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Combining ability for yield attributing traits in green gram (Vigna radiata (L.) Wilczek)

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Abstract

Six lines were crossed with four testers in Line \times Tester fashion to estimate the combining ability for yield and yield attributing traits in green gram. Analysis of variance revealed significant differences among crosses, lines, testers and line \times tester effect for most of the traits. Preponderance of non-additive gene effects was realized from higher values of specific combining ability compared to general combining ability. Parents *viz.*, ML-2056, TARM-2, Karjat local and TARM-1 were considered as superior parents as they recorded high per se performance with positive significant effects for grain yield per plant and other yield contributing traits. Cross combinations *viz.*, ML-2333 x TARM-1, NVL-641 x TARM-1, PUSA-1477 x TARM-1 and ML-2056 x Karjat local exhibited high per se performance with good specific combinations for grain yield per plant and other desirable traits. These cross combinations could be utilized for further amelioration of grain yield in green gram.

Keywords: Green gram, combining ability variance

Introduction

Green gram [*Vigna radiata* (L.) Wilczek] is the most important pulse crop in India. In the traditional vegetarian diet of Indian population, pulses occupy second place next to cereals and is the main source of protein, ranking after chickpea and pigeon pea. Green gram, an important seed legume having short duration (60 to 75 days) and plays vital role in meeting the quantitative and qualitative requirement of food and protein throughout the world. In India, it is grown on an area of 3.83 million hectares with a production of 1.60 million tonnes and productivity of 418 Kg/ha. In Maharashtra, green gram is cultivated on an area of 3.83 lakh hectares with the production of 0.72 lakh tonnes and the average productivity of 534.7 Kg/ha during 2015 -16 (Directorate of Economics and Statistic Ministry of Agriculture and Farmers welfare 2015-16).

The estimates of combining ability along with per se performance of genotypes in a crop improvement programme have a direct bearing upon the choice of breeding methodology to be followed and to identify the parent and crosses (Khattak *et al.*, 2004) ^[5] which, could be exploited for future breeding programme. In literature, both additive and non-additive genetic systems, controlling grain yield and yield-relating traits in green gram have been reported (Barad *et al.* (2008) ^[1]; Marappa (2008) ^[6]; Sathya and Jayamani (2011) ^[11]. Therefore, the present investigation was planned and executed to assess the nature of gene action involved and combining ability of parental genotypes for different characters utilizing Line × Tester mating design (Kempthorne, 1957) ^[4] for evolving productive varieties in green gram.

Materials and Methods

The experimental material comprised of ten parents (TARM-2, PUSA-147, NVL-641, ML-2333, PUSA-1477, ML-2056, TARM-1, PKVAKM-04, Karjat local and DGG-03) including standard check (DPLM-26), representing wide spectrum of variation were crossed in line x tester fashion to produce 24 F₁'s. The resultant 24 hybrids along with their ten parents were evaluated in Randomized Block Design with three replications at the Research farm, Department of Agricultural Botany, College of Agriculture, Dapoli during Rabi 2017-18. Each genotype was sown in two rows (20 plants) with row to row and plant to plant distance of 30 cm. The experiment was conducted under irrigated condition. Recommended agronomic and plant protection package were followed to raise healthy crop. Observations were recorded on five randomly competitive plants in parents and their hybrids for quantitative traits (days to

50% flowering, days to maturity, plant height, number of branches per plant, cluster per plant, pods per cluster, number of pods per plant, pod length (cm), number of grains per pods, 100-seed weight (gm) and grain yield per plant (gm). The mean data was analyzed to compute combining ability effect and their variance according to Kempthorne (1957)^[4].

Results and Discussion

Analysis of variance for combining ability (Table 1) showed significant differences among the crosses for all the characters except for number of branches per plant and grains per pod indicating significant variation among crosses under study. The variance due to lines showed significant differences for all the characters except for number of branches per plant, clusters per plant, pods per plant, number of grains per pod and grain yield per plant. The variance due to testers showed significant difference for 11 characters except for days to 50% flowering, number of branches per plant, clusters per plant, pods per cluster, pods per plant. Mean squares due to lines vs testers effects were non significantly different for all the characters except for days to 50% flowering, clusters per plant and pods per plant indicating specific combining ability involvement in the expression of this traits and importance of dominance or non additive variance for this minimum characters. The significant mean square of lines and testers indicated prevalence of additive variance for the yield and its components. Occurrence of both additive and non additive gene effects for yield and important yield components in green gram were reported in earlier studies by Anbumalarmathi et al. (2005) [12], Marappa et al. (2008) [6], Barad et al. (2008)^[1], Suresh (2014)^[10], Purohit et al. (2016) ^[13] and Nath *et al.* (2017) ^[14].

The gca effects reflect performance of parental lines in combination with all other lines, so parents with highest gca effects should have greater impact on the trait improvement. Among the lines, ML-2333 ranked top as it exhibited significant gca effect for clusters per plant, pods per cluster and earliness for flowering. This was followed by ML-2056 for hundred seed weight and late maturity. The PUSA-1477 for plant height and late flowering and maturity while, NVL-641 for pod length. The PUSA-1472 for late maturity while, TARM-2 has recorded non significant gca effects. The

estimates of gca effects further revealed that the parental lines showing high gca effect for all yield attributing traits. Similar results were reported by Rout et al. (2009) [8], Patil et al. $(2011)^{[7]}$ Narshimhulu *et al.* $(2014)^{[15]}$, Bhagora *et al.* $(2013)^{[2]}$ and Purohit *et al.* $(2016)^{[14]}$. Among the testers, TARM-1 was the best general combiner for most of the traits viz., grain yield per plant, branches per plant, pods per cluster, pods per plant and earliness for maturity followed by DGG-03 recorded significant gca effects for hundred seed weight, plant height and late maturity while, Karjat local for pods per plant and pod length was found to be good general combiners. Similar results were reported by Patil et al. (2011)^[7] and Narshimhulu et al. (2014)^[15] and Chuodhary et al. (2016)^[13]. Estimate of SCA effect (Table 3) revealed that none of cross combination recorded significantly desirable SCA effect for vield. Specific combining ability estimates demonstrated a very wide range of variation for all the characters. High SCA effects mostly from the dominance and interaction effects existed between the hybridizing parents. In present investigation, the cross ML-2333 x TARM-1 recorded high SCA effects and per se performance for clusters per plant and pods per plant while, the cross NVL-641 x Karjat local for pods per plant whereas, NVL-641 x TARM-1 and TARM-2 x DGG-03 for cluster per plant followed by ML-2056 x PKVAKM-04 for earliness of 50 per cent flowering. These crosses could be exploited effectively through heterosis breeding programme for getting desirable recombinants from the segregating population. These results supported by Marappa *et al.* (2008)^[6] Selvam *et al.* (2012)^[9] Bhagora *et al.* (2013)^[2], Chuodary *et al.* (2016)^[13] and Purohit *et al.* (2016) [14]

Predominance of non additive gene effects in the manifestation of all the characters was observed by higher value of specific combining ability variance than general combining ability variance except days to 50 per cent flowering, pods per cluster and pod length. The present results indicated the predominance of non additive gene action in the expression of most of the characters studied and scope for the exploitation of non additive genetic variation for the traits through heterotic breeding followed by selection at later generation.

Source of variation	d.f	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length (cm)	Grains per pod	Hundred seed weight (g)	Grain yield per plant (g)
Rep.	2	0.60	1.05	8.90	0.54	3.01	0.82	2.26	1.89	1.54	0.96	3.86
Crosses	23	6.26**	13.61**	20.60*	0.20	7.45**	0.44*	26.30**	3.51**	1.02	1.32**	12.22**
Line effect	5	17.45**	38.78**	36.82*	0.11	15.26	0.79*	28.09	4.94**	1.06	2.15**	15.32
Tester effect	3	1.05	27.82**	49.40*	0.36	4.49	0.79	58.37	13.33**	2.59*	4.56**	27.63*
Line x Tester effect	15	3.57**	2.37	9.42	0.19	5.43**	0.25	19.29**	1.07	0.69	0.40	8.10
Error	46	1.35	3.13	10.21	0.25	1.37	0.29	7.58	1.33	0.99	0.47	5.61

 Table 1: Analysis of variance of Line x Tester analysis for combining ability for eleven characters in green gram.

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

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Sr. No.	Source	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches/ Plant		Pods/ clusters	Pods/ plant	Pod length (cm)	Grains/ pod	100 seed weight (g)	Grain yield/ plant (g)
	Lines											
1.	TARM-2	-0.347	-1.369**	-1.500	0.050	-1.564**	0.006	-2.32**	-0.993**	-0.444	-0.575**	-2.046**
2.	PUSA-1472	-0.097	1.331**	-0.150	0.167	0.103	0.156	1.369	0.080	0.122	-0.317	-0.337
3.	NVL-641	-0.597	-1.336**	-0.517	-0.017	0.503	0.072	1.011	1.020**	0.322	-0.033	0.671
4.	ML-2333	-1.431**	-2.103**	-1.567	-0.083	1.469**	0.356*	1.486	0.075	0.289	0.292	1.229
5.	PUSA-1477	2.153**	2.097**	3.167**	-0.100	0.569	-0.31*	-0.847	-0.110	-0.144	0.017	0.179
6.	ML-2056	0.319	1.381**	0.567	-0.017	-1.081**	-0.278	-0.697	-0.073	-0.144	0.617**	0.304
	S.E. ±	0.32	0.44	0.99	0.12	0.32	0.14	0.76	0.29	0.26	0.19	0.66
	C.D at 5%	0.64	0.90	1.99	0.26	0.65	0.28	1.54	0.60	0.54	0.39	1.33
	C.D at 1%	0.86	1.19	2.66	0.34	0.86	0.37	2.05	0.80	0.72	0.52	1.78
					Т	esters						
7	TARM-1	-0.097	-1.675**	0.672	0.211*	0.469	0.289*	1.606*	-0.595*	0.311	-0.528*	1.549**
8	PKVAKM-04	-0.042	0.436	-1.461	-0.078	0.175	-0.044	-0.717	-0.718**	-0.50*	-0.317	-1.357*
9	Karjat Local	-0.208	-0.042	-1.239	-0.078	0.058	-0.033	1.322*	1.152**	0.278	0.311	0.321
10	DGG-03	0.347	1.281**	2.028*	-0.056	-0.703*	-0.211	-2.211**	0.161	-0.089	0.533**	-0.513
	S.E. ±	0.26	0.36	0.80	0.10	0.26	0.11	0.62	0.24	0.21	0.15	0.54
	C.D at 5%	0.53	0.73	1.63	0.21	0.53	0.23	1.26	0.49	0.44	0.32	1.09
	C.D at 1%	0.70	0.97	2.17	0.28	0.70	0.30	1.67	0.65	0.58	0.42	1.45

Table 2: Estimates of general combining ability (GCA) effects for lines and testers for yield contributing traits in green gram.

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

Table 3: Estimates of specific c	ombining ability (SCA)) effects for vield and	vield contributing characters	in 24 hybrids of green gram

N T	C C		Days to	Days to	Plant	Branches	Clusters	Pods per	Pods per		Grains		Grain	
No	5	ce	50%	maturity	height	per plant	per plant	clusters	plant	length		seed	yield/	
				flowering maturity (cm) per plant per plant clusters						-	(cm)	pod	wt. (g)	plant (g)
1.	TARM-2	х	TARM-1	0.181	-0.642	1.411	-0.361	-1.119	-0.439	-3.37*	0.136	-0.211	0.203	-2.78*
2	TARM-2 TARM-2	х	PKVAKM-04	0.458	-0.753	1.411	0.261	0.042	0.294	1.050	0.150	-0.211	-0.24	0.924
3	TARM-2 TARM-2	х	Karjat Local	-0.708	1.792*	-2.278	-0.072	-0.575	0.294	-0.156	-0.824	-0.244	0.364	-0.188
4	TARM-2 TARM-2	х	DGG-03	0.069	-0.397	-0.544	0.172	1.653*	0.083	2.478	0.228	0.856	-0.325	2.046
	PUSA -1472	х	TARM-1	-0.736	0.397	-0.339	-0.211	-1.119	0.001	-0.631	-0.377	0.830	0.011	-1.024
-	PUSA -1472	х	PKVAKM-04	-1.125	-0.586	-0.739	0.078	0.908	-0.122	2.592	-0.060	0.222	0.011	-0.518
		х	Karjat Local	0.708	-0.508	-0.428	0.078	1.092	-0.122	-2.91	0.150	0.433	-0.094	1.271
	PUSA -1472	х	DGG-03	1.153	0.703	1.506	-0.011	-0.881	0.178	0.953	0.130	-0.844	0.017	0.271
9	NVL-641	х	TARM-1	-0.236	-0.008	-0.372	0.106	1.414*	0.178	0.294	-0.104	0.089	-0.472	0.271
10	NVL-641 NVL-641	X	PKVAKM-04		0.281	-0.372	-0.206	-0.358	-0.239	-3.05	0.440	-0.033	0.550	-0.526
10	NVL-641 NVL-641	X	Karjat Local	-0.125	0.281	-0.194	0.128	-1.508*	0.017	3.311*	0.440	0.122	0.330	0.563
12	NVL-641	х	DGG-03	1.014	-0.831	1.272	-0.028	0.453	0.061	-0.556	-0.786	-0.178	-0.400	-0.704
12	ML-2333	х	TARM-1	0.264	0.158	-2.456	0.439	2.314**	0.411	4.953**	-0.139	0.122	0.036	2.110
13	ML-2333	X	PKVAKM-04	1.208	0.381	-0.056	-0.139	-1.258	0.144	-1.892	-0.815	-0.467	0.058	-0.351
15	ML-2333	X	Karjat Local	-0.292	-0.075	3.522	-0.139	0.325	-0.333	-1.631	0.628	-0.044	-0.03	-1.429
16	ML-2333	X	DGG-03	-1.181	-0.464	-1.011	-0.161	-1.381*	-0.222	-1.431	0.326	0.389	-0.058	-0.329
-	PUSA -1477	X	TARM-1	1.014	0.225	2.278	0.322	-0.253	-0.389	0.219	-0.147	-0.378	-0.189	1.026
	PUSA -1477	X	PKVAKM-04	-0.375	1.181	0.278	-0.122	-0.158	0.211	1.175	-0.210	0.233	-0.133	-1.201
	PUSA -1477	x	Karjat Local	0.125	-1.342	-2.078	-0.256	1.158	0.333	-0.297	0.593	0.522	-0.261	-1.179
	PUSA -1477	x	DGG-03	-0.764	-0.064	-0.478	0.056	-0.747	-0.156	-1.097	-0.236	-0.378	0.583	1.354
21	ML-2056	x	TARM-1	-0.486	-0.125	-0.522	-0.294	-1.236	0.244	-1.464	0.630	0.156	0.411	0.001
22	ML-2056	x	PKVAKM-04		-0.503	-0.189	0.128	0.825	-0.289	0.125	0.186	0.233	-0.300	1.674
23	ML-2056	x	Karjat Local	0.292	-0.425	1.456	0.120	-0.492	-0.033	1.686	-0.997	-0.544	-0.294	0.962
24	ML-2056	x	DGG-03	1.736**	1.053	-0.744	-0.028	0.903	0.078	-0.347	0.181	0.156	0.183	-2.638
			S.E ±	0.64	0.89	1.98	0.25	0.64	0.28	1.52	0.59	0.53	0.39	1.32
			C.D at 5%	1.28	1.79	3.99	0.51	1.29	0.57	3.08	1.20	1.08	0.79	2.68
			C.D at 1%	1.72	2.39	5.32	0.68	1.72	0.75	4.10	1.60	1.44	1.05	3.57

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

Conclusion

The present investigation revealed the importance of both additive and non additive gene effects in the inheritance for most of the polygenic traits in Mungbean. Under such situations, maximum yield can be achieved with a system that can exploit both additive and non additive gene effects simultaneously. Thus, mating of selected plants in early segregating generations could facilitate desirable gene combination in development of high yielding lines.

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