IR 6888 was used as the check. The details of the selected parents are furnished in Table 1. The seed materials were collected from Paddy Breeding Station, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore and Tamil Nadu Rice Research Institute, Aduthurai, Tamil Nadu.

Hybridization programme

The 21 parental seed materials [six Lines and 15 Testers (Testers = eight R lines and seven aerobic rice varieties)] were sown in a raised nursery bed during the month of June, 2009. The source materials of A, B and R lines were sown adopting line sowing in raised beds of one meter width and convenient length in a fertile well leveled plot. Thin sowing in the nursery was followed by good water and nutrient management to obtain healthy seedlings with three to four tillers at the time of planting.

Seedlings of A, B, R lines which attained the age of 29 days were transplanted in three meter length row with the spacing of 30 cm between rows and 15 cm between plants of each genotype in four rows. R lines were planted separately with an isolation of 300 meter. The row ratio obtained for planting the A and B lines was 8:2. Recommended package of practices and need based plant protection measures were adopted. Crosses were effected in a 'Line x Tester' mating design (Kempthorne, 1957).

The spikelets which were likely to open in the same day were selected during early hours between 6.30 and 8.30 A.M. in the female parents. Wet cloth method of emasculation as suggested by Chaisang et al. (1967) was followed to emasculate the selected spikelets. In this method, Panicles of the A lines on the 3rd or 4th day of its blooming were selected. The immature already opened top and lower spikelets were removed leaving only the middle spikelets. The panicle was covered with wet cloth and hot air was blown through the mouth. Due to increase in temperature and humidity inside the wet cloth, the spikelets were forced to open in the pre-anthesis time. All the six stamens that protruded out of the opened spikelets were removed one by one carefully by using a pointed forceps without damaging the style and stigma. The unopened spikelets were clipped off. At the time of anthesis, the matured anthers from the male parents were collected and dusted on the stigma of the emasculated spikelets of the female parents. The crossed panicles were labeled and covered with red colored butter paper covers. The butter paper covers were removed three days after pollination. Crossing was repeated till sufficient number of crossed seeds were obtained in each of the cross combinations. Selfing of parents was also done by putting white colored butter paper covers on the panicles before the opening of spikelets.

Thus, hybrid seeds of 90 cross combinations and selfed seeds from all the 21 parents were collected after maturity. The seeds were dried at 12 %moisture and preserved at room temperature (28±1°C).

Evaluation of F_1 hybrids and parents for yield traits under aerobic condition

Ninety hybrids along with six lines, 15 testers and one check were raised in a Randomized Block Design (RBD) with three replications under non-puddled and non flooded aerobic soil, during Rabi, 2010. Each treatment was accommodated in two rows of one metre length with a spacing of 30 x 15 cm in each replication. A uniform population of 20 hills per treatment with single seedling was maintained in each replication. Recommended doses of fertilizer and cultural practices were adopted. The hybrids along with their parents were maintained under irrigated condition upto 55 days. From the 56th day onwards the treatment plot was maintained under aerobic condition. For every irrigation thereafter, soil sampling was carried out before and after irrigation to assess the soil moisture content. Irrigation was given only when hair line crack was noticed in the treatment plot and the control plot was maintained under normal flooded condition till maturity. The rainfall received during the entire crop period was recorded. Five plants were selected at random and tagged. Data were recorded at panicle initiation(75 – 80 days), flowering and maturity stages for physiological and quantitative traits. Observations of B lines were recorded for the

Table 1. Details of parents.

S/ No	Symbol	Genotypes	Source
		Lines	
1	L_1	IR 79128A	IRRI, Phillipines
2	L_2	IR79156A	IRRI, Phillipines
3	L_3	IR73328A	IRRI, Phillipines
4	L_4	IR70369A	IRRI, Phillipines
5	L_5	CO MS- 14A	TNAU, Coimbatore
6	L_6	CO MS 24A	TNAU, Coimbatore
		Testers	
1	T_1	IR 69726-29-1-2-2R	IRRI, Phillipines
2	T_2	IR 81178-2T-2-2-3R	IRRI, Phillipines
3	T_3	IR 80286-22-3-6-1R	IRRI, Phillipines
4	T_4	IR 7925A-428-2-1-1R	IRRI, Phillipines
5	T_5	IR 79582-21-2-2-1R	IRRI, Phillipines
6	T_6	IR 79200-45-2-2-1R	IRRI, Phillipines
7	T_7	IR 80402-88-3-1-3R	IRRI, Phillipines
8	T_8	IR05 N496R	IRRI, Phillipines
9	T_9	MAS- 946-1	UAS, Bangalore
10	T_{10}	MAS -26	UAS, Bangalore
11	T_{11}	KMP-105	UAS, Bangalore
12	T_{12}	KMP -148	UAS, Bangalore
13	T_{13}	KMP -149	UAS, Bangalore
14	T_{14}	BR -2655	UAS, Bangalore
15	T_{15}	BI-33	UAS, Bangalore

corresponding A lines.

Characters studied

Observations were recorded for the drought tolerant, yield and its component traits *viz*., Days to 50 %flowering (DF), Plant height (PH), Number of Productive tillers per plant (PT), Number of panicles per plant (PP), Panicle length (PL), Filled grains per panicle (FG), Spikelet fertility (SF), Hundred grain weight (HGW), Proline content (PC), SPAD chlorophyll meter reading (SCMR), Chlorophyll stability index (CSI), Relative water content (RWC), Biomass yield (BMY), Dry shoot weight (DSW), Dry root weight (DRW), Root / shoot ratio (RS), Root length (RL), Harvest index (HI), Single plant yield (YLD) under water stress and fully irrigated (control) conditions as per the Standard Evaluation System (1996). Proline content was estimated as suggested by Bates *et al*. (1973). The relative water content was calculated using the formula suggested by Weatherley (1950).

$$\text{RWC (\%)} = \frac{\text{(Fresh Weight – Dry Weight)}}{\text{(Turgid Weight - Dry Weight)}} \times 100$$

Statistical analysis

The mean values of all the above observations recorded on five randomly selected plants were utilized for statistical analysis. Lines, testers and hybrids were tested for their significance based on their respective means.

Line x Tester analysis

Analysis of variance

The analysis of variance of RBD and their significance for all the characters were worked out as suggested by Panse and Sukhatme (1964) as shown in Table 2.

The test of significance was worked out as suggested by Snedecor and Cochran (1967).

Test of significance for mean values

$$\text{SEd of lines} = \sqrt{\left(\frac{1}{r}+\frac{1}{rt}\right)EMS}$$

$$\text{SEd of testers} = \sqrt{\left(\frac{1}{r}+\frac{1}{rl}\right)EMS}$$

$$\text{SEd of hybrids} = \sqrt{\left(\frac{1}{r}+\frac{1}{rlt}\right)EMS}$$

Where, SEd=Standard error difference; EMS=Error mean square.

To calculate the CD value, SEd values were multiplied with table 't' value at error degrees of freedom.

Table 2. Analysis of variance of RBD and their significance

Sources of variation	Degrees of freedom	Mean squares	Expectations of mean squares
Replication	r-1		
Genotype	t-1	M_1	$\sigma^2e + r\sigma^2g$
Error	(r-1) (t-1)	M_2	σ^2e
Total	rt-1		

Where, r=Number of replications; t=Number of genotypes;M1=Mean squares for genotypes;M2=Mean squares for error

Phenotypic and genotypic variances

These were estimated according to the formulae given by Lush Jay (1940).

$$\text{Genotypic variance} \quad (\sigma^2_g) = \frac{M_1 - M_2}{r}$$

$$\text{Phenotypic variance} \quad (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Phenotypic and genotypic co-efficient of variability (PCV and GCV)

For each character, PCV and GCV were computed based on the methods given by Burton (1952).

$$\text{PCV} = \frac{\sqrt{Phenotypic\ \text{var}\ iance}}{Grand mean} \times 100$$

$$\text{GCV} = \frac{\sqrt{Genotypic\ \text{var}\ iance}}{Grand mean} \times 100$$

Heritability

In general sense, heritability specifies the proportion of the total variability that is due to genetic causes or the ratio of genotypic variance to the total variance. It is a good index of the transmission of the characters from parents to their offspring (Falconer, 1967). Heritability (h^2) in the broad sense was calculated according to Lush Jay (1940).

$$h^2 \text{ (B.S.)} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,
σ^2_g = Genotypic variance and
σ^2_p = Phenotypic variance

The range of heritability was categorized as suggested by Johnson et al. (1955a):

Range: Frequency

0-30%: Low
31- 60%: Moderate
More than 60%: High

Genetic advance

It is a measure of genetic gain under selection. Genetic advance is defined as the difference between the mean genotypic value of the selected lines and the mean genotypic value of the parental population. It was derived according to the method of Johnson *et al.* (1955 a) for each character under study.

$$\text{Genetic advance (GA)} = \frac{\sigma^2_g}{\sigma_p} \times k$$

Where,
σ^2_g = Genotypic variance,
σ_p = Phenotypic standard deviation and
k = Selection differential at a particular level of selection intensity, which takes into account the mean phenotypic value of the selected families (Falconer, 1967).

Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson et al. (1955a).

$$\text{Genetic advance as percentage of mean} = \frac{Genetic\ advance}{Grand mean} \times 100$$

The range and frequency is as follows:

Less than 10: Low
10 to 20: Moderate
More than 20: High

Analysis of combining ability and gene action

Line x tester analysis was carried out to test parents and hybrids with respect to their general and specific combining ability respectively. The line x tester analysis of combining ability gives useful information regarding the choice of parents and elucidates the nature and magnitude of various types of gene action for the expression of yield and yield attributing characters.

The data on the hybrids and parents were subjected to L×T analysis.

The assumption of null hypothesis was tested for differences among the genotypes as detailed by Panse and Sukhatme (1964). The general combining ability effects of the parents and specific combining ability effects of the crosses were worked out as suggested by Kempthorne (1957). The mean squares due to different sources of variation as well as their genetic expectations

Table 3. ANOVA for combining ability.

Source of variation	Degrees of freedom	Mean squares	Expectations of mean squares
Lines	(l-1)	M_1	EMS + r(COV.F.S – 2.COV.H.S) + rt (COV.H.S)
Testers	(t-1)	M_2	EMS + r(COV.F.S – 2.COV.H.S) + rl (COV.H.S)
Line x Tester interaction	(l-1) (t-1)	M_3	EMS + r (COV.F.S – 2.COV.H.S)
Error	(r-1) (lt-1)	M_4	EMS
Total	(ltr -1)		

Where, r=number of replications; l=number of lines; t=number of testers.

were estimated as follows (Table 3).
From the genetic expectations, the covariance of full sib (COV.F.S) and half sibs (COV.H.S) were estimated as follows:

$$\text{COV.H.S.} = \frac{(M_1 - M_3) + (M_2 - M_3)}{r(l+t)}$$

$$\text{COV.F.S.} = \frac{(M_1 - M_4) + (M_2 - M_4) + (M_3 - M_4)}{3r} - \frac{r(l+t)\,\text{COV.H.S}}{3r}$$

From the covariances of full and half sibs, variances due to general combining ability (σ^2GCA) and specific combining ability (σ^2SCA) were computed as follows:

Variance due to general combining ability (σ2GCA)=COV.H.S.
Variance due to specific combining ability (σ2SCA)=COV.F.S - 2.COV.H.S.

From the variances of GCA and SCA, the gene action was calculated as follows:

Additive genetic variance (σ2A) = 2 σ2GCA (Inbreeding co-efficient, F=1)
Non additive genetic variance (σ2D) = σ2SCA (Inbreeding co-efficient, F=1)

Estimation of combining ability effects

General combining ability effects (*gca*) of parents and specific combining ability effects (*sca*) of hybrids of ijkth observation were arrived at using the mathematical model given below

$$X_{ijk} = \mu + \hat{g}_i + \hat{g}_j + \hat{s}_{ij} + \hat{e}_{ijk}$$

Where,

X_{ijk}= value of ijkth observation
μ= population mean
$\hat{g}_i$ = *gca* of ith line
$\hat{g}_j$ = *gca* of jth tester
$\hat{s}_{ij}$ = *sca* of ijth hybrid
$\hat{e}_{ijk}$ = error associated with ijkth observation
i= number of lines
j= number of testers
k= number of replications

$$\text{Mean } (\mu) = \frac{X...}{rlt}$$

Where, X…=total of all hybrids; r=number of replications; l=number of lines; t=number of testers

General combining ability effects

The individual *gca* effects were estimated as follows:

$$gca \text{ effect of lines } (g_i) = \frac{X_i..}{rt} - \frac{X...}{rlt}$$

$$gca \text{ effect of testers } (g_j) = \frac{X_{.j.}}{rl} - \frac{X...}{rlt}$$

Where, Xi..=Total of ith line over 't' testers and 'r' replications
X.j.=Total of jth tester over 'l' lines and 'r' replications.
X…=Total of all hybrids.

Specific combining ability effects

The individual *sca* effects were estimated as follows:

$$sca \text{ effects of hybrid } (s_{ij}) = \frac{X_{ij.}}{r} - \frac{X_i..}{rt} - \frac{X_{.j.}}{rl} + \frac{X...}{rlt}$$

Where, Xij.=Total of the hybrid between ith line and jth tester over 'r' replications.

Test of significance of combining ability effects

The standard error pertaining to *gca* effects of lines and testers and *sca* effects of hybrids were calculated as follows:

i. S.E. of *gca* of lines = $\sqrt{\frac{EMS}{rt}}$

ii. S.E. of *gca* of testers = $\sqrt{\frac{EMS}{rl}}$

iii. S.E. of *sca* of hybrids = $\sqrt{\frac{EMS}{r}}$

Where, S.E.= Standard error; EMS=Error mean square; 't'= $\frac{\text{Parameter}}{\text{S.E.}}$

The calculated 't' value was compared with table't' value at error degrees of freedom to test the significance. The significance of *gca* effect of lines, *gca* effect of testers and *sca* effects of hybrids was tested against twice the standard error at five %level and one %level. The ratio of σ^2A/σ^2D was worked out for each character to find out predominance of additive or non-additive gene action, assuming the simple additive dominance model.

Estimation of heterosis

The term heterosis was coined by Shull in 1914. It refers to the superiority of F_1 hybrid over its parents. In other words, heterosis refers to increase in fitness and vigour of F_1 over the parental values. While heterosis refers to the phenomenon (cause), hybrid vigour is the phenotypic expression (effect) of the genetical phenomenon.

The mean values of hybrids and their respective parents were used for estimation of heterosis %under three categories. The magnitude of heterosis in hybrids was expressed as percentage of increase or decrease of a character over mid parent (d_i), better parent (d_{ii}) and standard hybrid (d_{iii}) and was estimated following the formula of Fonseca and Patterson (1968).

Heterobeltiosis (d_{ii})

The superiority of F_1 over better parent was estimated as follows:

$$d_{ii} = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

Where, $\overline{F}_1$ = Mean value of hybrid; $\overline{BP}$= Mean value of better parent

Standard heterosis (d_{iii})

The superiority of F_1 hybrid over the standard commercial variety or hybrid is known as standard heterosis. The term useful heterosis was used by Meredith and Bridge (1972). It is also called as economical heterosis. This type of heterosis is of direct practical value in plant breeding. It is estimated as follows:

$$d_{iii} = \frac{\overline{F_1} - \overline{SV}}{\overline{SV}} \times 100$$

Where,

$\overline{F}_1$ = Mean value of hybrid, $\overline{SV}$ = Mean value of standard variety

The variety IR 6888 was used as standard variety for yield components and drought tolerant traits in the present study.

Test of significance

The significance of magnitude of heterobeltiosis and standard heterosis was tested at error degrees of freedom by the formula as suggested by Turner (1953).

$$\text{'t' for heterobeltiosis} = \frac{\overline{F_1} - \overline{BP}}{\sqrt{\frac{2EMS}{r}}}$$

$$\text{'t' for standard heterosis} = \frac{\overline{F_1} - \overline{SV}}{\sqrt{\frac{2EMS}{r}}}$$

Where, EMS=Error Mean Square; r=Number of replications

RESULTS AND DISCUSSION

Variability studies

Progress in any crop improvement venture depends mainly on the variability existing in the metric traits of the base population. Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. The variability for 19 traits was estimated on the basis of phenotypic and genotypic co-efficient of variations. The PCV value was found to be higher in all the 19 characters studied than the GCV. The differences between PCV and GCV for the 19 characters were very less indicating less environmental influence on those characters (Table 4). Similar findings were reported by Muhammad et al. (2007).

Selection of biometrical techniques

The analysis of variance for combining ability indicated that the lines and testers differed significantly among themselves for all the traits under aerobic condition. Further, the analysis of GCA/SCA variances indicated that the nature of gene action was non additive due to dominance with non fixable genetic variation for all the characters studied. The results are in accordance with the earlier reports of Babu et al. (2001).

The presence of greater magnitude of non additive gene action offers scope for exploiting hybrid vigour through heterosis breeding and hence, these parents can be exploited for production of commercial hybrids. Similar results were also reported by Banumathy (2001). The proportional contribution to total genetic variance by the lines was found to be higher for 100 grain weight. For other characters contribution from line x tester interaction was higher. These results indicate the predominance of non additive gene action. This is in accordance with the earlier reports of Muhammad et al. (2010) and Malathi (2010).

Table 4. Variability parameters for different traits.

Characters	PCV (%)	GCV (%)	Heritability (%)	Genetic advance as %of mean
Days to 50 %flowering	6.71	4.73	50.00	6.88
Plant height	7.52	7.36	96.00	14.83
Productive tillers per plant	13.49	13.09	94.00	26.16
Panicles per plant	20.61	20.39	98.00	41.57
Panicle length	5.37	3.33	38.00	4.25
Spikelet fertility	8.74	8.62	97.00	17.49
Filled grains per panicle	13.91	13.78	98.00	28.13
100 grain weight	12.10	7.34	37.00	9.18
Harvest index	16.96	16.81	98.00	34.33
Single plant yield	7.65	7.62	99.00	15.61
Proline content	11.55	11.43	98.00	23.31
SPAD Chlorophyll meter reading	35.58	35.51	65.00	73.02
Chlorophyll stability index	10.96	10.85	98.00	22.10
Relative water content	6.75	6.30	87.00	12.13
Biomass yield	30.81	23.33	57.00	36.39
Dry root weight	23.21	18.62	64.00	30.77
Dry shoot weight	32.50	18.03	18.03	20.60
Root : Shoot ratio	20.64	20.50	99.00	41.93
Root length	14.35	14.29	99.00	29.32

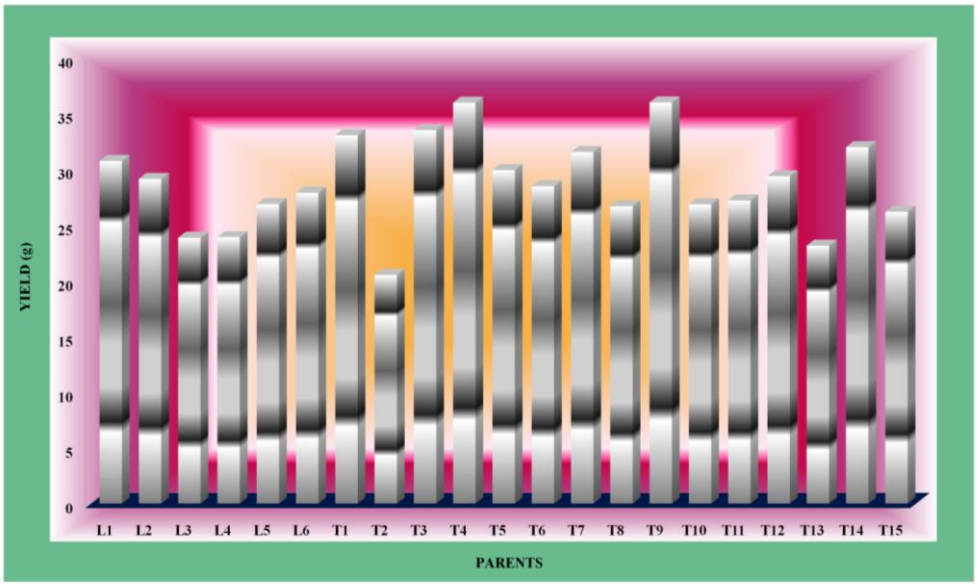

Figure 1. Mean performance of parents for single plant.

Evaluation of parents based on mean performance

As said by Gilbert, 1958 and Nadarajan, 1986 that the parents with high mean performance would result in good performing offspring, the lines IR79128A (L_1), IR79156A (L_2), COMS14A (L_5) and COMS24A (L_6) and the testers, IR 80286-22-3-6-1R (T_3), IR7925A-428-2-1-1R (T_4) and KMP -148 (T_{12}) were adjudged as the best parents as it had significantly desirable mean values for drought and yield traits (Figure 1).

Evaluation of parents based on general combining ability

Since the Combining ability effect is one of the most important parameters commonly used by plant breeders to evaluate the genetic potential of the materials handled,

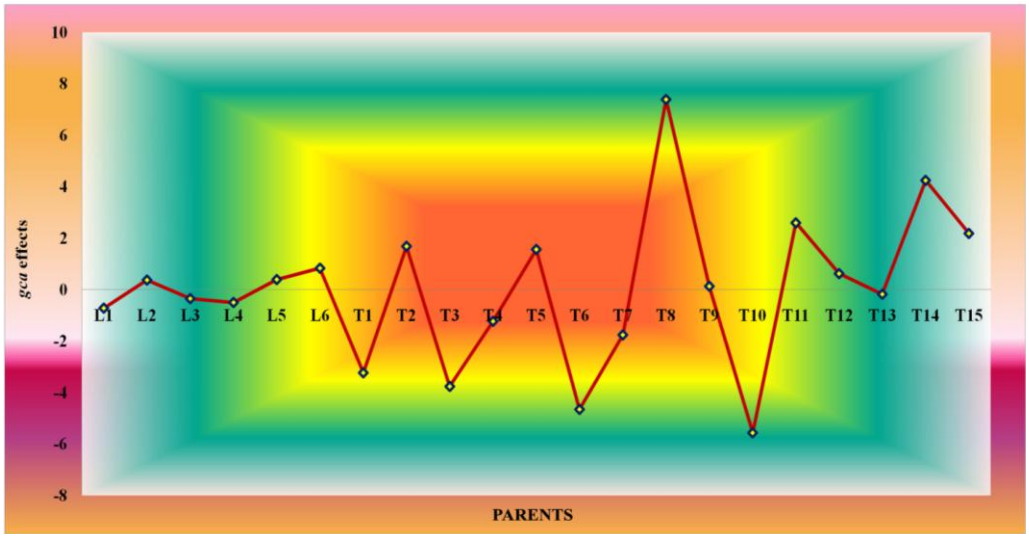

Figure 2. General combining ability of parents for single plant yield.

IR79128A (L_1), IR70369A (L_4) and IR79156A (L_2) among lines and BI-33 (T_{15}), IR79582-21-2-2-1R (T_5), KMP-105 (T_{11}), T_1 (IR 69726-29-1-2-2R) and MAS- 946-1 (T_9) (Figure 2) among testers were found to be the best general combiners as earlier reported by Simmonds (1979) emphasizing that *gca* effect gives the intrinsic genetic value of the parent for a trait. High *gca* effectsshow presence of favorable genes with additive type of gene action. Therefore, a multiple crossing programme involving good general combiners isolated in the present study is recommended to identify superior genotypes as suggested by Nadarajan and Gunasekaran (2005).

Evaluation of parents based on *per se* performance and *gca* effects

Evaluation of parents based on *per se* performance and *gca* effects separately might lead to contradiction in selection of promising parents since *per se* performance of parents was not always associated with high *gca* effects. IR79128A (L_1), IR79156A (L_2) and IR70369A (L_4) among lines and IR7925A-428-2-1-1R (T_{11}), KMP -148 (T_{12}) and BI-33 (T_{15}) among testers were the best parents for most of the traits since they had high *per se* performance and *gca* effects. Earlier studies also indicated that the parallelism between *per se* performance and *gca* effects did not always exist (Selvaraj et al., 2006).

Evaluation of hybrids

Hybridization is the most important method of crop improvement. The basic idea of hybridization is to combine favourable genes present in different parents into a single genotype.

Evaluation of hybrids based on mean performance

The hybrids IR79156A **/** KMP-105 (L_2 x T_{11}), IR70369A **/** MAS -26 (L_4 x T_{10}), IR79156A **/** IR05 N496 (L_2 x T_8), IR79156A **/** BI-33 (L_2 x T_{15}) and CO MS- 14A **/** BR -2655 (L_5 x T_{14}) exhibited significantly desirable mean performance for most of the characters which included drought tolerant, yield and yield components under aerobic condition. These results are in conformity with the earlier findings of Sabesan et al. (2009) and Saravanan et al. (2006).

Evaluation of hybrids based on *sca* effects

The second important criterion for the evaluation of hybrids is the specific combining ability effects which could be related with hybrid vigour. The *sca* effects signify the role of non-additive gene action in character expression (Sprague and Tatum, 1942). The hybrids IR70369A **/** IR 7925A-428-2-1-1R (L_4 x T_4), IR 79128A / BR -2655 (L_1 x T_{14}) and IR70369A **/** KMP-105 (L_4 x T_{11}) expressed superior *sca* effects for majority of drought tolerant and yield attributing characters including single plant yield.

Evaluation of hybrids based on heterosis

Significant standard heterosis over check IR6888 was observed in IR79156A **/** IR 79582-21-2-2-1R (L_2 x T_5) for 16 traits except plant height, 100 grain weight and root:

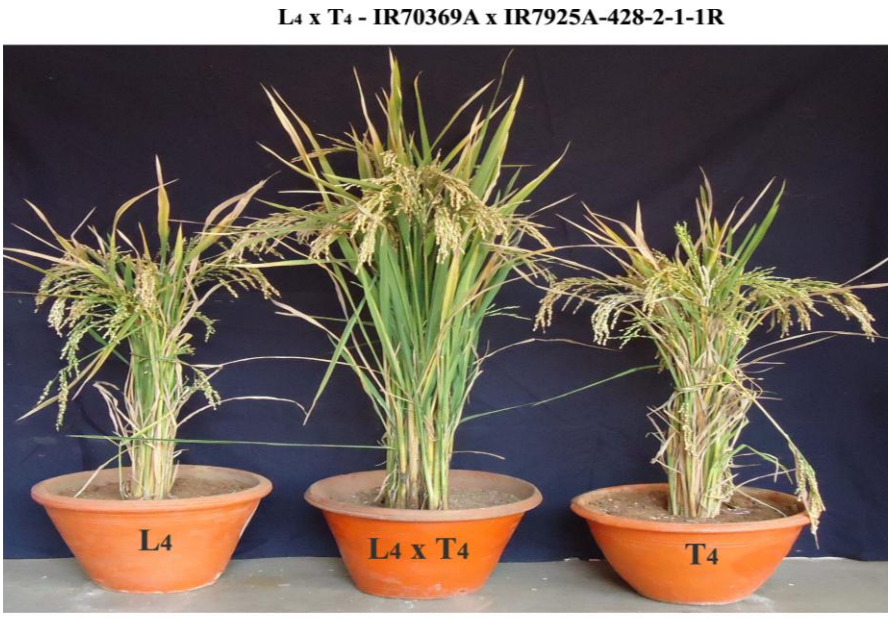

Plate 1. Hybrid recommended for heterosis breeding.

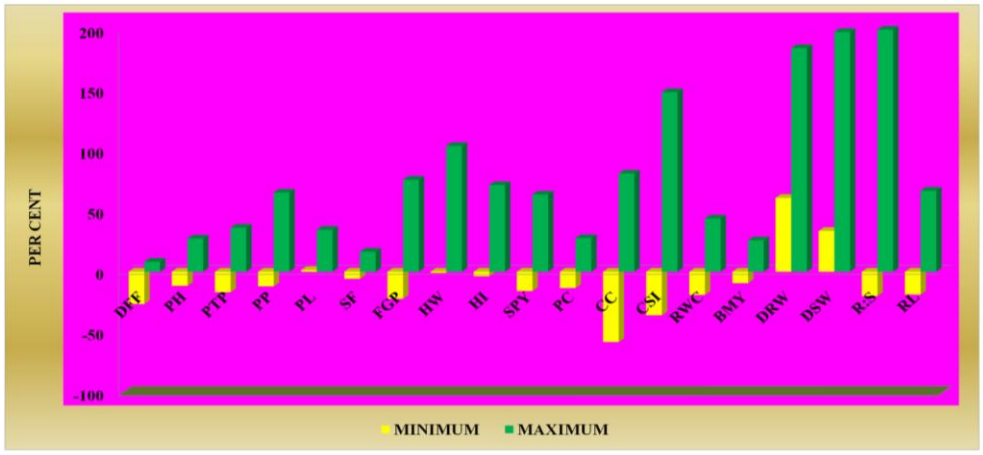

Figure 3. Range of standard heterosis for different traits.

shoot ratio. Similar results have been reported by Khoyumthem et al. (2005) and Soni et al. (2005).

Selection of best Parents and hybrids for utilization in plant breeding programme

The utilization of hybrids directly for commercial seed production mainly depends on the genetic constitution of hybrids. The genetic constitution from the parameter like mean performance, *sca* effects and extent of heterosis. The hybrids IR70369A / IR 7925A-428-2-1-1R (L_4 x T_4) and IR70369A / KMP-105 is suitable for heterosis breeding (Plate 1) under aerobic condition (Figure 3). This is in accordance with the reports of Malarvizhi et al. (2010).

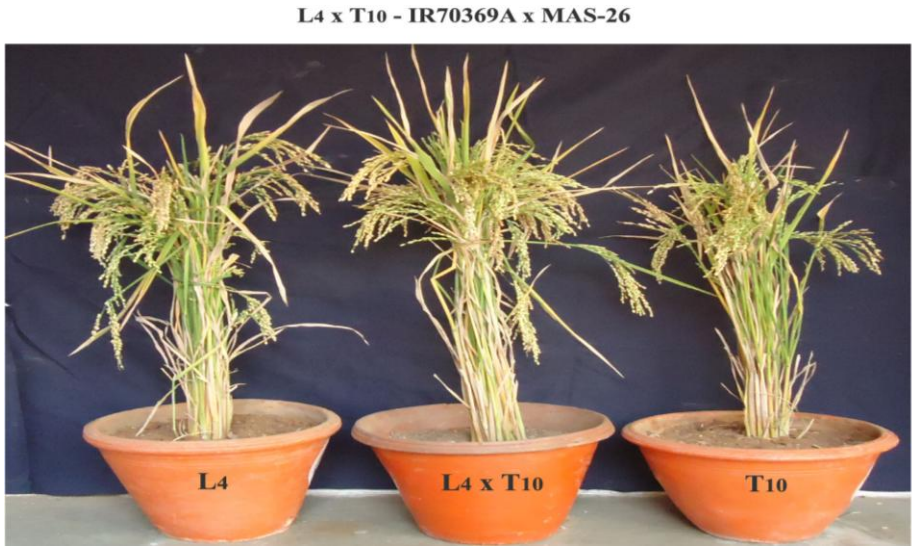

Plate 2. Hybrid recommended for recombination breeding.

Considering the hybrids showing non- significant *sca* effects with significantly favourable *gca* effects of parents for more than one character, the hybrid IR70369A ***/*** MAS -26 (L_4 x T_{10}) is suitable for recombination breeding to get desirable segregants in early segregating generations for drought tolerant and yield attributes (Plate 2). These results are supported by the findings of Utharasu (2007) and Sheeba et al. (2010).

Conflict of Interest

The authors have not declared any conflict of interest.

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