Combining ability analysis for quantitative traits and yellow mosaic virus in mungbean [*Vigna radiata* (L.) Wilczek]

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SUMMARY

Combining ability analysis was carried out involving diverse genotypes in one-way diallel in mungbean. Both additive and non-additive genetic variances were found important for inheritance of seed yield and its components. The parents, PDM-11, GM-4 and GM-9918 were good general combiners for seed yield and two and more yield attributing traits. The highest sca effect for seed yield was observed in cross PDM-11 x GM-4 followed by PDM-143 x GM9918. These cross combinations also had sca effect in the desire direction for branches per plant, pods per plant, harvest index, 100-seed weight and YMV incidence. In case of MYMV resistance, the parental lines PDM-143, PDM-11 and PDM-14 have potentiality to donate resistant gene. The crosses PDM-143 x GM-9918, PDM87 x GM-4 and PDM-87 x GM-4 were superior combinations for MYMV incidence. These promising crosses gave superior trasgressive segregants in advance generation.

Key words :
Mungbean,
Quantitative
traits,YMV

India is one of the major pulses growing countries in the world, but average productivity level, 397 kg /ha is the lowest in the world of the mungbean [*Vigna radiata* (L.) Wilczek]. Several reasons have been suggested for low productivity of this crop, which include inheritent low productivity of yield, damages caused by several diseases like yellow mosaic virus (YMV), pests, abiotic stress factors and poor management. It is generally felt that there is an urgent need to break the bottlenecks for increasing productivity of this crop. To breed resistant variety, it is necessary to know mechanism of resistance and its genetic control. However, very scanty information is available on this aspect of yellow mosaic virus in mungbean (MYMV). Identification of suitable parents for hybridization is an important means to meet the objectives of breeding programme. It helps to identify parents and crosses which are likely to give the maximum improvement for the trait under consideration but also provide means of understanding regarding gene action involved in it. An attempt was, therefore, made to identify the best general combiners and specific cross combinations for seed yield, YMV incidence and its components in mungbean.

MATERIALS AND METHODS

A set of 36 genotypes comprising of 8 genotypes and 28 F_1 crosses were sown in randomized block design with three replication during *summer* season of 2004 at Main Pulses Research Station, Gujarat Agricultural University, Sardarkrushinagar. Each genotype consisted of single row of two meter length. The infector row of GM-3 variety (susceptible to YMV) was grown in alternate rows, so as increase the incidence of yellow mosaic virus. The hybrid cotton and okra were also sown around the plot for increasing the incidence of the whitefly (*Bamisia tabaci*), which acts as a vector of the YMV. Five random plants were selected from each parents and crosses in each replication. The observations were recorded for eight important characters. The important character YMV incidence recorded prior to leave senession on standard scale 0-5. International mungbean breeding nursery follows 5 point scale system for YMV incidence. Data were subjected to analysis of variance for mean performance (Panse and Sukhatme, 1967) and combining ability analysis as per Model-I and Method -2 of Griffing (1956).

RESULTS AND DISCUSSION

The mean squares for combining ability for different traits are presented Table 1. It indicated that both gca and sca variances were highly significant for all the characters. This

indicated the importance of additive as well as non-additive genetic effects for inheritance of all traits.

The variances due to gca and sca may not give correct picture of gene action and therefore, the ratio of estimates of variance due to gca and sca were calculated. The ratio of estimates of variance due to gca to sca indicated predominance of non-additive variance for all the trait. The ratio of σ^2gca/σ^2sca was less than unity for seed yield and all other traits under study. This indicated that non-additive components play greater role in the inheritance of these characters. These results are in accordance with the findings of Masuria and Joshi (1994) and Aher and Dahat (1999).

The gca effect is controlled by fixable additive genes and the crosses involving parents with high gca will give better trasngressive segregants in later generations. Therefore, selection of parents based on gca effects would have an impact in breeding programme. Hence, both mean performance and gca effects may be taken into account for parental selection (Table 1).

However, the parent PDM-143 was found to be good general combiner for days to maturity, harvest index, 100 seed weight and YMV incidence. The parent GM-9918 exhibited significant desirable gca registered in to days to maturity and seed yield. PDM-11 displayed significant gca in seed yield, pod per plant, harvest index and YMV incidence. Hence, it may be considered as the best source of favourable genes for increasing seed yield as well as resistant against YMV. The parent GM-4 exhibited good

gca effect for most of the traits except days to maturity (Table 2). The parent GM-3 proved to be poor general combiners for most of the traits due to highly susceptibility to YMV. In respect of resistance YMV, the parental line PDM-11, PDM-14 and PDM-143 were noted good general combiners. Therefore, it would be worthwhile to use these parental lines in hybridization, aimed at getting segregants in the advance generation.

In the present study highest sca was recorded in PDM-14 x GM- 9918 (-4.59) for days to flowering, PDM-14 x GM-9918 (-3.89) for days to maturity, PDM-14 x PDM-87 (1.20) for branches per plant, PDM -11 x GM-4 (5.46) for pods per plant, PDM-11 x GM-4 (2.54) for seed yield per plant, PDM-11 x GM-9918(0.61) for 100 seed weight, PDM-143 x GM-9918 (5.49) for harvest index and PDM-87 x GM-4 (-1.70) for YMV incidence (Table 3). In the above crosses, at least one of the parents is either good or average general combiners for the respective traits. Similar view has been expressed by Sandhu *et al.* (1994) and Aher *et al.*(2001)

The perusal of data on specific combining ability revealed that nine crosses exhibited significant positive sca effect for seed yield per plant. The highest sca effect for seed yield was observed in cross PDM-11 x GM-4 (2.54) followed by PDM-143 x GM-9918 (2.45) and PDM11 x GM9918 (2.44). These cross combinations also reported significant sca effect in desire direction for branches per plant, pod per plant, harvest index, 100 seed weight and YMV incidence. This suggested the role of

Table 1 : Analysis variance (mean squares) for combining ability for different traits in mungbean

Source of variance	df	Days to flowering	Days to maturity	Branches per plant	Pod per plant	Seed yield per plant (g.)	100-seed weight (g.)	Harvest index (%)	YMV incidence
GCA	7	6.98**	27.58**	0.56**	0.81**	5.63**	0.08**	8.26**	2.72**
SCA	28	9.33**	6.48**	0.47**	10.63**	2.34**	0.18**	2.71**	0.88**
Error	70	0.26	0.42	0.02	1.16	0.09	0.06	0.03	0.17
σ^2gca/σ^2sca		0.07	0.05	0.21	0.04	0.24	0.28	0.11	0.15

* and ** indicate of significance of values at P = 0.05 and 0.01, respectively,

Table 2 : General combining ability effects of parents for different traits in mungbean

Parents	Days to flowering	Days to maturity	Branches per plant	Pod per plant	Seed yield per plant (g.)	100-seed weight (g.)	Harvest index (%)	YMV incidence
PDM-143	-1.88**	-0.27	0.17**	-0.29	-0.14	0.05*	0.93**	-0.55**
PDM-11	0.22	1.34**	0.27**	0.97**	0.69**	-0.03	2.51**	-0.25**
PDM-14	0.25	1.42**	0.06	-0.37	-0.52**	-0.15**	-0.38	-0.29*
PDM-87	0.02	1.74**	-0.18**	0.19	0.06	-0.06**	-1.08**	0.17
K-581	0.83**	-0.62**	-0.02	-0.84*	-0.26**	0.04	-1.81**	0.00
GM-4	0.31*	-3.04**	0.15**	1.84*	1.16**	0.15	1.59**	-0.09
GM-3	0.27	0.84	-0.47**	-1.16**	-1.28**	-0.02	2.19**	1.17**
GM9918	0.59**	-1.40**	0.02	0.31	0.29**	0.03	0.43	-0.15
S.E.±	0.22	0.29	0.07	0.83	0.14	0.03	0.53	0.18

* and ** indicate of significance of values at P = 0.05 and 0.01, respectively,

Table 3 : Specific combining ability effects of crosses for different traits in mungbean								
Cross	Days to flowering	Days to maturity	Branches per plant	Pod per plant	Seed yield per plant (g.)	100-seed weight (g.)	Harvest index (%)	YMV incidence
PDM14 x PDM87	-0.01	-1.05	1.20**	4.92**	1.26**	0.40**	2.67*	-0.50
PDM14 X GM9918	-4.59**	-3.89**	-0.50**	-1.49	-0.80**	-0.05	-0.39	0.49
PDM87 x GM-4	2.55**	0.62	-0.18	5.07**	0.87**	0.27**	-0.45	-1.70**
PDM11x GM-4	-3.64**	-1.18*	0.95**	5.46**	2.54**	0.49**	4.65**	-1.27**
PDM11 x GM9918	-3.53**	-2.38**	0.68**	2.69**	2.44**	0.61**	4.54**	-0.53
PDM 143 X GM9918	-0.44**	-2.89**	0.58**	2.76**	2.45**	0.33**	5.49**	-1.23**
PDM 143 X PDM14	3.68**	2.96**	0.54**	1.45	0.17	0.02	1.84	1.23**
SE± s_{IJ}	0.46	0.59	0.14	0.20	0.22	0.07	1.07	0.38
SE± s_{IJ}- s_{IK}	0.56	0.71	0.17	0.22	0.26	0.08	1.30	0.46

* and ** indicate of significance of values at P = 0.05 and 0.01, respectively,

yield attributing traits towards high yield.

The negative sca value is desirable for YMV incidence, only four crosses registered significant negative effects, suggesting that they were good cross combinations for YMV resistance. The best combination for YMV resistance was PDM- 87 x GM-4 (-1.70) followed by PDM-11 x GM-4 (-1.27) and PDM-143 x GM-9918 (-1.23)

These promising crosses of seed yield and YMV incidence with high sca involving parents with good sca can be exploited effectively by conventional breeding procedure like pedigree method. However, those crosses which involved one good combiner parent and the other medium combiners parent could be exploit through selection followed by intermating of segregnts in early generation. Also, such crosses could produce desirable trasgressive segregants, if additive genetic system was operating in good combining parent and epistatic effects also act in same direction.

Considering preponderance of non-additive component of variance for most the traits under study, mainly yield, yield components and YMV resistance, non-conventional method such bi-parental mating, *inter-se* mating, multiple crossing and recurrent selection would be more effective to break undesirable linkage selection in later generation would be more fruitful as dominance genes could be dilute due to inbreeding and additive genes could be fixed. It is difficult to go for reciprocal recurrent selection being cleistogamous nature of mungbean. Hence, *bi-parental* mating and inter-se mating are most desirable breeding methods to be used for the improvement of this crop for different traits.

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