Estimation of Gene Action and Variance Components of Some Reproductive Traits of Rice \((Oryza sativa L)\) Through Line x Tester Analysis

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Abstract

Twenty one parents (five cm S lines and sixteen Restorer lines) were considered for through line x tester analysis to study gene action and combining ability effects of developed cmS and restorer lines. Experiment was carried out at the experimental farm, Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Bangladesh in Boro 2011-12 following RCBD design in three replications. Significant genotypic variances for yield related traits indicated that there were significant variations among the genotypes. Significant gca variances along with additive variance component for reproductive traits indicated the accessibility of additive gene action. Degree of dominance were found negative for most of traits which reveals that regression lines passing below the origin i.e., this character are responsible for over dominance. The linear non-significant relationship between female vs male indicates the reliability of the crosses to go through heterosis breeding. The contributions of lines were found significant indicating preponderance of dominant genes among the lines with tester. The significant interaction of line x tester indicated higher estimates for sca variances. Four restorer lines showed significant negative effects for days to 1st flowering, 80% flowering and days to maturity. Three pollen parents and one cmS line, showed significant positive gca effects for pollen fertility while six pollen parents showed significant positive effects for spikelet’s fertility but two pollen parents showed significant positive gca effects for both panicle and stigmas exertion rate. The estimated of gca effects of parents indicated that five pollen parents contributed highly significant negative effects for plant height which were responsible for dwarfing character. Fifteen crosses showed significant negative sca estimates for days to first flowering, sixteen crosses for days to 80% flowering and twenty crosses for days to maturity. Among 80 crosses fifty two crosses showed significant positive sca effects along with above average perse performances for grain yield.

Keywords: General combining ability; Specific combining ability; gca effects; sca effects; Perse performances

Introduction

Combining ability analysis is one of the powerful available evaluation tools to estimate the combining ability variance and effects for selecting the desirable parents and crosses for exploitation of heterosis. Combining ability variance is usually used for estimate of genetic control of a specific trait .The estimates of additive and non-additive gene action through this technique may be useful in determining the possibility of commercial exploitation of heterosis and isolation of pure line. Hybrid rice offers an opportunity to boost the yield potential of rice. It has a yield advantage of 15-20% over conventional high-yielding varieties. Hybrid rice research now concentrates on the conversion and identification of stable local cytoplasmic male sterile (CMS) lines and effective restorers from local elite lines through repeated backcrossing. To exploit maximum heterosis using male sterile system in hybrid breeding program, we must know the combining ability of different male sterile and restorer lines. The development and use of hybrid rice varieties on commercial scale utilizing cm S fertility restoration system has proved to be one of the mile stones in the history of rice improvement. General combining ability effect is used to select the desirable parents to be used in crosses. Selection of heterotic hybrid depends on expected level of heterosis as well as the specific combining ability effect. Combining ability is a powerful tool in identifying the best combiners that may be used in crosses either to exploit heterosis or to accumulate fixable genes and obtain desirable segregates that helps to understand the genetic architecture of various characters that enable the breeder to design effective breeding plan for future upgradation of the existing materials. Breeding strategies based on selection of hybrids require expected level of heterosis as well as the specific combining ability. In breeding high yielding varieties of crop plant, the breeders often face with the problem of selecting parents and crosses. Line x tester analysis provides information about general combining ability (gca) effects of parents and is helpful in estimating various types of gene actions. [1-3] Therefore, the present investigation was carried out to estimate combining ability effects for yield components involving cm S and restorer lines. Considering the above idea the present investigation was undertaken

1. To determine the extent of general combining ability variances in some morpho-reproductive strains for selection of suitable parents.

2. To determine the extent of specific combining ability effects and perse performances in some morpho-reproductive trains for selection of suitable parents.

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Material and methods

To study combining ability effects of developedcmS and restorer lines an experiment was carried out at the experimental farm, Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur during Aman and Boro following RCBD design in three replications. Five knowncmS lines and sixteen developed R-lines were considered for through line x tester analysis. Data were collected from 10 hills of each genotype on 10

| Sl no | Parents/F1s Status | Sl no | Parents/F1s Status |
|-------|------------------|-------|------------------|
| 1     | RG-BU 08-001 (RG-BU 08-001 R) | 17    | IR 56025A Female Parent (Line) |
| 2     | RG-BU 08-002 (RG-BU 08-002 R) | 18    | GAN 46 A Female Parent (Line) |
| 3     | RG-BU 08-005 (RG-BU 08-003 R) | 19    | IR 62829A Female Parent (Line) |
| 4     | RG-BU 08-006 (RG-BU 08-004 R) | 20    | IR 68888A Female Parent (Line) |
| 5     | RG-BU 08-007 (RG-BU 08-005 R) | 21    | BRRI 1 A Female Parent (Line) |
| 6     | RG-BU 08-013 (RG-BU 08-006 R) | 22    | GAN 46 A Female Parent (Line) |
| 7     | RG-BU 08-016 (RG-BU 08-007 R) | 23    | GAN 46 A Female Parent (Line) |
| 8     | RG-BU 08-018 (RG-BU 08-008 R) | 24    | GAN 46 A Male Parent (Tester) |
| 9     | RG-BU 08-025 (RG-BU 08-009 R) | 25    | GAN 46 A Male Parent (Tester) |
| 10    | RG-BU 08-034 (RG-BU 08-010 R) | 26    | GAN 46 A Male Parent (Tester) |
| 11    | RG-BU 08-038 (RG-BU 08-011 R) | 27    | GAN 46 A Male Parent (Tester) |
| 12    | RG-BU 08-046 (RG-BU 08-012 R) | 28    | GAN 46 A Male Parent (Tester) |
| 13    | RG-BU 08-057 (RG-BU 08-013 R) | 29    | GAN 46 A Male Parent (Tester) |
| 14    | RG-BU 08-063 (RG-BU 08-014 R) | 30    | GAN 46 A Male Parent (Tester) |
| 15    | RG-BU 08-097 (RG-BU 08-015 R) | 31    | GAN 46 A Male Parent (Tester) |
| 16    | RG-BU 08-105 (RG-BU 08-016 R) | 32    | GAN 46 A Male Parent (Tester) |

And eighty crosses from these parents in winter 2011-12, and winter 2012-13.

| Sl | Crosses (F1s) | Sl | Crosses (F1s) |
|----|--------------|----|--------------|
| 1  | IR 58025A × RG-BU08-001R | 21 | GAN 46A × RG-BU08-007R |
| 2  | IR 58025A × RG-BU08-002R | 22 | GAN 46A × RG-BU08-013R |
| 3  | IR 58025A × RG-BU08-005R | 23 | GAN 46A × RG-BU08-016R |
| 4  | IR 58025A × RG-BU08-006R | 24 | GAN 46A × RG-BU08-018R |
| 5  | IR 58025A × RG-BU08-007R | 25 | GAN 46A × RG-BU08-025R |
| 6  | IR 58025A × RG-BU08-013R | 26 | GAN 46A × RG-BU08-034R |
| 7  | IR 58025A × RG-BU08-016R | 27 | GAN 46A × RG-BU08-038R |
| 8  | IR 58025A × RG-BU08-018R | 28 | GAN 46A × RG-BU08-046R |
| 9  | IR 58025A × RG-BU08-025R | 29 | GAN 46A × RG-BU08-057R |
| 10 | IR 58025A × RG-BU08-034R | 30 | GAN 46A × RG-BU08-063R |
| 11 | IR 58025A × RG-BU08-038R | 31 | GAN 46A × RG-BU08-069R |
| 12 | IR 58025A × RG-BU08-046R | 32 | GAN 46A × RG-BU08-105R |
| 13 | IR 58025A × RG-BU08-057R | 33 | BRRI 1ª × RG-BU08-001R |
| 14 | IR 58025A × RG-BU08-063R | 34 | BRRI 1ª × RG-BU08-002R |
| 15 | IR 58025A × RG-BU08-097R | 35 | BRRI 1ª × RG-BU08-005R |
| 16 | IR 58025A × RG-BU08-105R | 36 | BRRI 1ª × RG-BU08-010R |
| 17 | GAN 46A × RG-BU08-001R | 37 | GAN 46A × RG-BU08-007R |
| 18 | GAN 46A × RG-BU08-007R | 38 | GAN 46A × RG-BU08-013R |
| 19 | GAN 46A × RG-BU08-009R | 39 | GAN 46A × RG-BU08-016R |
| 20 | GAN 46A × RG-BU08-025R | 40 | GAN 46A × RG-BU08-018R |

Table 1: List of parental lines (five CMS and sixteen restorer lines).
similar contribution of lines was found significant (13.77**) indicating preponderance of fertile genes among the lines followed by (3.73*) with tester for plant height. The interaction of line x tester was found significant (82.50**) that indicated higher estimates for variances among the preponderance of non-additive gene action. Significant genotypic variances for days to first (310.49**) flowering, days to 80% flowering (3937.62**) and days to maturity (4501.57**) indicates that there is significant variations among the genotypes. But significant negative variances parents of these traits; days to first (-47.52**) flowering, days to 80% flowering (-602.70**) and days to maturity (-602.70**) indicates that short duration materials are present among these parents. Like parents, significant negative variances were also recorded for female parents for these traits but significant positive variances were recorded for male parents which indicate that restorer lines are mostly long duration materials. The linear non-significant relationship between female vs male (-9704.37, -69886.36 and -82993.74) indicates the reliability of these traits to go through heterosis breeding. While parent vs hybrid (11605.32**, 93994.24* and 110554.38**) were found highly significant. [5, 6] has observed significant differences between parents and hybrids. Significant negative gca variances (-6.455*, -40.556** and -38.864**) along with negative additive variance component (-1.614*, -10.139* and -9.716*) indicates the accessibility of additive gene action towards short duration parents. Like gca variance (f-gca) significant negative sca (f2) variances were also recorded -61.427**, -137.922** and -164.943** along with significant negative dominant variance component (-24.857**, -36.481** and -41.736**) indicates the accessibility of dominant gene action through short duration hybrids among these 80 cross combinations. Degree of dominance (-0.2779, -0.2964 and -0.40937) were found negative which reveals that regression lines passing below the origin i.e., these characters are responsible for over dominance. Yield is considered as the most important character among these 80 cross combinations. The analysis of variance due to genotypes showed a highly significance (6.85**) indicating a wide range of variability for grain yield highly significant variances for male (8.21**), female (2.79**) and parents (11.01**) indicating equal contribution of male, female and parents which might lead to a wide range of variability among the offspring’s. The linear non-significant relationship between female vs male (132.07 ns) indicates the reliability of the parents to go through heterosis breeding. Non-significant contribution of female in hybrid (1.78 ns) indicates there is no significant differences between the female lines for grain yield. Significant contribution of male in hybrid (8.66**) was estimated followed by parents vs hybrid (7.29**) implies that there is a significant difference between parents and hybrids. These results were supported [7,8] (Table 2).

Non-significant general combining ability variances (0.069 ns) reveals that grain yield was not controlled by the additive gene but highly significant specific combining ability variances (1.390**) were observed which reveals that this character is completely controlled by the dominant gene action. The result was completely supported by non-significant additive variance (0.017 *) and significant dominant genetic variance (0.848*). While selection of suitable cross combination might be done on the basis of significant specific combining ability variances along with dominance variance. Observed that gca and sca variances were highly significant for yield and the yield attributing characters which indicated the importance of both additive and non-additive gene action. Degree of dominance (0.020) was found near zero which reveals that this character is responsible for complete dominance. Conducted experiments on combining ability using eight lines and four testers in rice and observed non-additive gene action governing the characters. While non-significant (1.24 ns ) error sum squares of tester indicates no significant deviations among the testers. Reported highly significant variance for combining ability in different characters among lines, testers and line x tester interactions. In fact, five recognized cm S (Cytoplasmic male sterile) lines were used as testers and among the cm S-lines there was no significant difference for pollen fertility and spikelet fertility. The interaction of line x tester was found significant (76.26**) that indicated higher estimates for variances due to dominant gene action [9-12].

**Estimation of general combining ability (GCA) effects**

The general combining ability effects of the parents in the present

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**Table 2:** Estimates of mean sum of squares for lines, testers, line x tester as well as variance components (additive, dominance and degree of dominance) in 80 F1 hybrids and their parents.

| Source of Variation | df | Plant height (cm) | Days first flowering | Days 80 % flowering | Days to maturity | Yield (t/ha) |
|--------------------|----|------------------|---------------------|---------------------|-----------------|-------------|
| Replication (r-1)  | 1  | 529054.36        | 47523.73            | 602697.02           | 689015.99       | 1007.38     |
| Genotypes (g-1)    | 100| 3456.49**        | 310.49**            | 3937.62**           | 4501.57**       | 6.58**      |
| Parents (p-1)      | 20 | 529.05**         | -47.52**            | -602.70**           | -689.02**       | 11.01**     |
| females (f)        | 4  | 1381.70**        | 449.59**            | 2580.82**           | 3216.64**       | -2.79**     |
| males (m)          | 15 | 2694.95**        | -463.70**           | -3167.27**          | -4521.46**      | 8.21**      |
| f vs m              | 1  | 56532.15         | -9704.37            | -69886.36           | -82993.74       | -132.07     |
| Hybrids (c)        | 79 | 3525.77**        | -258.15**           | -3947.11**          | -4473.208**     | 6.40**      |
| female in hybrids (f) | 1 | 77694.32**       | 11605.32**          | 93994.24**          | 110554.38**     | 172.36**    |
| male in hybrid (m) | 15 | 4703.29**        | 317.74**            | 5304.04**           | 6013.42**       | 76.29**     |
| fh x mh (Line x Testers) | 60 | 1051808.72 | 95047.47           | 1205394.05          | 1378031.99      | 2024.76     |

| Variance components | f2 gca | -51.26 | -6.455 | -40.556 | -38.864** | 0.068 |
|---------------------|--------|--------|--------|---------|-----------|-------|
| f2 sca              | 125.22 | -61.427** | -137.922** | -164.943** | 1.390** |
| f2 A                | 12.82  | -1.614 | -10.139 | -9.716* | -0.017** |
| f2 D                | 31.31** | -24.857** | -36.481** | -41.736** | 0.848** |
| f2 gca / f2sca      | -0.40937 | 0.1051 | -0.2294 | -0.2356 | -0.0497 |
| f2A/f2D (Degree of dominance) | -0.2328 | -0.2779 | -0.2964 | -0.40937 | -0.0204 |

*p=0.05, **p=0.01 and ***=non-significant.
study have brought to light the parents with high gca effects for five different traits. A total of 16 crosses were found having significant negative heterosis for plant height. Where three crosses of IR 58025A, three crosses of BRRI 1A, four crosses of GAN46A, two crosses of IR 68888A and four crosses of IR 62829A are significant negative heterosis for plant height. This result indicates that the following crosses are semi dwarf in nature. The crosses of IR58025A showed significant positive specific combining ability effects with RG-BU-08-006R & RG-BU-08-034R. As these crosses showed highly significant positive sca effects and above average perse performances, might not be selected as suitable hybrid. The crosses of GAN46A also found significant positive sca effects and above average perse performances with RG-BU-08-007R, RG-BU-08-018R & RG-BU-08-105R. The crosses of IR68888A showed significant positive sca effects and above average perse performances with RG-BU-08-002R, RG-BU-08-006R, RG-BU-08-018R and RG-BU-08-016R which can be considered as good specific combination for tallness. As the above crosses showed positive specific effects which could be used as above average combinations for tall stature. These results are in line with the findings of Good specific combinations for tallness were evolved from high × high, general combiner parents. Low × above average general combiner parents produced above average specific combination for tall plant height in rest of the crosses also found similar findings. Semi-dwarf plant height is needed to protect the crop from lodging. The estimated gca effects of parents indicated that the parent, RG-BU-08-001R, RG-BU-08-002R, RG-BU-08-0046R, RG-BU-08-0057R, RG-BU-08-0097R, BRRI 1A and IR6829A contributed highly significant negative effects. These facts indicated that the former parents possessed more negative alleles for the dwarf stature of the parents. Perse performance also supported that RG-BU-08-001R (89.03 cm), RG-BU-08-006R (96.72 cm), RG-BU-08-007R (90.39 cm), RG-BU-08-097R (81.39 cm) and BRRI 1A (90.59 cm) except RG-BU-08-002R (103.69 cm) and IR6829A (108.57 cm) were dwarf in stature. Although general gca effects found significant negative but perse performances did not correlate with RG-BU-08-002R (103.69 cm) and IR6829A (108.57 cm) which might be due to pseudo recessive gene effect or wide environmental fluctuation. Therefore, RG-BU-08-001R, RG-BU-08-046R, RG-BU-08-057R, RG-BU-08-097R and BRRI 1A are potential parents and have highly significant gca effect in the desirable direction (negative direction) for plant height. These findings are in accordance with [13-16], Out of sixteen restorer lines eight restorer lines showed significant negative effects for days to 1st flowering, seven showed significant negative effects for days to 80% flowering and five showed significant negative effects for days to maturity. But among these 16 restorer lines, only four showed significant negative gca effects for all these three traits. The restorer lines showing significant negative gca effects for all three traits are RG-BU-08-005R (-7.434**, -8.647**, -7.590**), RG-BU-08-006R (-6.073**, -6.177**, -7.412**), RG-BU-08-007R (-3.743**, -5.057**, -7.564**), RG-BU-08-097R (-8.743**, -6.177**, -5.532**). Such lines could be used as male parent for development of early maturing hybrids in rice. performed line x tester analysis using five lines and four testers to study the combining ability and heterosis for yield and its contributing characters in rice and observed that IR58025A and IR6829A were good general combiners for earliness, grain yield per plant and per day productivity [17] (Table 3).

While estimating the life cycle of these five cmS lines, it was observed that IR 6829A (-2.996**) showed significant negative effects for day 1st flowering and IR 6829A (-3.224*) for days to 80% flowering while GAN 46A (-2.236**, -2.994**, -5.740**) showed significant negative effects for all three traits. Such estimates indicated that these female parents possessing more negative alleles for first flowering. Perse

| Source of Variation | Plant height (cm) | Days first flowering | Days 80% flowering | Days to maturity | Yield (ton/ha) |
|---------------------|------------------|---------------------|--------------------|-----------------|---------------|
| Lines               | g/gh             | Mean               | g/gh               | Mean            | g/gh          |
| IR 58025A           | -0.466           | 89.02 ± 12.07      | 0.824              | 106.66 ± 1.12   | -1.074        |
| IR 68888A           | 0.194            | 107.13 ± 12.07     | 0.076              | 105.13 ± 1.12   | 0.866         |
| BRRI 1A             | -3.836           | 108.57 ± 12.07     | 5.114              | 110.95 ± 1.12   | 6.226**       |
| SE (gi)             | 12.074           | 1.129              | 2.085              | 2.455           | 0.026         |
| SE (gi - gj)        | 30.185           | 2.222              | 3.711              | 3.387           | 0.057         |
| Testers             |                  |                    |                    |                 |               |
| RG-BU-08-001 R      | -5.123**         | 89.03 ± 2.27       | -2.403             | 103.01 ± 3.48   | 3.153**       |
| RG-BU-08-002 R      | -5.823**         | 103.69 ± 2.27      | -4.743             | 100.67 ± 3.48   | -1.177        |
| RG-BU-08-005 R      | -1.788           | 99.40 ± 2.27       | -7.743             | 97.67 ± 3.48    | -8.447**      |
| RG-BU-08-006 R      | -12.536**        | 96.72 ± 2.27       | -6.073**           | 99.34 ± 3.48    | -6.177**      |
| RG-BU-08-007 R      | -1.394           | 136.52 ± 2.27      | -3.743             | 101.67 ± 3.48   | -5.507**      |
| RG-BU-08-009 R      | -0.188           | 99.23 ± 2.27       | -1.928**           | 117.34 ± 3.48   | 1.653         |
| RG-BU-08-010 R      | 0.320            | 91.23 ± 2.27       | 4.598**            | 110.01 ± 3.48   | 4.153**       |
| RG-BU-08-012 R      | 0.511            | 86.79 ± 2.27       | -3.743**           | 101.67 ± 3.48   | -8.447**      |
| RG-BU-08-013 R      | 10.682**         | 92.94 ± 2.27       | 11.258**           | 116.67 ± 3.48   | 6.493**       |
| RG-BU-08-014 R      | 0.199            | 91.11 ± 2.27       | 9.599**            | 115.01 ± 3.48   | 5.823**       |
| RG-BU-08-016 R      | -3.282**         | 96.13 ± 2.27       | -9.073**           | 96.34 ± 3.48    | -6.507**      |
| RG-BU-08-017 R      | -7.027**         | 100.39 ± 2.27      | -1.403             | 104.01 ± 3.48   | -4.177**      |
| RG-BU-08-018 R      | 2.580**          | 87.41 ± 2.27       | -6.073**           | 99.34 ± 3.48    | -0.177        |
| RG-BU-08-019 R      | -4.083**         | 81.93 ± 2.27       | -7.843**           | 96.76 ± 3.48    | -6.177**      |
| RG-BU-08-020 R      | 2.942**          | 97.95 ± 2.27       | 12.258**           | 117.67 ± 3.48   | 6.1493**      |
| SE (gi)             | 2.278            | 3.483              | 3.067              | 3.581           |               |
| SE (gi - gj)        | 4.594            | 5.730              | 5.677              | 5.039           | 0.784         |

*p = 0.05, **p = 0.01 and *** = insignificant.

Table 3: GCA effects of parents for different yield and yield contributing character of rice.
performances also recorded similar results supported parents RG-BU 08-005R (0.879*), RG-BU 08-005R (0.439*), RG-BU 08-006R (1.069*), RG-BU 08-007R (0.449*), RG-BU 08-013R (0.449*), RG-BU 08-016R (0.449*) and RG-BU 08-034R (0.439*) and positive general combining ability effects of cmS parents IR 58025A (0.074**) and IR 68888A (0.346**). Perse performances revealed that among 21 parents (16 pollen parents and 5 cmS parents) 2 cmS lines IR 58025A (2.66 t/ha) were superior to others. These facts indicated that among 21 parents these nine parents possessed more positive alleles for the increase of grain yield. Observed good general combiner performances with RG-BU08-002R, RG-BU08-005R, RG-BU08-006R, RG-BU08-007R, RG-BU08-013R, RG-BU08-016R and RG-BU08-034R were the best general combiner due to highly significant positive gca effects and above average perse performances with RG-BU08-007R, RG-BU08-018R & RG-BU08-105R. The crosses of IR68888A showed significant positive sca effects and above average perse performances, might not be selected as suitable hybrid. The crosses of GAN46A also found significant positive sca effects and above average perse performances with RG-BU08-007R, RG-BU08-006R, RG-BU08-018R and RG-BU08-016R which can be considered as good specific combination for tallness. As the above crosses showed positive sca effects which could be used as above average combinations for tall stature. These results are in line with the findings of. Good specific combinations for tallness were evolved from high x high, general combiner parents. Low x above average general combiner parents produced above average specific combination for tall plant height in the rest of the crosses also found similar findings [13-15]. Out of 80 test crosses fifteen crosses showed significant negative sca estimates for days to first flowering and sixteen crosses showed significant negative sca estimates for days to 80% flowering. Out of 80 crosses twenty crosses showed significant negative sca estimates for days to maturity, where seven with IR 58025A, two with GAN46A, six with IR 62829A, two with IR 68888A and three with BRRI 1A. In all the cases it was observed that maximum number of crosses were found showing significant negative sca estimates with IR 58025A. The F1s crosses of IR58025A with seven restorer lines showed significant negative sca estimates for days to first flowering, 6 F1s for days to 80% flowering and seven for days to maturity (Tables 4,5).

**Table 4:** SCA effects (Sij vis-a-vis per-se mean performance of hybrids for plant height (cm) in 80 F1 hybrids.

| Line Testers | Plant height (cm) | Sij effect | Mean | Sij effect | Mean |
|-------------|------------------|------------|------|------------|------|
| **Line (Sij)** | **IR 58025A** | **GAN 46A** | **IR 62829A** | **IR 68888A** | **BRRI 1A** |
| RG-BU 08-001 R | -4.98 | 98.79 ± 7.26 | -4.28 | 99.49 ± 7.78 | -9.95* | 93.82 ± 7.39 | -5.93* | 92.84 ± 7.39 | -3.45 | 107.32 ± 7.25 |
| RG-BU 08-002 R | -5.50* | 98.27 ± 7.26 | -3.91 | 98.86 ± 7.78 | -8.86** | 94.91 ± 7.85 | 4.4 | 108.22 ± 7.39 | -15.27** | 88.50 ± 7.25 |
| RG-BU 08-005 R | -2.74 | 101.03 ± 7.26 | -7.50* | 97.62 ± 7.78 | 6.60* | 110.38 ± 7.39 | -1.01 | 102.76 ± 7.39 | -4.28 | 99.49 ± 7.25 |
| RG-BU 08-006 R | 10.71** | 114.49 ± 7.26 | 1.59 | 105.37 ± 7.78 | 46.40** | 150.18 ± 7.85 | 7.88** | 111.66 ± 7.85 | -3.91 | 99.86 ± 7.25 |
| RG-BU 08-007 R | -0.34 | 103.43 ± 7.26 | -4.87 | 108.65 ± 7.85 | -2.31 | 101.46 ± 7.85 | -1.67 | 102.19 ± 7.85 | -7.50* | 95.27 ± 7.25 |
| RG-BU 08-013 R | -3.49 | 100.28 ± 7.26 | -15.64** | 88.13 ± 7.78 | 12.34** | 116.12 ± 7.78 | -0.11 | 103.66 ± 7.85 | 1.59 | 105.37 ± 7.25 |
| RG-BU 08-016 R | -0.74 | 103.03 ± 7.26 | -3.54 | 100.23 ± 7.78 | -3.47 | 100.30 ± 7.85 | 1.95 | 105.73 ± 7.79 | 4.87 | 106.65 ± 7.25 |
| RG-BU 08-018 R | 1.06 | 104.84 ± 7.26 | 4.76 | 105.54 ± 7.78 | 8.02* | 111.83 ± 7.79 | 3.36 | 107.14 ± 7.85 | -15.64** | 88.13 ± 7.25 |
| RG-BU 08-025 R | 0.10 | 103.68 ± 7.26 | -1.91 | 101.86 ± 7.78 | 5.37* | 109.15 ± 7.85 | 2.53 | 106.31 ± 7.39 | -3.54 | 100.23 ± 7.25 |
| RG-BU 08-034 R | 6.60* | 112.38 ± 7.26 | -1.75 | 102.02 ± 7.78 | 45.17** | 148.95 ± 7.85 | -3.38 | 100.39 ± 7.39 | 4.76 | 108.54 ± 7.25 |
| RG-BU 08-038 R | -0.20 | 103.57 ± 7.26 | -2.21 | 101.56 ± 7.78 | 9.04* | 112.82 ± 7.85 | -3.71 | 100.08 ± 7.39 | -1.91 | 101.86 ± 7.75 |
| RG-BU 08-046 R | -3.93 | 99.84 ± 7.26 | -7.22 | 96.65 ± 7.78 | -5.74* | 98.03 ± 7.85 | 2.25 | 106.03 ± 7.85 | -1.75 | 102.02 ± 7.25 |
| RG-BU 08-057 R | -6.56* | 97.21 ± 7.26 | -4.25 | 99.52 ± 7.78 | -17.54** | 86.23 ± 7.85 | -4.55 | 99.22 ± 7.79 | -2.21 | 101.56 ± 7.25 |
| RG-BU 08-063 R | 1.71 | 105.49 ± 7.26 | -2.62 | 101.15 ± 7.78 | 17.52** | 121.30 ± 7.85 | 3.51 | 107.29 ± 7.79 | -7.22* | 96.55 ± 7.25 |
| RG-BU 08-097 R | -5.38* | 99.39 ± 7.26 | -5.88* | 97.89 ± 7.85 | -5.66** | 98.44 ± 7.85 | -6.55* | 97.22 ± 7.79 | -4.25 | 99.52 ± 7.25 |
| RG-BU 08-105 R | 3.24 | 107.02 ± 7.26 | 4.78 | 108.56 ± 7.78 | 7.19* | 110.97 ± 7.85 | 2.10 | 105.88 ± 7.93 | -2.62 | 101.15 ± 7.75 |

Mean | 103.31 | 100.98 | 110.68 | 103.97 | 99.94

| SE (Sj) | 3.113 |
| SEd (Sj) | 5.153 |
| SEd (Sj-Sk) | 7.561 |

\*p=0.05, \**p=0.01 and ***non-significant.
Ten crosses of IR 58025A, seven crosses of GAN46A, fourteen crosses of IR 62829A, nine crosses of IR 68888A and ten crosses of BRRI 1A showed significant positive specific combining ability effects along with mean values. Ten crosses of IR 58025A with the restorers showed significant positive specific combining ability effects along with above average SCA effects and above average per se performances for days to first flowering with RG-BU 007R (0.81**, 4.67 t/ha), RG-BU 008R (3.50*, 7.59 t/ha), RG-BU 007R (3.426**, 7.33 t/ha), RG-BU 08-018R (0.722*, 4.86 t/ha), RG-BU 08-063R (1.544**, 5.63 t/ha), RG-BU 08-097R (2.452**, 6.54 t/ha).

Fourteen crosses of IR62829A resulted highly significant positive specific combining ability effects. These were found in the crosses with RG-BU08-001R (1.16**, 5.26 t/ha), RG-BU08-002R (2.06*, 6.02 t/ha), RG-BU08-005R (2.350**, 6.44 t/ha), RG-BU08-013R (1.138**, 5.23 t/ha), RG-BU08-016R (0.960*, 5.05 t/ha), RG-BU08-025R (2.239**, 6.33 t/ha), RG-BU08-034R (1.056**, 5.15 t/ha), RG-BU08-057R (2.855**, 6.97 t/ha), RG-BU08-063R (1.459**, 5.63 t/ha) and RG-BU08-097R (1.83*, 6.26 t/ha) (Tables 6,7). Nine crosses of IR68888A showed significant positive SCA effects and above average per se performance were found in the crosses with RG-BU08-001R (0.98**, 5.10 t/ha), RG-BU08-006R (2.66**, 5.93 t/ha), RG-BU08-007R (1.62**, 5.71 t/ha), RG-BU08-018R (3.09**, 7.18 t/ha), RG-BU08-057R (0.84**, 4.93 t/ha), RG-BU08-063R (0.81**, 4.88 t/ha) and RG-BU08-097R (1.16**, 5.26 t/ha).

Ten crosses of BRRI 1A showed significant positive specific combining ability effects and above average per se performance were found in the crosses with RG-BU08-001R (1.972**, 6.06 t/ha), RG-BU08-002R (1.97*, 6.06 t/ha), RG-BU08-005R (1.570**, 5.66 t/ha), RG-BU08-006R (1.47**, 5.62 t/ha), RG-BU08-007R (2.21**, 6.10 t/ha), RG-BU08-016R (3.491**, 7.48 t/ha), RG-BU08-025R (3.278**, 6.37 t/ha), RG-BU08-063R (1.572**, 5.66 t/ha) and RG-BU08-097R (2.21**, 6.18 t/ha) [10,11] observed non-additive gene action governing the characters. Banumathy and Thiyagarajan 2005 also found similar results while studying sca variances of rice. The crosses of five R-lines, RG-BU08-001R, RG-BU08-002R, RG-BU08-006R, RG-BU08-007R and RG-BU08-097R were found resulting significant positive SCA effects and above average per se performances with all five cm 5 lines for grain yield. RG-BU08-002R and RG-BU08-097R were found resulting significant positive SCA effects with all yield contributing characters like pollen fertility, spikelets fertility, panicle exertion rate, stigma exertion rate, effective tillers per plant, primary branches per panicle and secondary primary branches.
flowering and maturity. In rice found similar results in SCA effects of panicle and significant negative SCA values in days to 1st flowering, 80% plant, primary branches per panicle, secondary primary branches per fertility, panicle exertion rate, stigma exertion rate, effective tillers per be due to significant positive SCA values in pollen fertility, spikelet's.

\*p=0.05, **p=0.01 and ns

\textbf{Table 6:} SCA effects (Sij) vis-à-vis per-se mean performance of hybrids for days to 80% flowering in 80 F1 hybrids.

\textbf{Table 7:} SCA effects (Sij) vis-à-vis per-se mean performance of hybrids for days to maturity in 80 F1 hybrids.

per panicle with all five cm S lines. Increased sca effect in yield might be due to significant positive sca values in pollen fertility, spikelet's fertility, panicle exertion rate, stigma exertion rate, effective tillers per plant, primary branches per panicle, secondary primary branches per panicle and significant negative sca values in days to 1st flowering, 80% flowering and maturity. In rice found similar results in sca effects of several cross combinations [3] found high specific combinations of crosses of rice from high x high general combiner parents (Table 8).

\textbf{Conclusion}

Significant genotypic variances for yield related traits indicated that there were significant variations among the genotypes. Significant
gca variances along with additive variance component for reproductive traits indicated the accessibility of additive gene action. Degree of dominance were found negative for most of traits which reveals that regression lines passing below the origin i.e., character are responsible for over dominance. The linear non-significant relationship between female vs male indicates the reliability of the crosses to go through heterosis breeding. The contributions of lines were found significant, indicating preponderance of dominant genes among the lines with tester. The significant interaction of line x tester indicated higher estimates for sca variances. Four restorer lines showed significant negative effects for days to 1st flowering, 80% flowering and days to maturity. Three pollen parents and one cm S line, showed significant positive gca effects for pollen fertility but two pollen parents showed positive gca effects for pollen fertility while six pollen parents showed significant positive effects for spikelets fertility but two pollen parents showed significant positive effects for both panicle and stigma exertion rate. The estimated gca effects of parents indicated that five pollen parents contributed highly significant negative effects for plant height which were responsible for dwarifying character. Fifteen crosses showed significant negative sca estimates for days to first flowering, sixteen crosses for days to 80%flowering and twenty crosses for days to maturity. Among 80 crosses fifty two crosses showed significant positive sca effects along with above average per se performances for grain yield.

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