

## Combining Ability in Mungbean (*Vigna radiata* (L.) Wilczek) I. Agronomic Traits

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**ABSTRACT :** Combining ability in mungbean was studied in 15 quantitative traits through a 6 × 6 diallel cross. Both additive and non-additive gene effects were found conditioning the inheritance of nodes of the first peduncle, clusters per plant, clusters on main stem and branches, pods per plant, 1000 seed weight, grain yield per plant, biomass, and harvest index. The additive gene action was found significant for nodes on main stem, average internodal length, branches per plant, pods per cluster, pod length, and seeds per pod. The predominance of additive genetic variance was observed in all traits. For grain yield and yield components, the best combiner were VC3902A, VC1560D and ML-5, while the best combinations were the crosses VC3902A × ML-5, VC1560D × ML-5, and NM 92 × VC1560D.

**Keywords :** *vigna radiata*, mungbean, combining ability, agronomic traits.

The superiority of F<sub>1</sub>-hybrids over their parents may not indicate their potential to produce desirable transgressive segregants, as the components of heterosis include many types of unfixable gene effects. It is therefore, important for a plant breeder to obtain information on the inheritance of characters under improvement. The knowledge about genetic architecture of the character's components would help understanding nature of the character itself. Diallel analysis is a popular method employed to assess inheritance of quantitative characters and provide valuable clues for selection of parents for a hybridization programme (Pooni *et al.*, 1984; Wright, 1985).

Grain yield and its components were studied through 6 parent diallel crosses with the objectives to identify the nature of gene action and isolation of superior genotypes which combine well and throw transgressive segregants for grain yield and its components.

## MATERIALS AND METHODS

Six mungbean genotypes, i.e. NM 92, Var. 6601, and NM 89 from Pakistan, VC1560D and VC3902A from the Asian Vegetable Research and Development Center (AVRDC), Taiwan, and ML-5 from India exhibited wide spectrum of variation, were crossed in a diallel fashion excluding reciprocals. The parents and their 15 F<sub>1</sub>'s were grown in a randomized complete block design with three replications during spring 1998 at the research farm of the Nuclear Institute for Agriculture and Biology, Faisalabad (latitude 31.5°N), Pakistan. Each plot consisted of a single row of ten plants, with row to row spacing of 30 cm and plant to plant spacing of 10 cm. Data on average internodal length [(plant height from 1<sup>st</sup> node to last node)/(total no. of nodes)], number of nodes of the first peduncle, number of nodes on main stem, clusters per plant, clusters on main stem, branches per plant, clusters on branches, pods per plant, pods per cluster, pod length, seeds per pod, 1000-seed weight, grain yield per plant, biomass, and harvest index were recorded on five randomly selected competitive plants from each plot in a replication. Mean of five plants was subjected to diallel analysis using MSTAT-C (Michigan State University Statistical Package Version C) micro computer statistical program.

## RESULTS AND DISCUSSION

The analysis of variance showing mean square values for blocks, genotypes, general combining ability (gca), and specific combining ability (sca) is presented in Table 1. The mean squares of genotypes were significant in respect of all traits. This indicated an adequate amount of variability present in the parental materials.

The significant mean squares due to gca and sca effects for number of nodes of the first peduncle, clusters per plant, clusters on main stem, clusters on branches, pods per plant, 1000-seed weight, grain yield per plant, biomass, and harvest index revealed the presence of additive as well as non-additive gene action for the expression of these traits. The significance of gca and non-significance of sca for number

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**Table 1.** Analysis of variance for genotypic difference and combining ability of some metric traits in 6 parent diallel crosses of mungbean.

Sources of Variation	df	Mean square														
		Nodes of the first peduncle	Nodes on main stem	Average Internodal Length (cm)	Clusters per plant	Clusters on main stem	Branches per plant	Clusters on branches	Pods per plant	Pods per cluster	Pod length (cm)	Seeds per pod	1000 seed wt. (gm)	Grain yield per plant (gm)	Biomass (gm)	Harvest index (%)
Blocks	2	0.23	0.25	0.43	1.87	0.61	0.83	0.42	0.40	0.08	0.71	1.16	0.90	0.83	8.38	0.32
Genotypes	20	1.54**	2.33**	0.26*	12.12**	1.02**	0.87**	8.90**	109.88**	0.13*	1.36**	1.22**	348.25**	17.80**	322.73**	34.47**
gca	5	5.06**	7.46**	0.75**	36.48**	1.40**	2.70**	28.28**	322.32**	0.26**	4.98**	3.23**	130.65**	28.70**	876.31**	30.74**
sca	15	0.37*	0.62	0.10	4.00**	0.89**	0.25	2.44*	39.06**	0.09	0.15	0.55	28.11**	14.17**	138.20**	35.71**
Error	40	0.16	0.40	0.13	0.83	0.29	0.23	0.98	8.30	0.06	0.11	0.40	2.07	1.80	10.69	4.81

\*, \*\*Significant at P = .05 and P = .01, respectively.

**Table 2.** Estimates of gca effect and mean performance (in parenthesis) of some metric traits in 6 parent diallel crosses of mungbean.

Genotypes	Nodes of the first peduncle	Nodes on main stem	Average Internodal length (cm)	Clusters per plant	Clusters on main stem	Branches per plant	Clusters on branches	Pods per plant	Pods per cluster	Pod length (cm)	Seeds per pod	1000 seed wt. (gm)	Grain yield per plant (gm)	Biomass (gm)	Harvest index (%)
NM 92	-0.75 (3.3)	-0.86 (7.1)	-0.32 (3.9)	-1.71 (7.4)	-0.08 (4.9)	-0.54 (1.0)	-1.64 (2.5)	-4.14 (21.2)	0.06 (2.9)	-0.001 (7.5)	-0.68 (8.7)	2.78 (55.5)	-1.77 (10.9)	-10.25 (37.1)	1.46 (29.4)
Var. 6601	0.08 (4.9)	-0.09 (8.1)	0.1 (5.0)	0.21 (9.3)	-0.14 (4.1)	0.05 (1.7)	0.35 (5.2)	2.04 (26.5)	0.14 (2.8)	-0.43 (6.8)	0.19 (11.0)	-7.07 (36.5)	-0.54 (10.8)	0.3 (55.7)	-1.07 (19.5)
NM 89	-0.34 (3.9)	-0.16 (8.3)	-0.02 (4.5)	-0.07 (11.2)	0.21 (5.4)	-0.18 (1.7)	-0.28 (5.8)	-0.77 (27.5)	-0.05 (2.4)	0.01 (7.5)	0.14 (11.3)	-2.58 (43.1)	-0.03 (15.8)	2.22 (69.0)	-1.17 (22.8)
VC 1560D	0.26 (5.5)	-0.09 (8.9)	-0.03 (4.4)	-0.66 (9.5)	-0.32 (4.5)	-0.03 (1.7)	-0.34 (5.1)	-2.62 (20.6)	-0.09 (2.2)	0.44 (8.5)	0.10 (10.8)	6.39 (60.9)	0.09 (13.1)	-2.62 (53.3)	1.11 (24.5)
VC 3902A	0.47 (5.5)	0.43 (9.1)	0.11 (4.5)	0.19 (9.7)	-0.02 (4.5)	0.35 (2.6)	0.21 (5.2)	-0.67 (24.1)	-0.12 (2.5)	0.57 (9.1)	-0.11 (10.3)	9.38 (73.5)	1.28 (17.6)	7.63 (68.3)	-0.66 (25.8)
ML-5	0.28 (4.9)	0.77 (9.5)	0.17 (5.0)	2.04 (12.9)	0.35 (4.9)	0.35 (2.5)	1.69 (8.0)	6.16 (35.1)	0.08 (2.7)	-0.58 (6.4)	0.36 (11.3)	-8.90 (32.3)	0.96 (13.9)	2.72 (57.0)	0.33 (24.5)
S.E. gi	0.07	0.12	0.07	0.17	0.10	0.01	0.18	0.54	0.05	0.06	0.12	0.27	0.25	0.61	0.41
S.E.(gi-gi)	0.11	0.18	0.11	0.26	0.15	0.14	0.29	0.83	0.07	0.09	0.18	0.14	0.39	0.94	0.63

of nodes on main stem, average internodal length, branches per plant, pods per cluster, pod length, and seeds per pod indicated significant additive gene action in their inheritance. For all the traits, except harvest index, the magnitude of *gca* was higher than that of the *sca*, which suggested the predominance of additive gene action.

Grain yield and yield components, viz. pods per plant, seeds per pod, and 1000-seed weight in mungbean were predominantly controlled by loci with additive gene effects (Malhotra *et al.* 1980; Basaeruddin & Nagur, 1981; Rao *et al.*, 1984; and Wilson, *et al.*, 1985). Non-additive gene actions were found most important in the inheritance of grain yield and seed weight (Lal *et al.*, 1982). The significance of additive gene action was reported earlier by Luthra *et al.* (1979), Reddy & Sreeramulu (1982), Malik & Singh (1983), and Wilson *et al.* (1985) for clusters per plant and pod length. The additive gene action for branches per plant and non-additive gene effects for pods and seed yield per plant were predominant in mungbean (Tiwari *et al.*, 1993). The difference in mode of inheritance of a trait is due to difference in genetic background of the genotypes used for inheritance estimation. There would be the need for specific breeding procedures appropriate for mode of inheritance of the trait to be improved.

The estimate of *gca* effect and mean value of the parents for all characters are given in Table 2. The genotype ML-5 showed higher *gca* effect for number of nodes on main stem,

average internodal length, clusters per plant, clusters on main stem, branches per plant, clusters on branches, pods per plant, and seeds per pod. Thus the genotype ML-5 could be used as a good combiner for increasing grain yield per plant through increasing branches per plant, clusters per plant, pods per plant, and seeds per plant. In mungbean, the top fruiting and uniform maturity is a prerequisite for mechanical harvesting. Top fruiting is usually observed in cultivars that set pods at upper nodes on long peduncles. The genotype ML-5 and accession VC3902A were the best combiners for average internodal length and number of nodes of the first peduncle, respectively. The combination of such genotypes could be very useful for breeding mungbean with top fruiting behavior suitable for mechanical harvesting. The genotype VC3902A was also good combiner for branches per plant, pod length, 1000-seed weight, biomass, and grain yield per plant. The variety NM 92 was among the poorest combiners of most traits but was good combiner only for harvest index. Mean performance of the parents in many traits positively coincided with their *gca* effects. This relationship leads to the suggestion that mean performance can be improved by selecting parents with higher *gca*. A similar positive association between mean performance and *gca* of the parents was reported earlier in mungbean by Tiwari *et al.* (1993).

The *sca* and mean performance of the crosses showing significant *sca* effects are presented in Table 3. The param-

**Table 3.** Estimates of *sca* effects and mean performance (in parenthesis) of some metric traits in 6 parent diallel crosses of mungbean.

Cross combinations	Nodes of the first peduncle	Clusters per plant	Clusters on main stem	Clusters on branches	Pods per plant	1000-seed weight (gm)	Grain yield per plant (gm)	Biomass (gm)	Harvest index (%)
NM 92 × Var. 6601	-0.08(3.7)	-0.23(8.8)	0.33(5.3)	-0.56(3.5)	-3.18(22.2)	-1.50(43.3)	-0.83(11.4)	-0.28(49.0)	-1.95(23.2)
NM 92 × NM 89	0.33(3.7)	0.46(9.2)	-0.35(5.0)	0.18(4.2)	2.04(24.6)	-0.96(48.3)	0.46(13.1)	1.81(53.0)	-0.27(24.8)
NM 92 × VC 1560D	-0.27(3.7)	-0.23(7.9)	-0.23(4.6)	0.001(3.3)	-0.32(20.4)	1.90(60.2)	-0.46(12.4)	2.64(49.0)	-2.15(25.2)
NM 92 × VC 3902A	-0.54(3.6)	0.26(9.3)	0.47(5.6)	-2.22(3.7)	0.01(22.7)	-0.09(60.1)	1.75(15.8)	-0.28(56.3)	2.41(28.0)
NM 92 × ML-5	-0.15(3.8)	-0.79(10.1)	0.17(5.7)	-0.96(4.4)	-2.63(26.9)	-0.97(42.0)	-0.79(12.9)	-0.70(51.0)	-1.44(25.1)
Var. 6601 × NM 89	-0.23(3.9)	-0.14(10.5)	0.45(5.7)	-0.59(4.8)	1.72(30.5)	2.26(41.7)	0.49(14.4)	4.92(66.7)	-0.98(21.6)
Var. 6601 × VC 1560D	-0.49(4.3)	0.65(10.7)	0.37(5.1)	0.27(5.6)	4.96(31.9)	-1.94(46.5)	2.71(16.8)	-6.25(54.0)	8.61(33.4)
Var. 6601 × VC 3902A	0.22(5.2)	1.13(12.1)	-0.06(5.0)	1.19(7.1)	1.69(30.5)	-2.40(49.0)	2.05(17.3)	10.51(77.7)	-0.76(22.3)
Var. 6601 × ML-5	-0.12(4.7)	1.82(14.6)	0.51(5.9)	1.32(8.7)	4.99(40.7)	0.45(33.6)	0.84(15.8)	-0.58(61.7)	1.45(25.5)
NM 89 × VC 1560D	-0.01(4.3)	-1.47(8.3)	-0.31(4.8)	-1.16(3.5)	-3.29(20.8)	-1.21(51.7)	-1.57(12.9)	-1.16(57.7)	-2.25(22.5)
NM 89 × VC 3902A	-0.16(4.4)	-0.65(10.0)	0.39(5.8)	-1.04(4.2)	-2.03(24.0)	-0.49(55.4)	-2.42(13.3)	-14.41(54.7)	1.38(24.3)
NM 89 × ML-5	-0.17(4.2)	0.11(12.6)	0.29(6.1)	-0.19(6.5)	-1.53(31.3)	2.13(39.7)	0.34(15.8)	-1.83(62.3)	1.33(25.3)
VC 1560D × VC 3902A	-0.35(4.8)	-0.14(9.9)	-0.09(4.8)	-0.05(5.1)	-1.05(23.1)	-0.67(64.2)	-2.31(13.6)	-1.25(63.0)	-3.73(21.5)
VC 1560D × ML-5	0.04(5.0)	0.56(12.5)	0.48(5.7)	0.07(6.7)	2.98(34.0)	3.92(50.5)	4.72(20.3)	7.34(70.0)	4.51(30.7)
VC 3902 × ML - 5	0.49(5.7)	1.77(14.5)	0.65(6.2)	1.12(8.3)	5.51(38.5)	-7.65(41.9)	-0.21(16.5)	11.09(80.7)	-3.96(20.5)
S.E. Sij	0.20	0.47	0.27	0.51	1.47	0.74	0.69	1.67	1.12
S.E.(Sij-Sik)	0.30	0.69	0.41	0.76	2.20	1.10	1.03	2.50	1.68
S.E.(Sij-Skl)	0.28	0.64	0.38	0.70	2.04	1.02	0.95	2.31	1.55

ters for number of nodes on main stem, average internodal length, branches per plant, pods per cluster, pod length, and seeds per pod were not given as these traits did not show significant sca effects (Table 1). The best crosses on the basis of sca effects were VC3902A  $\times$  ML-5 for number of nodes of the first peduncle, clusters on main stem, pods per plant, and biomass; Var. 6601  $\times$  ML-5 for number of clusters per plant and branches per plant; VC1560D  $\times$  ML-5 for 1000-seed weight and grain yield per plant; and Var. 6601  $\times$  VC 1560D for harvest index. The crosses with high sca effects were resulted from the combination in which both or one parent exhibited high gca and mean. The high grain yield per plant of the cross VC3902A  $\times$  ML-5 may be explained on the basis that a parent superior for one component should be crossed with a parent superior for another, to obtain heterosis for a complex trait like yield (Williams, 1959). A complementary combination of higher 1000-seed weight was detected from the best combiner VC3902A while more pods per plant from another good combiner ML-5 (Table 2). This cross combination can give some desirable segregants useful in mungbean breeding programs.

The present studies indicated predominance of additive gene action controlling the expression of all traits. However, the non-additive gene action was also important in many traits. Therefore, a breeding program involving infusion of desirable genes in the population such as diallel selective mating or multiple crossing as suggested by Redden & Jensen (1974) may prove useful in breaking the yield barriers in mungbean.

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