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Research Article

Combining ability and gene action for yield traits in greengram [*Vigna radiata* (L.) wilczek]

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Abstract
The combining ability analysis of 225 F_3s in greengram developed from half diallel crosses among six parents revealed importance of both additive and non-additive gene actions in the inheritance of pods per plant, seeds per pod, 100-seed weight and yield per plant. There were significant differences in gca and sca effects for the characters studied. OGG-12 was the best general combiner for pods/ plant and grain yield per plant where as OGG-57 was for seeds/ pod, OGG-12 and LGG-460 for 100-seed weight. Among the 15 crosses, six crosses showed significant positive and seven crosses had significant negative SCA effects for seed yield/plant. Significant positive SCA effects were observed in two crosses for pods/plant, four crosses for seeds/ pod and three crosses for 100-seed weight. Although some crosses were showing positive SCA effect for yield and its components, the frequency of unfavorable cases were more. Only TARM-1 × OGG-12 exhibited favorable SCA effect for all characters. Considering all the characters simultaneously, OGG-12 was the best combiner followed by TARM-1 and LGG-460.

Key words
Greengram, Combining ability, GCA, SCA, Gene action

Introduction

Greengram [*Vigna radiata* (L)R. Wilczek] is a short duration legume crop cultivated primarily for its dry seed in tropical, subtropical and temperate zone of Asia including India, Bangaladesh, Pakistan, Myanmar, Indonesia, Philippines, Srilanka, Nepal, China, Korea and Japan (Shanmugasundaram, 2001). However, its yield is much lower than that of other legume crops such as grasspea, chickpea and lentil (FAO, 2007). India is the leading greengram cultivator, with about 55% of the total world acreage and 45% of total production (Singh *et. al.,* 2013). According to the report of AICRP MULLaRP (2016), the annual greengram production in India was around 1.5 million tonnes from about 3.02 million ha area during the year 2014-15. Thus, there is an urgent need to increase production and productivity for food and nutritional security which requires efforts to enhance genetic yield potential of the existing varieties by restructuring their plant type. In order to accomplish this task, combining ability analysis was performed which furnishes information to identify desirable parents and genetic architecture of the crosses. It also provides information about the nature of gene action and relative magnitude of fixable and non-fixable genetic variances, which can be used in selecting superior parents and hybrids for production of superior inbreds having desirable character(s). It also furnishes the information on additive and non additive portions of genetic variances present in material for the character under study. Several workers have used combining ability analysis in different crops to study gene effect and genetic worth of parents. But the information on greengram is scanty. Hence the half diallel analysis was adopted in present study to gather information on GCA (general combining abilities) and SCA (specific combining abilities) of parents and simultaneously estimating various types of gene effects involved in the expression of seed yield and related attributes in greengram.

Material and Methods

The experimental material for study comprised of the six parents and 225 F_3 (fifteen crosses and 15 families/cross) progenies of a half diallel cross among six varieties of greengram out of which three (OGG-12, OGG-57 and OUM-11-5) were improved varieties from Orissa, and rest three TARM-1, LGG-460 and Pant-M-4 were prominent varieties from different parts of India like Western, Southern and Northern part, respectively. The crosses (F_3s) along with the parental varieties were grown in a compact family block design (CFBD) with 2 replications at Central Research Station, Department of Plant Breeding and Genetics, Orissa University of Agriculture and Technology, Bhubaneswar. The experimental material was sown on 25th October, 2008. Each parental line and F_3 progeny of a cross was represented by one row of 4 meters long in each replication. One parent of a cross was sown at the beginning and the other one at the end of F_3 progenies of that cross. All together each parent was repeated 5 times per replication. A spacing of 30 cm between rows and 10 cm between plant to plant within a row was maintained after thinning. Fertilizers were applied at the rate of 20 kg N_2, 40 kg P_20_5 and 20 kg of K_20 per hectare in terms of Urea, SSP and MOP respectively along with 12 cart loads of FYM per hectare.

Observations on four quantitative traits such as pods/plant, seeds/pod, 100-seed weight and single plant yield were recorded on ten selected plants from each replication of each cross. The mean data were subjected to statistical analysis. Analysis of variance for combining ability was carried out on the parental and F_3 means following the experimental method-II, model II of Griffing (1956). The components of variance due to general combining ability (σ^2_{gca}) and due to specific combining ability (σ^2_{sca}) were estimated from the observed and expectations of mean squares under model- II to examine the relative roles of GCA and SCA and hence the nature of gene action. In a half diallel cross, the total genetic variance of the progeny families is given by $2\sigma^2_{gca}+\sigma^2_{sca}$ and the phenotypic variance is given by $2\sigma^2_{gca}+\sigma^2_{sca}+\sigma^2_{e}$.

Results and Discussion

The analysis of variance for combining ability for the four characters revealed highly significant differences in GCA effects and which mean that the parent varieties differ in their general combining ability for these characters and highly significant differences in specific combining ability of the crosses for all characters indicating the importance of both additive and non-additive genetic components of variation in expression of these characters (Table 1). Cheralu *et al.* (1999), Pandiyan (2006), Jena (2008) and Yadav and Lavanya (2011) had reported similar finding.

The estimates of general combining ability effects for parental lines revealed that no parents had significant GCA effects for all the traits together (Table-2). Only one parent, OGG-12 was the best general combiner for three traits, *viz* pods/plant, 100 seed weight and yield/plant where as LGG-460 for 100 seed weight and OGG-57 for seeds/pod. The GCA effects for pods/plant ranged from -0.468 to 1.286. Using the symbol '>' for better parent, the order of superiority in respect of GCA for pods/ plant is OGG-12 > TARM-1 > OUM-11-5 > LGG-460 > Pant M-4 > OGG-57. Similarly the range of GCA for seeds/ pod varied from -0.188 to 0.144 and the orders of superiority of the parents in respect of GCA for seeds/pod is OGG-57 > OUM-11-5 > OGG-12 > PantM-4 > TARM-1 > LGG-460. In case of 100-seed weight, the range of GCA was -0.119 to 0.106. The order of superiority of the parents in respect of GCA for this character is OGG-12 > LGG-460 > Pant M-4 > OGG-57 > OUM-11-5 > TARM-1. The range of GCA for seed yield /plant was -0.114 to 0.363 and the order of superiority of the varieties for grain yield/plant is OGG-12 > TARM-1 > Pant M-4 > LGG-460 > OGG-57 > OUM-11-5. On the basis of the magnitude of GCA effects for favorable expression of the traits, none of the parents was a good general combiner for all the traits. However, OGG-12 was the best general combiner for seed yield/ plant, pods/ plant and 100-seed weight. LGG-460 was a good combiner for 100-seed weight and moderate for seed yield/ plant while OGG-57 was best combiner for seeds/pod. OUM-11-5 was a good combiner for seeds /pod and moderate for pods × plant while Pant M-4 was moderate combiner for 100-seed weight and yield/plant. The parents having high GCA effects are due to additive gene effects and is fixable component of genetic variance (Sprague, 1966). In view of this, breeders may utilize the good general combiners in specific breeding programme for amelioration of grain yield in greengram. In general, good combiner for seed yield/plant had significant GCA effect for some other yield component character suggesting their potential use in further breeding programme to isolate desirable transgressive segregants for seed yield and its component characters in greengram (Dethe *et al.*, 2008). It is, therefore, recommended that breeders should breed for the component traits having superior combining ability with an ultimate objective to improve the overall GCA for grain yield in greengram. Based on a simultaneous consideration of the GCA effects for yield and its direct component OGG-12 was found to be best combiner followed by TARM-1 and LGG-460.

Good general combining inbred parents have not always showed high SCA effects in their cross combinations. Thus it may be concluded that the information on GCA effects alone may not be sufficient to predict the extent of hybrid vigor by a particular cross combination (Chakraborty *et al.*, 2010).Therefore, information on GCA effects of the inbred need to be supplemented with that on SCA effects. The specific combining ability is the deviation from the performance predicted on the basis of general combining ability (Allard, 1956). The SCA effects represent non-fixable components of genetic variance, related with heterosis. SCA effects for yield and its direct components are present in Table 3. Five crosses recorded significant SCA effect ranging from – 1.894 to 2.297 for pods/plant of which two crosses showed significant positive and three crosses showed significant negative SCA effects for this character. The cross OGG-12 × OGG-57 had high significant positive effect followed by LGG-460 × Pant M-4, while OUM-11-5 × Pant M-4 had highest negative effects. Ten crosses showed significant SCA effects ranging from -1.113 to 1.497 in seeds/pod out of which four were positive and six were negative. OGG-57 × OUM-11-5 showed highest positive effects followed by TARM-1 × OGG-12 and OGG-57 × Pant M-4. Three crosses showed significant positive and four crosses showed significant negative effects for 100-seed weight ranging from -0.784 to 0.605. Among the crosses showing significant SCA effects, high positive effect was exhibited by OGG-12 × LGG-460 followed by TARM-1 × OGG-57 and OGG-12 × Pant M-4 while OGG-12 × OUM-11-5 showed high negative effects for the character under study. Only TARM-1 × OGG-12 exhibited favorable SCA effect for all characters.

On the basis of values of F_3 population of 15 crosses, six crosses showed significant positive and seven crosses had significant negative SCA effects for seed yield/plant. However, the highest positive and significant SCA effect was exhibited by TARM-1 × OGG-12 followed by OGG-12 × LGG-460 for seed yield × plant. The other promising crosses which showed significant positive SCA effect for seed yield/plant were LGG-460 × Pant-M-4, OGG-57 × OUM-11-5, OGG-12 × Pant M-4 and TARM-1 × OUM-11-5. These crosses also exhibited average to high SCA effects for some of the yield components. This may be because the seed yield is a complex character and is generally dependent upon its component characters. The results are in agreement with Kujur and Lavanya (2011). An examination of the SCA effects of different crosses revealed that the crosses showing high SCA effects did not necessarily involve good general combiners as their parents as observed by Jena (2008) and Tiwari *et al*., (1993). The crosses with significant positive SCA have potential for further improvement in seed yield through its component traits. It is, therefore, suggested that such crosses should be exploited vigorously in the future breeding programme to obtain good segregants which will lead to building up a population with high genetic yield potential.

The crosses, TARM-1 × OGG-12, OGG-12 × LGG-460 and OGG-12 × Pant M-4 with high SCA for seed yield/plant and other yield contributing characters involving parents with high gca × high gca combination indicated that additive and additive × additive gene effects were predominant in the expression of the characters. Therefore, single plant selection could be practiced in segregating generations to isolate transgressive segregants from such combinations due to possibility of fixation (Dethe *et al.*, 2008).

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Table 1. ANOVA of combining ability for yield and its components in F_3 of a 6-parent half diallel cross in greengram

Source	Df	Pods / plant	Seeds / pod	100-Seed weight	Yield / plant
Genotypes	20	2.211**	0.502**	0.121**	0.236**
GCA	5	3.513**	0.123*	0.077**	0.263**
SCA	15	1.777**	0.629**	0.136**	0.227**
Error	20	0.447	0.038	0.016	0.001
σ^2_{gca}		0.217	- 0.063	- 0.060	0.004
σ^2_{sca}		1.330	0.591	0.120	0.226

* Significant at 5 % level ** Significant at 1% level

Table 2. GCA effects of the parental varieties for yield and its components in F_3 of a 6-parent half diallel cross in greengram

Parental variety	Pods / plant	Seeds / Pod	100-Seed weight	Yield / Plant
1. TARM-1	0.109	-0.011	-0.119**	-0.019
2. OGG-12	1.286**	0.007	0.106*	0.363**
3. LGG-460	-0.371	-0.188**	0.085*	-0.069**
4. OGG-57	-0.468*	0.144*	-0.019	-0.107**
5. OUM-11-5	-0.183	0.122	-0.110*	-0.114**
6. Pant M-4	-0.372	0.073	0.057	-0.063**
SE (g_i)	0.216	0.063	0.041	0.010
SE (g_i - g_j)	0.334	0.098	0.063	0.016

* Significant at 5 % level ** Significant at 1% level

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Table 3. SCA effects of the crosses in F_3 of a 6-parent half diallel cross for yield and its components in greengram

Crosses	Pods plant	Seeds / pod	100-Seed weight	Yield / Plant
1. TARM-1 × OGG-12	1.155	0.768**	0.224	0.704**
2. TARM-1 × LGG-460	-1.078	-0.562**	-0.296*	-0.572**
3. TARM-1 × OGG-57	-1.456*	0.444*	0.284*	-0.306**
4. TARM-1 × OUM-11-5	0.814	-0.233	-0.100	0.096**
5. TARM-1 × Pant M-4	-0.491	-1.082**	-0.158	-0.435**
6. OGG-12 × LGG-460	-0.215	0.115	0.605**	0.376**
7. OGG-12 × OGG-57	2.297**	-1.113**	-0.211	0.012
8. OGG-12 × OUM-11-5	0.167	-0.671**	-0.784**	-0.806**
9. OGG-12 × Pant M-4	0.391	-0.010	0.268*	0.289**
10. LGG-460 × OGG-57	-1.341*	-0.883**	-0.350**	-0.629**
11.LGG-460 × OUM-11-5	-0.866	0.764**	0.161	0.048
12. LGG-460 × Pant M-4	1.374*	0.195	-0.061	0.327**
13. OGG-57 × OUM-11-5	-0.664	1.497**	0.231	0.279**
14. OGG-57 × Pant M-4	-0.199	0.482*	-0.532**	-0.261**
15.OUM-11-5 × Pant M-4	-1.894**	0.174	0.009	-0.390**
SE (S_{ij})	0.593	0.173	0.112	0.028
SE (S_{ij}-S_{ik})	0.884	0.260	0.167	0.041
SE (S_{ij}-S_{ki})	0.819	0.240	0.155	0.039

* Significant at 5 % level ** Significant at 1% level