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Genetic control and character association estimates of yield and yoeld attributing traits in some mungbean genotypes

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ABSTRACT

A field experiment was conducted to evaluate the genetic variability and character association on 27 genotypes of greengram (Vigna radiata L.) at Instructional Farm Jaguli, Bidhan Chandra Krishi Viswavidyalaya during 2012 and 2013.The experiment was laid out in Randomized Block Design with two replications. Analysis of variance revealed significant differences among genotypes for all the eleven characters which provides enough scope for significant improvement of the traits through selection. Marginal difference between GCV and PCV was observed predicting least environmental influence. High heritability accompanied by high genetic advance was observed for seed yield plant $^{-1}$ followed by 100 seed weight, number of branches plant $^{-1}$ and number of pods plant $^{-1}$ indicating importance of additive gene effects which may facilitate the adoption of simple breeding strategies to obtain desirable changes with respect to these characters. Seed yield plant^{-1} had shown significant positive correlation with number of pods plant^{-1},100 seed weight and positive correlation with pod width, protein content which also exerted positive direct effect on yield.

Keywords: Greengram, GCV, PCV

Green gram also known as mungbean is the third most important pulse crop in India covering an area of 34.4 lakh hectare with a total production of 14 lakh tonnes and the average productivity of 406.98 kg ha^{-1} (ZPDK, 2011). India is the largest producer and consumer of pulses in the world accounting for 33 per cent of world area and 25 per cent of world production (FAOSTAT 2007). At present, the total area under pulses is 23.63 million hectare with a total production of 17.29 million tonnes (ICAR, 2011-12). However, its production in India in 2011-12 crop year has fallen by 5.3 per cent to 17.28 tonnes in addition to its consumption of 30 per cent of the world pulse production with 2-3 million tonnes from its own production as reported by trade officials. Thus, there is a need to increase the production and productivity by more intensive interventions. Important green gram growing states in India include Odisha, Andhra Pradesh, Maharashtra, Karnataka and Bihar. Green gram seeds 25%-28% protein, 1-1.5% oil, 3.5-4.5% ash and 52-65% carbohydrates. High lysine content makes its protein an excellent complement to rice in terms of balanced human nutrition. Though an important pulse crop of India the average yield of greengram is low owing to low genetic yield potentiality, indeterminate growth habit, canopy architecture, low partitioning efficiency, cultivation in marginal land and also for many other biotic and abiotic stresses. The growing knowledge on the importance of pulses in our diet has driven us to make numerous efforts for increase in production of pulses in the country where much concentration and efforts was given on improvement of cereals which so long dominated the agricultural sector. In this context, the present investigation was undertaken to evaluate mungbean genotypes for yield and its attributing traits along with protein content to identify desirable genotypes to be utilised in combination breeding.

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MATERIALS AND METHODS

The experiment was conducted on 27 mungbean genotypes (Sonali, Kopergaon , WBM-220, Hum-12, PS-16, K-851, Malda-95-13, WBM-4131, Pusa Visal, WBM-659, Sublobata-2, Basanti, Samrat, TM-99-50, Tarm-2, TM-99-37, Sublobata-14, TM-99-21, Pant Mung-2, TM-99-30, Midnapur Local, WBM-314, Bireswar, WBM04-05, WBM-611-3, TM-98-50, PDM-54) at the Instructional Farm Jaguli, BCKV., Mohanpur during *kharif* 2012-13, following Randomized Block Design with two replications. The row to row distance was 30 cm. Standard Package of practices were followed for raising and maintenance of the plants. Five plants were selected at random from each entry in each replication for recording data. The different characters considered included plant height (cm), days to 50% flowering, days to maturity, number of branches plant $^{-1}$, number of pods per plant, number of seed pod^{-1}, pod length (cm), pod width (mm), hundred seed weight (g), seed yield plant $^{-1}$ and Protein content. Protein estimation was carried out using Lowry's method. Genotypic coefficients of

Table1: ANOVA for different characters and yield in twenty seven mungbean genotypes

Sl. No.	Characters	Source of Variation			
		Replication	Treatment	Error	CD
1	Days to 50% flowering	4.1693	5.5514**	0.705	1.726
2	No.of days to maturity	15.5752	12.8690**	0.151	0.799
3	Plant height	0.0220	152.5445**	0.091	0.620
4	No. of branch/plant	0.0015	1.4398**	0.012	0.229
5	No. of pods/plant	0.0584	29.0048**	0.063	0.518
6	No. of seeds/pod	0.0057	3.1236**	0.016	0.267
7	Pod length	0.0537	0.6527**	0.034	0.384
8	Pod width	0.0000	0.0032**	0.000	0.013
9	100 seed weight	0.0803	1.7280**	0.006	0.167
10	Protein content	0.0109	7.1551**	0.049	0.457
11	Seed yield/plant	0.033	12.7779**	0.032	0.371

*** Significant at 1% level*

Table 2: Mean, range and other genetic parameters in mungbean

Sl.No	Characters	Range		Mean	SED	Variances		CV	GCV	PCV	H^2	GA	GA
		Min.	Max.			PV	GV						(% of mean)
1	Days to 50% flowering	46.530	53.500	48.944	0.840	3.128	2.423	1.716	3.180	3.613	77.46	4.991	5.766
2	No. of days to maturity	73.500	82.500	77.130	0.389	6.510	6.359	0.504	3.269	3.308	97.68	13.099	6.656
3	Plant height (cm)	34.006	68.441	50.794	0.302	76.318	76.227	0.594	17.188	17.198	99.88	157.026	35.387
4	No. of branches/plant	2.25	5.550	3.276	0.112	0.726	0.714	3.399	25.787	26.011	98.29	1.469	52.665
5	No. of pods plant^{-1}	13.20	28.005	18.709	0.252	14.534	14.471	1.347	20.332	20.376	99.56	29.808	41.793
6	No. of seeds pod^{-1}	7.850	12.450	10.287	0.130	1.570	1.553	1.264	12.115	12.181	98.92	3.199	24.823
7	Pod length (cm)	5.603	8.352	6.591	0.187	0.344	0.309	2.834	8.432	8.896	89.85	0.636	16.465
8	Pod width(cm)	0.307	0.467	0.386	0.006	0.002	0.002	0.000	10.345	10.474	97.56	0.004	21.050
9	100 seed weight (g)	2.174	5.611	3.282	0.081	0.867	0.861	2.475	28.268	28.376	99.24	1.772	58.010
10	Protein content (%)	18.040	25.025	20.825	0.223	3.602	3.553	1.068	9.051	9.114	98.62	7.317	18.516
11	Seed yield plant^{-1} (g)	3.292	14.320	6.841	0.181	6.405	6.373	2.639	36.900	36.994	99.49	13.127	75.820

Table 3: Mean of eleven characters of twenty seven genotypes in mungbean (*Vigna radiata* L. Wilczek)

Sl. No	Genotype	Days to 50% flowering	No. of days to maturity	Plant height (cm)	No. of branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	Pod length (cm)	Pod width (cm)	100 seed weight(g)	Protein content (%)	Seed yield plant^{-1} (g)
1	Sonali	48.500	75.500	59.140	2.950	21.000	10.700	6.901	0.307	2.297	18.040	6.665
2	Kopergaon	48.000	76.500	53.370	2.250	21.350	10.150	6.571	0.420	3.263	23.440	7.422
3	WBM-220	47.500	75.500	45.887	2.750	16.000	8.350	6.201	0.405	2.618	22.015	4.457
4	Hum-12	49.500	77.500	42.006	2.300	17.100	9.150	6.403	0.424	4.056	20.050	7.384
5	PS-16	47.000	75.500	57.025	4.000	14.950	11.200	6.852	0.336	2.607	20.035	8.607
6	K-851	53.500	82.500	57.975	3.250	21.450	11.150	6.552	0.418	3.682	19.680	9.700
7	Malda-95-13	52.500	82.000	54.221	4.250	18.550	11.250	7.061	0.395	3.704	22.320	5.767
8	WBM-4151	51.000	74.500	46.994	4.250	16.950	9.750	6.266	0.328	2.716	19.015	4.791
9	Pusa Visal	50.500	74.500	55.153	3.350	16.950	9.950	6.157	0.327	2.338	20.060	4.962
10	WBM-659	49.500	79.500	44.120	2.250	16.500	9.850	5.603	0.427	2.174	19.920	5.688
11	Sublobata-2	49.000	79.000	64.095	5.350	17.050	8.850	6.250	0.350	2.378	19.025	5.007
12	Basanti	49.500	76.500	58.030	3.250	17.600	10.650	6.401	0.407	3.862	21.595	5.391
13	Samrat	48.500	75.500	34.006	2.550	28.000	12.350	7.050	0.421	4.959	23.500	14.320
14	TM-99-50	47.000	73.500	35.091	2.700	27.250	11.700	6.266	0.410	4.472	21.995	10.479
15	Tarm-2	47.500	74.500	55.445	3.600	25.450	12.450	7.210	0.389	4.664	24.885	9.962
16	TM-99-37	48.500	76.500	60.395	3.400	20.100	9.950	6.903	0.359	3.589	20.385	5.276
17	Sublobata-14	48.500	76.500	68.441	5.550	18.000	8.950	5.957	0.373	2.283	19.810	4.175
18	TM-99-21	46.500	76.000	56.078	3.250	17.050	10.650	6.168	0.359	2.181	20.405	4.307
19	Pant mung-2	48.500	76.500	45.072	3.200	15.300	9.950	7.504	0.399	3.663	19.895	6.294
20	TM-99-30	48.500	76.500	60.030	3.250	16.550	11.450	6.807	0.369	3.152	19.340	5.958
21	Midnapur local	49.000	78.500	47.805	3.450	20.000	10.600	5.693	0.396	2.603	20.270	7.120
22	WBM-314	47.500	74.500	47.475	2.400	17.650	10.250	6.836	0.422	3.688	21.480	9.227
23	Bireswar	47.000	74.500	40.040	2.600	24.200	8.000	6.406	0.467	5.611	25.025	10.105
24	WBM-04-05	49.000	79.500	43.987	2.300	13.200	7.850	6.647	0.439	3.877	19.055	7.605
25	WMB-611-3	50.000	81.500	41.943	3.000	15.900	12.000	8.352	0.375	2.997	23.160	6.582
26	TM-98-50	51.000	81.000	45.048	3.450	16.050	9.450	6.159	0.370	2.512	19.195	3.292
27	Pdm-54	48.500	78.500	52.575	3.550	15.000	11.150	6.782	0.321	2.663	18.675	4.166
	Grand mean	**48.500**	**77.130**	**50.794**	**3.276**	**18.709**	**10.287**	**6.591**	**0.386**	**3.282**	**20.825**	**6.841**
	CV	**1.716**	**0.504**	**0.594**	**3.399**	**1.347**	**1.264**	**2.234**	**0.000**	**2.475**	**1.068**	**2.639**
	SEm (±)	**0.840**	**0.389**	**0.302**	**0.112**	**0.252**	**0.130**	**0.187**	**0.006**	**0.081**	**0.223**	**0.181**
	LSD(0.05)	**1.726**	**0.799**	**0.620**	**0.229**	**0.518**	**0.267**	**0.384**	**0.013**	**0.167**	**0.457**	**0.371**

Table 4: Genotypic and Phenotypic correlation among the eleven characters of mungbean (*Vigna radiata* L.Wilczek)

Characters		Days to maturity	Plant height (cm)	No. of branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	Pod length (cm)	Pod width (cm)	100 seed weight(g)	Protein content (%)	Seed yield plant^{-1} (g)
Days to 50% flowering	**G**	0.742**	0.102	0.220	-0.198	0.046	0.024	-0.064	-0.144	-0.303	-0.214
	P	0.666*	0.093	0.186	-0.168	0.054	0.007	-0.064	-0.126	-0.253	-0.189
No. of days to maturity	**G**		0.075	0.119	-0.359	0.005	0.126	0.095	-0.219	-0.235	-0.254
	P		0.074	0.119	-0.353	0.006	0.122	0.093	-0.217	-0.235	-0.250
Plant height(cm)	**G**			0.660*	-0.258	-0.009	0.109	-0.529	-0.480	-0.369	-0.476
	P			0.655*	-0.257	-0.009	0.100	-0.522	-0.477	-0.368	-0.474
No. of branches/plant	**G**				-0.178	-0.020	0.109	-0.555	-0.398	-0.294	-0.421
	P				-0.176	-0.013	0.098	-0.541	-0.389	-0.291	-0.415
No.of pods/plant	**G**					0.412	0.032	0.305	0.634*	0.608*	0.733**
	P					0.409	0.024	0.305	0.629*	0.602*	0.731*
No.of seeds/pod	**G**						0.488	-0.236	0.134	0.247	0.387
	P						0.465	-0.227	0.135	0.248	0.387
Pod length(cm)	**G**							-0.074	0.331	0.318	0.280
	P							-0.073	0.319	0.299	0.266
Pod width (cm)	**G**								0.671*	0.562	0.515
	P								0.661*	0.549	0.510
100 seed weight(g)	**G**									0.678*	0.757**
	P									0.670*	0.751*
Protein content(%)	**G**										0.556
	P										0.551

significant at 5% level of significance* * significant at 1% level of significance*

Table 5: Path coefficient analysis at genotypic level of eleven characters in (*Vigna radiata* L. Wilczek)

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	Pod length (cm)	Pod width (cm)	100 seed weight(g)	Protein content (%)	Seed yield plant^{-1} (g)
Days to 50% flowering	**-0.05890**	-0.14969	-0.01333	0.01837	-0.10770	0.01157	0.00786	-0.03988	-0.00755	0.12519	-0.214
No. of days to maturity	-0.04370	**-0.20175**	-0.00973	0.00995	-0.19518	0.00129	0.04053	0.05911	-0.01149	0.09696	-0.254
Plant height(cm)	-0.00602	-0.01505	**-0.13038**	0.05513	-0.14036	-0.00238	-0.03518	-0.32897	-0.02519	0.15267	-0.476
No. of branches/plant	-0.01295	-0.02405	-0.08609	**0.08349**	-0.09672	-0.00497	-0.03517	-0.34512	-0.02089	0.12167	-0.421
No. of pods/plant	0.01165	0.07234	0.03362	-0.01483	**0.54438**	0.10351	0.01034	-0.18974	0.03331	-0.25133	0.733
No.of seeds/pod	-0.00271	-0.00104	0.00123	-0.00165	0.22404	**0.25152**	0.15678	-0.14638	0.00703	-0.10210	0.387
Pod length (cm)	-0.00144	-0.02543	0.01426	-0.00913	0.01750	0.12262	**0.32159**	-0.04620	0.01738	-0.13156	0.280
Pod width (cm)	0.00378	-0.01919	0.06901	-0.04636	0.16619	-0.05924	-0.02390	**0.62153**	0.03520	-0.23225	0.515
100 seed weight(g)	0.00847	0.04417	0.06255	-0.03321	0.34533	0.03369	0.10645	0.41674	**0.05250**	-0.28011	0.757
Protein content (%)	0.01784	0.04733	0.04816	-0.02458	0.3310303	0.06213	0.10237	0.34935	0.03558	**-0.41331**	0.556

Residual effect: 0.439

variation (GCV) and Phenotypic coefficients of variation (PCV) were calculated by the formulae given by Burton, 1952. The percentage of heritability (H) was estimated by the formula suggested by Hanson *et al.,* 1956.The expected genetic advance (GA) as percentage of mean and phenotypic and genotypic correlation coefficients was computed according to the formula suggested by Johnson *et al.,* 1995.

RESULTS AND DISCUSSION

Analysis of variance (Table 1) revealed significant differences among genotype for all the eleven characters studied in the present investigation which provide enough scope for significant improvement on the traits through selection (Khairner *et al*., 2003, Siddique *et al*., 2006, Rao *et al*., 2006). Table 2 depicted the estimated value on genetic parameters like PCV, GCV, heritability, genetic advance etc. where PCV was found to be marginally higher than GCV. The characters like number of days to 50 % flowering, number of branches plant^{-1}and pod length showed wider differences between GCV and PCV which might be due to higher environmental influence on these characters. Higher genetic advance was observed in plant height, number of branches plant$^{-1,}$ number of pods plant^{-1}, 100 seed weight and seed yield plant^{-1}and the characters are predominantly influenced by additive genes. Characters such as number of days to 50% flowering, number of days to maturity, number of seeds pods^{-1}, pod length, pod width and protein content showed lower genetic advance which suggested that the clusters of characters are governed predominantly by non-additive gene action, Vikas *et al*., (1998). The genotypic and phenotypic correlation coefficients among eleven characters are presented in table 3. Number of days to 50 % flowering showed positive significant correlation at both the phenotypic and genotypic levels with number of days to maturity. Plant height also showed significant positive correlation with number of branches^{-1}. Number of pods plant^{-1} exhibited significant positive correlation with 100 seed weight, protein content and seed yield^{-1} at genotypic and phenotypic levels. Pod width was also found to have significant positive correlation at both the levels with 100 seed weight. The character 100 seed weight exhibited significant positive correlation with protein content and seed yield plant^{-1}. Selection for pods plant $^{-1}$ has frequently been regarded as important for seed yield production of mungbean by various authors like (Makeen *et al*., 2007, Gul *et al*., 2008, Hakim *et al*., 2008, Tabasum *et al*., 2010). The direct and indirect effects of different characters on the yield are presented in Table 4. Residual effect was low (0.4) indicating the number of characters chosen for the study was sufficient for yield determination in mungbean. Pod weight imparted the highest direct effect on yield plant^{-1} followed by number of pods plant^{-1}, pod length, number of seeds pod^{-1}, number of branches plant^{-1} and 100 seed weight. Number of pods plant^{-1} and 100 seed weight had significantly positive relation with yield plant^{-1}. Therefore, direct selection through this trait would be effective to improve yield potential of a genotype. On the basis of path analysis studied number of pods plant^{-1} and 100 seed weight were found to be the most important attributable components for yield improvement (Kausendra *et al*., 1995, Rahim *et al*., 2010) also reported similar findings.

Thus, from the above study it could be inferred that the genotypes *Samrat, Bireswar, Tarm-2 and TM-99-50* identified as superior with respect to yield along with a number of yield attributing traits and high protein content in the first three genotypes and earliness in the last genotype could be employed to develop early maturing protein rich high yielding lines. Also seed yield plant^{-1} which had shown significant positive correlation with number of pods plant^{-1}, 100 seed weight and positive correlation with pod width, protein content which also exerted positive direct effect on yield except protein content may provide simultaneous improvement in yield, number of yield related characters and protein content.

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