



COMBINING ABILITY ANALYSIS FOR YIELD AND YIELD CONTRIBUTING TRAITS OF GROUNDNUT

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ABSTRACT

A 10×10 diallel experiment was conducted on groundnut (*Arachis hypogaea* L.) to ascertain the genetic mechanism of yield and its related traits. The observations were recorded on no. of pod/plant, no. primary branch/plant, plant height (cm), harvest index (%), 100 pod weight (gm), 100 kernel weight (g), pod index (%), disease incidence (%) and yield/plot (g). The analysis of combining ability suggested that both additive and non additive gene actions were involved in the genetic system. The GCA: SCA ratio was more than one found in no. of pod/plant, plant height (cm), harvest index (%), 100 pod weight (g), pod index (%), disease incidence (%) and yield/plot (g). It indicates preponderant additive gene action for controlling those traits. However, primary branches plant⁻¹ and 100 kernel weight were predominantly controlled by non-additive gene action. Ranking of the parents on GCA performance for nine characters indicated that the parent P₄ (J×87015-SL-1) was the best general combiner for harvest index (%), 100 pod weight (g) and yield /plot (g) and that of hybrids on SCA performance suggested that the F₁ (P₃×P₅) was the best specific combiner for plant height (cm) and F₁ (P₃×P₄) for disease incidence and yield/plot (g).

Key words: Combining ability, groundnut, specific combining ability, yield

INTRODUCTION

Groundnut (*Arachis hypogaea* L.) rank is the second most important oilseed crop in Bangladesh after mustard/rapeseed with an annual production of 143,000 metric tons (AIS 2012). Its seeds contain 45-56% high quality edible oil, 25-30% protein and 20% carbohydrate along with vitamins E and B. Being a multipurpose crop, there are many constraints responsible for low yield of groundnut. Among them, biotic factors, diseases play a vital role in reducing groundnut yield. The world record indicates that groundnut is suffering from 60 different diseases (Westcott 1974) of which 21 are known to occur in Bangladesh (Talukder 1974; Anonymous 1983; Ahmed and Hossian 1985). Among the diseases, cercospora leaf spot (*Cercospora arachidicola*) is reported as major due to its high incidence, distribution and detrimental diallel cross effect on yield (Khaleque 1986).

Among the mating designs widely used in characterizing quantitative genetic variation in numerous cross and self-pollinated crops. A dialled crossing system involves the selection and intercrossing of a number of genotypes. Statistical

genetic analysis using the diallel method can divided the genotypic variance into two components: the general combining ability (GCA) or the average performance of a cultivar in hybrid combination and the specific combining ability (SCA) or the deviation of a line from its average performance in certain combinations. Estimates of GCA and SCA can be translated into measures of additive and dominance components of genetic variation, respectively, in a given population (Griffing 1956a). Breeding for improved and high-yielding peanut cultivars has been hampered through the lack of information of the genetics of yield and yield components (Hammons 1973; Norden 1973; Gibori *et al.* 1978). Wynne and Coffelt (1983) pointed out that despite the availability of methods for characterizing the genetic variability in self-fertilizing species; little information has been obtained on the various types of gene action and their relative importance in the inheritance of important traits in peanuts. This study were conducted to measure the magnitude of GCA and SCA mean squares and effects for some quantitative traits in peanut and to evaluate the breeding potential of the population.

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MATERIALS AND METHODS

Among the ten groundnut genotypes; two genotypes are tolerant, two genotypes are susceptible and the rest of them are moderate tolerant to *cercospora* leaf spot. The cultivars used are presented in Table 1. Ten cultivars were crossed in diallel, excluding reciprocal to get 45 F₁ hybrids. Selfed seeds of the plants used as parents were also obtained for the ten parental cultivars. Hybrid seeds of the 45 crosses together with the selfed seeds of parental cultivars were planted in the field during the 2010-2011 using as randomized complete block design with three replications. Plot size was (1m×0.80m). Plants were spaced at 20cm within each row. The experimental area was thoroughly prepared and appropriate cultural management practices such as weeding, cultivation, Fertilizers were applied at the recommended dose following BARC fertilizer recommendation guide (2005). The whole amount of Urea 44 kg/ha, TSP 178 kg/ha, MOP 138 kg/ha and Gypsum 111 kg/ha were applied at the time of final land preparation, artificial inoculation spraying @ 15,000 conidia per ml using hand sprayer and irrigation were equally applied to all plots. The following measurements were taken for each of the 45 F₁ genotypes and ten parental cultivars in each replication. Number of pod/plant, number of primary branch/plant, plant height (cm), harvest index (%), 100 pod weight (gm), 100 kernel weight(gm), pod index (%), disease incidence (%) and yield / plot(gm). The replicated data on different characters were subjected to the preliminary ANOVA using for RCBD design. ANOVA, Mean and range were calculated by computer using MSTATC software. The data were then analyzed for combining ability.

For the genetic analysis of diallel cross, data were subjected to analyse by Griffing's (1956). An understanding of general and specific combining ability and the genetic system controlling important traits of groundnut were thus attempted. Griffing's (1956) method 2, Model 1 (Fixed effects model) was used for combining ability analysis for each of the trait. In model 1, the experimental materials are regarded as the population about which inferences are to be made. Presuming when reciprocal differences were absent or negligible then following the method 2.

RESULTS AND DISCUSSION

The analysis of variance for combining ability both GCA and SCA variances were highly significant for all the characters. It reveals that both additive as well as non additive gene action were involved in the inheritance of these traits. Moreover, GCA:SCA ratio revealed that (GCA mean squares were much higher than SCA mean squares) for no. of pod/plant (2.05:1), plant height (1.52:1), harvest index (2.89:1), 100 pod weight (2.65:1), pod index (1.91:1), disease

incidence (1.17:1) and yield/plot (3.49:1) which indicated additive gene action was more important in controlling the character. Primary branch/plant (GCA= 0.48 and SCA= 2.07) and 100 kernel weight (GCA= 20.16 and SCA= 26.25)) which revealed the preponderance non additive gene action for controlling the characters. For yield and yield related traits, Wynne *et al.*, (1975) recorded significant GCA and SCA for pod weight and pod number where GCA were greater than SCA. Jogloy *et al.* (1999) found that GCA mean squares were important for pod length and pod size, but SCA mean squares were less important for this trait. Green *et al.* (1983) and Swe and Branch (1986) found that GCA and SCA mean squares were significant for yield and yield component traits. Similar results were also reported by Holbrook (1990). Redona and Lantican (1985) reported highly significant effects of GCA and SCA for pod yield/plant. Isleieb *et al.* (1978) found that persistent significance of SCA mean squares for yield and seed traits were observed in F₁ through F₅ generation from the crosses of diverse origin. The analytical methods and the procedures of them, often quoted with worked out examples, could be found in several reference literature (Mather and Jinks 1982; Singh and Chaudhary 1979; Dabholkar 1992; Sharma 1998).

General combining ability effects: The estimates of GCA effect of the parents are shown in Table 2. The GCA effect is a good estimate of additive gene action. The estimate of significant GCA effect showed that Dacca-1 was the best general combiner in case of 100 kernel weight (g), diseases incidence (%) and yield/plot (g). This parent could be the best donor for high yielding resistant variety. Binachinabadam-4 had a desirable general combining ability because this parent showed positive significant GCA effect for no. of pod/plant. The GCA effect indicates that genotype Zhinghabadam was the best general combiner for plant height (cm), 100 pod weight (g) and yield/plot (g) because of positive significant GCA effect. Genotype J×87015-SL-1 was the strong general combiner for harvest index (%), 100 pod weight (gm) and yield / plot (g). ICGV-95063 genotype showed significant positive GCA effect for no. primary branch / plant and plant height (cm). The Genotypes BARI Chinabadam-7 showed significant negative GCA effect for yield/plot (g). Genotypes Binachinabadam-2, Binachinabadam-3 and ICGV-90227 exhibited poor general combiner for all the traits.

Specific combining ability effects: Estimates of the SCA effects of the 45 crosses for the quantitative characters measured are presented in Table 3. The SCA constants ranged from -5.84 to 11.66 for no. of pod/plant, -2.24 to 2.70 for no. primary branch/plant, -14.42 to 39.16 for plant height (cm), -13.91 to 18.08 for harvest index (%), -19.29 to 21.18

for 100 pod weight (g), -6.55 to 7.81 for 100 kernel weight (g), -18.40 to 9.29 for pod index (%), -13.24 to 14.26 for disease incidence (%) and -125.54 to 145.66 for yield/plot (g). The largest positive SCA effect was found in the cross P₅×P₈ for no. of pod/plant and harvest index (%). Another cross P₂×P₅ had the largest positive SCA effect for no. primary branch/plant. The hybrid P₃×P₅ exhibited the highest SCA effect for plant height (cm). Cross P₃×P₉ gave the highest SCA effect for 100 pod

weight (gm). The highest SCA effect was found in the cross P₉×P₁₀ for 100 kernel weight (g). For pod index (%), disease incidence (%) and yield/plot (g) the largest positive SCA effects were observed in crosses P₂×P₇, P₂×P₃ and P₃×P₄ respectively. Jivani *et al.* (2007) reported significant GCA and SCA variance for pod yield plant⁻¹. Upadhyaya *et al.* (1992) found same result which supported the present result.

Table 1. Name and source of the genotypes of groundnut along with reaction to *cercospora* leaf spot (CLS) disease

Sl No.	Varieties/ genotypes	Source	Reaction to CLS
1	Dacca-1	BARI	Susceptible
2	Zhinghabadam	BARI	Tolerance
3	BARI Chinabadam-7	BARI	Moderate tolerance
4	J × 87015-SL-1	ICRISAT	Moderate Susceptible
5	ICGV-95063	ICRISAT	Moderate tolerance
6	Binachinabadam-1	BINA	Moderate tolerance
7	Binachinabadam-2	BINA	Moderate tolerance
8	Binachinabadam-3	BINA	Moderate tolerance
9	Binachinabadam-4	BINA	Susceptible
10	ICGV-90227	ICRISAT	Tolerance

Table 2. Estimation of General Combining Ability (GCA) effects for different morpho-physiological agronomic traits in 10×10 half diallel cross of groundnut

Parent	No. of pod/pl ant	No. of primary branch/plant	Plant height (cm)	Harvest index (%)	100 Pod weight (g)	100 kernel weight (g)	Pod index (%)	Disease incidence (%)	Yield /plot (g)
P ₁ (Dacca-1)	0.23	-0.34	-0.12	1.85	2.03	1.59**	-1	4.42**	22.76**
P ₂ (Zhinghabadam)	0.12	-0.12	3.61**	0.19	11.39**	-0.52	2.71*	-5.99**	27.96**
P ₃ (BARI Chinabadam-7)	-1.58	0.1	-3.14**	-1.77	-7.92	-2.32**	-1.65	2.23**	-27.59**
P ₄ (J×87015-SL-1)	0.95	-0.4*	1.74	3.28*	3.22*	0.59	1.22	-1.16	41.16**
P ₅ (ICGV-95063)	-0.41	0.74**	8.16**	-6.65**	-5.36**	-0.07	-2.98*	2.89**	-55.69**
P ₆ (Binachinabadam-1)	-0.33	0.13	-2.56*	2.42	-1.78	1.34	4.04	-2.08**	28.11**
P ₇ (Binachinabadam-2)	-0.41	-0.18	-5.28**	3.75	2.03	0.4	0.75	0.01	11.91*
P ₈ (Binachinabadam-3)	-1.27	0.27	-1.2	1.31	4.92	0.62	0.001	-0.94	-0.89
P ₉ (Binachinabadam-4)	4.39**	-0.34	2.61*	2.67	-2.75	-2.02**	1.69	-0.38	9.26
P ₁₀ (ICGV-90227)	-1.69*	0.16	-3.81**	-7.04**	-5.78	0.37	-4.94**	1.22	-56.99**
SE(gi)	0.73	0.17	0.88	1.07	1.32	0.39	1.26	0.62	4.81

* and ** indicates significance at 0.05 and 0.01 level of probability, respectively

Table 3. Estimates of Specific Combining Ability (SCA) effects for different morpho-physiological agronomic traits in 10×10 half diallel cross of groundnut.

Cross No.	NPP	NPBP	PH	HI	100 PWt	100 KWt	PI	DI	Y
P1 × P2	0.3	-1.21**	-8.98**	-0.06	15.43**	3.09**	-5.89**	-11.27**	101.91**
P1 × P3	5.66**	-1.10**	-11.56**	-0.01	3.07	-1.78**	-1.84	1.51	-71.74**
P1 × P4	-0.54	-0.93**	-0.45	-3.12*	11.27**	2.31**	5.59**	-2.77**	35.91**
P1 × P5	2.49*	1.59**	15.13**	-1.89	2.85	4.31**	5.91**	-7.16**	11.56
P1 × P6	-1.92	0.2	-6.81**	7.68**	13.93**	4.89**	-9.67**	-9.52**	34.56**
P1 × P7	-5.84**	0.51*	5.58**	-7.73**	0.46	5.17**	0.4	-12.27**	15.96*
P1 × P8	-4.65**	-0.93**	6.49**	-2.04	5.90**	1.95**	3.58*	0.34	11.96
P1 × P9	0.35	0.34	-4.98**	1.6	5.24**	-2.75**	4.45*	-5.88**	-11.39
P1 × P10	-1.56	1.51**	-1.9	-3.02*	4.27*	-1.80**	-1.15	-3.60**	-28.54**
P2 × P3	2.77**	2.01**	3.71**	-13.87**	-19.29**	-3.66**	-9.63**	14.26**	-125.54**
P2 × P4	1.58	0.51*	22.83**	4.30**	16.90**	1.75**	-2.95	-5.69**	68.51**
P2 × P5	-3.73**	2.70**	0.08	-10.29**	-13.85**	-1.91**	-2.95	0.92	-35.64**
P2 × P6	-2.81**	-0.02	14.46**	-1.71	-5.10**	2.67**	0.04	-3.10**	15.56*
P2 × P7	-1.06	-1.05**	-3.48**	9.95**	-3.23	6.28**	9.29**	-7.52**	86.96**
P2 × P8	-2.54*	-1.49**	-12.23**	-3.12*	4.54*	3.72**	-0.54	1.09	-13.64*
P2 × P9	5.80**	-1.55**	0.96	6.38**	5.54**	2.03**	6.29**	3.87**	-32.79**
P2 × P10	-1.79	1.62**	-1.29	-4.52**	-15.10*	-3.03**	0.06	5.15**	-40.34**
P3 × P4	0.6	-0.05	2.58*	10.00**	16.54**	5.56**	2.79	-13.24**	145.66**
P3 × P5	0.63	-0.52*	39.16**	-13.91**	-7.87**	-2.11**	7.29**	-9.96**	-1.69
P3 × P6	-3.79**	-0.91**	-11.12**	-8.56**	-12.46**	6.81**	-2.19	3.67**	-96.29**
P3 × P7	1.96	0.4	-3.06*	16.12**	11.74**	5.42**	5.54**	-4.74**	78.31**
P3 × P8	2.16*	-1.05**	-11.48**	-0.29	7.52**	-0.14	6.18**	-1.46	46.11**
P3 × P9	-3.17**	-1.43**	2.38*	5.63**	21.18**	2.17**	4.88**	-11.69**	81.56**
P3 × P10	-5.09**	-1.60**	-7.54**	-5.33**	-11.79**	-1.22*	-11.08**	7.59**	-21.99**
P4 × P5	-2.56*	1.98**	-8.40**	2.83	-18.35**	-5.36**	-9.06**	3.09**	-78.84**
P4 × P6	1.35	-1.41**	-4.67**	2.38	5.74**	4.56**	6.68**	-1.27	19.16*
P4 × P7	1.44	0.23	-6.29**	-7.06**	-13.40**	0.84	-7.57**	5.98**	-113.44**
P4 × P8	-3.70**	0.45*	5.63**	-2.27	-1.62	0.95	-1.05	-4.41**	39.16**
P4 × P9	2.30*	1.40**	2.49*	-3.04*	0.38	1.25*	-1.42	-2.63**	-3.99
P4 × P10	-3.29**	-1.10**	-4.42**	-0.93	-1.6	0.2	-3.4	4.65**	-9.14
P5 × P6	-3.29**	-2.55**	-14.42**	-2.04	7.99**	4.56**	-6.05**	-5.33**	30.21**
P5 × P7	-1.87	2.09**	15.96**	-1.87	-1.82	-2.83**	-7.53**	0.26	-35.79**
P5 × P8	11.66**	0.65**	-0.79	18.08**	12.29**	6.28**	-2.49	-5.46**	42.41**
P5 × P9	0.33	-0.74**	-6.59**	4.58**	4.63*	4.59**	3.47*	-11.02**	28.06**
P5 × P10	1.41	-2.24**	-9.17**	-3.60*	-2.35	-4.14**	5.15**	7.92**	3.71
P6 × P7	-2.29*	-0.63**	-11.31**	-3.81*	2.6	1.42**	-0.39	5.23**	-67.99**
P6 × P8	-0.42	2.26**	8.60**	-4.03**	0.71	4.86**	3.79*	-1.16	1.21
P6 × P9	3.91**	1.20**	5.46**	-3.57*	-0.29	-3.50**	-3.03	-5.05**	23.46**
P6 × P10	-0.67	2.37**	23.21**	-1.95	-11.26**	-6.55**	-2.34	-2.10*	-41.09**
P7 × P8	-6.01**	0.23	6.66**	-11.76**	-9.76**	-6.19**	-13.08**	5.42**	-51.59**
P7 × P9	10.66**	-0.49*	-3.48**	2.90*	20.24**	0.45	3.78*	-10.13**	120.66**
P7 × P10	-1.26	-1.32**	-4.73**	-8.18**	0.27	6.06**	-8.40**	8.81**	-56.69**
P8 × P9	-4.15**	0.4	15.44**	-7.62**	-8.98**	-0.44	-18.40**	-3.19**	-84.94**
P8 × P10	2.60*	-0.77*	-2.81*	5.95**	8.71**	5.84**	4.87**	-10.58**	60.51**
P9 × P10	-5.06**	2.18**	5.71**	-13.48**	4.04*	7.81**	2.57	11.20**	-73.24**
SE(±)	0.99	0.22	1.18	1.44	1.78	0.53	1.7	0.83	6.48

* and ** indicates significance at 0.05 and 0.01 level of probability, respectively. Legend: NPP= No. of pod/plant NPB= No. of primary branch/plant, PH= Plant height, HI=harvest index, 100PWt=100 Pod weight, 100KWt= 100 kernel weight, PI= Pod index, DI= Disease incidence and Y= Yield / plot.

The largest negative SCA constants were obtained from crosses within the varieties. Cross $P_1 \times P_7$ gave the largest negative SCA effect for no. of pod/plant. The highest negative SCA effect was found in cross $P_5 \times P_{10}$ for no. primary branch/plant. $P_2 \times P_5$ cross showed highest negative SCA effect for 100 pod weight (g) and yield/plot (gm). Highest negative SCA effect was found in cross $P_3 \times P_4$ for disease incidence (%). Other crosses $P_5 \times P_6$, $P_3 \times P_5$, $P_6 \times P_{10}$ were recorded in the highest negative SCA effect for plant height (cm), harvest index (%) and 100 kernel weight (g) respectively. The estimates of GCA and SCA mean squares and effect were probably biased by genotype x environment interaction which could not be measured in this study. These experiments suggest that additive and non additive genetic effects were important in crosses between the varieties. The preponderance of the variance due to GCA in all traits can be exploited through the use of conventional selection methods that take advantage of additive genetic variation such as mass selection, pedigree selection, family selection and multiple line selection (Rachie and Roberts, 1974). Improvement in yield should be attained through direct selection for yield, indirect selection for yield through the traits correlated with the yielding ability or through a combination of direct and indirect selection. Considering all the traits under study, the cross combination $P_3 \times P_4$ was best for less disease incidence and higher yield by hybridization.

CONCLUSION

Additive gene effects were found covering the inheritance of no. of pod/plant, plant height, harvest index, 100 pod weight, pod index, disease incidence and yield / plot. Non additive gene effects were not important for this trait. P_4 (Jx87015-SL-1) proved to be the best general combiner for harvest index, 100 pod weight and yield/plot. Other genotype P_1 (Dacca-1) was also found good combiner for 100 kernel weight and yield/plot. The highest SCA effect was obtained in the cross ($P_3 \times P_4$) which was the best specific combiner for the lowest diseases infection and the highest yield/plot and yield components and may be utilized in hybrid seed production.

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