

Regular Article

Genetic variability and association studies for root infection to *Piriformospora indica*, nodulation, yield and its contributing traits in mungbean [*Vigna radiata* (L.) Wilczek]

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A study was carried out in mungbean to estimate the nature and magnitude of genetic parameters for root infection to *Piriformospora indica*, nodulation, N and P uptake, seed yield and yield components. PCV was higher than GCV for all the characters indicating influence of environmental factors on their expression. High heritability accompanied with high genetic advance was observed for 100-seed weight, seed yield, plant height, pods/plant, branches/plant and N and P content in seeds. Seed yield exhibited positive correlation with pods/plant, branches/plant, 100-seed weight, nodules/plant, nodules dry weight, N content in shoot and seeds, P content in seeds and *P. indica* infection in roots. Nodulation exhibited positive correlation with nodules dry weight, shoot dry weight, N content in shoot and seeds, P content in seeds and seed yield. Number of pods/plant exerted the maximum positive direct effect on seed yield followed number of nodules/plant and number of branches/plant.

Key words: correlations, mungbean, nodulation, path coefficients, *Piriformospora indica*

Mungbean [*Vigna radiata* (L.) Wilczek], also known as green gram, is an important pulse crop of *kharif* season in India. Now it is also grown during spring/summer season in northern parts and during *rabi* season in southern parts of India. Being a short duration crop, it fits well into the intensive rice-wheat cropping system of Indo-Gangetic plains of India. It can also be grown as intercrop with sugarcane, pigeonpea, poplar and orchards. Thus, there is a great scope for increasing area and production of summer mungbean. It is nutritionally as well as economically very important to vegetarians and poor population of the country to whom it is a major source of protein.

Biological nitrogen fixation is an important aspect of sustainable and

environment friendly agriculture and role of pulses in this context hardly need any emphasis. Legumes, besides helping in maintaining the soil fertility through biological nitrogen fixation, are major source of protein for human consumption and provide high quality crop residue for animal feed. It complements the deficiency of lysine in cereals and their combinations have shown higher biological values. Rhizobia have shown to increase root and shoot weight, plant vigor, nitrogen fixation and seeds yield in various legumes (Yadegari *et al.*, 2008).

Studies have also been conducted on co-inoculation of *Rhizobium* with other microbes and have shown very encouraging results. Significant effect of *Rhizobium* and Vesicular-arbuscular

mycorrhizal (VAM) fungi on nodulation, yield parameters, yield, NPK content in seeds and straw and the crude protein content in seeds of mungbean was reported (Bhat *et al.*, 2010). Substantial evidence has accumulated in recent years about how rational use of these microsymbionts could significantly contribute to decreasing use of fertilizer in agriculture if combined with other beneficial soil microorganism. VAM fungi perform many different functions such as mineral solubilization, uptake and abiotic stress resistance. However, VAM cannot be cultivated under laboratory conditions. Alternatively, a novel plant growth promoting, root colonizing endophytic fungus, *Piriformospora indica* isolated from orchid plants in the Thar desert in India, are able to grow axenically on a variety of simple and complex media and mimics most of the beneficial characteristics of VAM fungi. This fungus functions as a plant growth promoter and biofertilizer in nutrient deficient soils, as a bioprotector against biotic and abiotic stresses including root and leaf fungal pathogens and insect invaders and as a bioregulator for plant growth development and as a bio-agent for the hardening of tissue culture raised plants (Varma *et al.*, 2009).

Yield is the most important and complex trait governed by polygenes and influenced by many physiological processes within the plant and is highly affected by environment. Availability of genetic variability for yield and component trait is a major asset for initiating any fruitful crop improvement programme. Information on genetic variability and heritability is useful to formulate selection criteria for improvement of seed yield. Since mungbean is primarily grown under rainfed conditions, yield stability is a major problem, which can be overcome by better understanding of the component traits contributing to final yield. Study of inheritance of these traits through estimation of different genetic parameters will be helpful in formulation of an effective breeding programme. During last two

decades considerable amount of knowledge has been generated with regard to yield and component traits, however, very few studies have been made with regard to co-inoculation of *Rhizobium* and *P. indica*. Combined inoculation of *Rhizobium* and *P. indica* has been reported to increase the nodulation, dry matter content, seed yield and nitrogen (N) and phosphorus (P) uptake significantly over the uninoculated control in many crops. However, no study has been reported on genotypic variability for response to these microbial inoculants in mungbean. Thus, present investigation was undertaken to assess the magnitude of phenotypic and genotypic variability, correlation and path coefficients so that the results may be utilized in future breeding programmes for development of superior genotypes of mungbean.

Material and Methods

The present study was conducted at Pulses Research Area of Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar during *khari* 2013-14. The experimental material consisting of 10 mungbean genotypes *viz.*, Basanti, IPM-02-3, MH-318, MH-810, MH-721, MH-560, MH-805, Sattya, MH-421 and COGG-912 were grown in RBD Factorial with three replications. These genotypes were grown in four rows of 4m length each. Row to row spacing was kept at 30 cm and plant to plant at about 10 cm. The initial and final N and P status of the soil was analyzed. The mungbean rhizobial strain MB-703 and fungus *Piriformospora indica* procured from the Department of Microbiology, CCS Haryana Agricultural University, Hisar, were used to inoculate the seeds of the above mentioned genotypes and four microbial treatments [Mungbean rhizobial strain- MB-703, *P. indica*, Mungbean rhizobial strain MB-703 + *P. indica* and Control (Uninoculated)] were applied through seed treatment.

Observations were recorded on days to 50% flowering, days to maturity and seed yield on plot basis. Five randomly selected plants from every plot in each

replication were used to record number of nodules/per plant, dry weight of nodules/plant, nitrogen and phosphorous content in shoot and seeds, plant height, number of branches/plant, number of pods/plant, number of seeds/ pod, 100-seed weight, dry weight of shoot/plant and per cent root infection of *P. indica*. N and P contents were determined following standard methods. *P. indica* infection in roots was recorded on five random plants uprooted 55 days after sowing with intact roots. The roots of these were stained with trypan blue dye and their per cent *P. indica* infection was recorded using Phillips and Hayman (1970) method.

Genotypic and phenotypic coefficients of variation were estimated based on the estimates of genotypic and phenotypic variances. Heritability in broad sense was calculated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage. Genetic advance and genetic advance as percentage over mean was worked out by adopting the formula given by Johnson *et al.* (1955). The phenotypic and genotypic correlation coefficients were estimated as per Al-Jibouri *et al.* (1958). Path coefficient analysis was carried out as per method of Dewey and Lu (1959).

Results and Discussion

Assessment of genetic variability is the first step in any breeding programme and the progress depends on the extent of genetic variability present for various biometric characters. It is also crucial for any breeding programme as it provides an opportunity for selection of desirable genotypes. In the present study, analysis of variance revealed significant genotypic differences for all the sixteen characters studied indicating presence of considerable amount of variability and thus justifying the use of material. This implied that there is ample scope for selecting superior and desirable genotypes to achieve the ultimate goal. This was in agreement with the findings of Aziz *et al.* (2010) and Narasimhulu *et al.* (2013). Microbial

treatments differed significantly for plant height, number of pods/plant, 100-seed weight, number of nodules/plant, nodules dry weight/plant, shoot dry weight/plant, N and P content in shoot and seeds, *P. indica* infection in roots and for seed yield whereas, non significant differences were observed for days to 50% flowering, days to maturity, branches/plant and number of seeds/pod. Interaction between genotypes and microbial treatments was found significant for plant height, number of pods/plant, 100 seed weight, number of nodules/plant, nodules dry weight/plant, N and P content in shoot and seeds, *P. indica* infection in roots and for seed yield meaning thereby that the genotypes interacted differently with different microbial treatments.

As most of the traits of economic importance are polygenic in nature and are highly influenced by environment, therefore, it becomes difficult to judge whether the observed variability is due to environment or has genetic basis. Hence, it becomes imperative to partition the phenotypic variation into its heritable and non-heritable components. A bird eye view of the data (Table 1) revealed wide differences between phenotypic (PCV) and genotypic (GCV) coefficient of variance in traits like days to 50% flowering, days to maturity, number of branches/plant, number of seeds/pod and shoot dry weight, which indicated their susceptibility to environmental fluctuations than other characters with narrow differences. Further, the PCV was higher than their respective GCV for all the characters indicating influence of environmental factors on their expression. The genotypic coefficient of variation ranged from 2.21 to 112.78%. Moderate to high estimates of GCV and PCV estimates were observed for P content in shoot, seed yield, 100-seed weight, number of nodules/plant, plant height, nodules dry weight, number of branches/plant and number of pods/per plant which indicated greater amount of genetic variability among the genotypes prevailed thereby confirming earlier reports

by Rao *et al.* (2006), Khedar *et al.* (2006), Singh *et al.* (2009) and Narasimhulu *et al.* (2013). Low GCV and PCV were observed for days to 50% flowering, days to maturity, number of seeds/pod and shoot dry weight which were also reported earlier by Venkateshwarlu *et al.* (2001), Khedar *et al.* (2006), Singh *et al.* (2009) and Reddy *et al.* (2013).

The coefficient of variation indicates only the extent of variability present does not indicate the heritable portion which could be ascertained from heritability estimates. Heritability in broad sense, as it includes both additive and non-additive gene effects, shall be reliable only if accompanied by high genetic advance. High heritability together with high genetic advance is an indication of additive genetic effects and improvement of these quantitative characters is possible in subsequent generations. In the present investigation high heritability (broad sense) estimates accompanied with high genetic advance were observed for 100-seeds weight, seed yield/plant, plant height, number of pods/plant, number of branches/plant, N and P content in seeds. Similar results were reported by Rao *et al.* (2006), Wani *et al.* (2007), Singh *et al.* (2009) and Narasimhulu *et al.* (2013) in mungbean. Low estimates of heritability with low genetic advance were observed for number of seeds/pod and shoot dry weight meaning thereby that these have high component of non-heritable variance verifying results reported by Gupta *et al.* (2004) for seed yield and direct selection will be ineffective.

Maximization of yield is major objective in all the crops. There are many traits which individually or in combination affect the seed yield in mungbean. Seed yield is a complex character and considering it as unitary character appears to be faulty. Seed yield can be viewed as the end product of component characters like number of pods per plant, number of seeds/pod, 100-seed weight, number of nodules/plant and nodules dry weight as these characters tend to show inter

relationship. Infection of *Rhizobium* and other micro-organisms along with their interaction is of paramount importance in deciding the ultimate yield in mungbean. They are not only plant species specific but also interact differently with different genotypes of a same species. These inoculants are promising biofertilizer as they are cheap, easy to handle and improves plant growth.

Although increase in biomass can lead to increase in economic yield, in practice that is not always so and increase in biomass can occur without this. It is, therefore, necessary to examine the main traits which might be of use to breeders in relation to crop processes and yield characteristics which they are most likely to affect. An understanding of inter-character genotypic and phenotypic correlations is essential to evaluate the possibility of simultaneous improvement of many characters and more so as selection for one trait may affect the other related traits in both the directions.

In the present study, genotypic correlation coefficients were found to be higher than their corresponding phenotypic correlation coefficients (Table 2) indicating inherent association among different characters and selection based on the phenotype will be effective. Similar results were earlier reported by Tabasum *et al.* (2010) and Degefa *et al.* (2014) in mungbean. Seed yield exhibited positive correlation with number of branches/plant, number of pods/plant, 100-seed weight, number of nodules/plant, nodules dry weight, N content in shoot and seeds, P content in seeds and *P. indica* infection in roots. Positive correlation of seed yield have been earlier reported with number of pods/plant, number of seeds/pod, 100-seed weight, number of branches/plant and plant height (Rao *et al.*, 2006; Wani *et al.*, 2007 and Tabasum *et al.*, 2010). However, seed yield showed significant negative correlation with days to 50% flowering which is in concurrence with the results reported by Tabasum *et al.* (2010) and Degefa *et al.* (2014) in mungbean.

Table 1: Estimates of GCV, PCV, heritability and genetic advance for different characters in mungbean

Sr. No.	Characters	Range	GCV (%)	PCV (%)	h ² (bs)	GA % mean
1.	Days 50% flowering	36.09 - 40.74	3.98	5.25	57.50	6.22
2.	Days to maturity	62.61-73.58	2.21	3.037	52.85	3.31
3.	Plant height (cm)	54.68- 78.76	12.11	12.33	96.42	24.48
4.	Number of branches per plant	1.68- 2.66	14.97	20.54	53.13	22.48
5.	Number of pods per plant	15.16- 27.58	14.26	15.67	82.80	26.73
6.	Number of seed per pod	11- 12.42	3.26	8.29	15.47	2.64
7.	100-seed weight (g)	3.45-4.62	10.77	11.67	85.04	20.45
8.	Number of nodules per plant	18.41- 35.83	19.60	20.59	90.57	38.42
9.	Nodules dry weight (mg)	203.24- 365.26	15.59	15.91	95.92	31.45
10.	Shoot dry weight (g)	10.25-12.05	5.11	11.75	18.90	4.57
11.	N-content in shoot (%)	2.29- 3.10	14.87	15.17	96.00	30.01
12.	P- content in shoot (%)	0.15-0.21	21.52	24.76	75.53	38.53
13.	N-content in seed (%)	2.25-3.60	13.83	13.99	97.80	28.18
14.	P- content in seed (%)	0.20-0.25	17.59	19.16	84.28	33.26
15.	<i>P. indica</i> infection in roots (%)	13.67-83.34	112.78	112.86	99.87	232.18
16.	Seed yield per plot (g)	193.67- 404.42	18.08	19.69	84.28	34.18

Positive genotypic and phenotypic correlation of 100-seed weight with number of nodules/plant, nodules dry weight, N and P content in seeds, *P. indica* infection in root and seed yield were observed and it had negative association with days to 50% flowering, plant height and seeds per pod. Positive association of 100-seed weight with harvest index and seed yield was also reported by Narasimhulu *et al.* (2013) and Lalinia *et al.* (2014) and negative correlation with plant height, branches per plant, pods per plant, clusters per plant, seeds per pod and biological yield by Gul *et al.* (2008). Significant positive genotypic and phenotypic correlation of number of seeds/pod with number of nodules/plant, nodules dry weight, P content in shoot and *P. indica* infection in root and significant negative correlation with branches per plant and 100 seed weight were observed in this study.

Nodulation exhibited positive correlation with nodules dry weight, shoot dry weight, N content in shoot and seeds, P content in seeds and seed yield. Similar results have also been reported by Das and Bandyopadhyay (2011). Nitrogen N content in shoot and seeds exhibited positive association with number of pods/plant, 100-seed weight, number of nodules/plant, nodules dry weight, shoot dry weight and seed yield verifying earlier report by Rosario *et al.* (1997). They found that the proportion of the N in the plant contributed by fixation was highly correlated with plant vigor, plant height, shoot dry weight and seed yield.

P. indica infection in roots exhibited positive relationship with plant height, pods per plant, number of seeds/pod, 100-seed weight, P content in shoot and seeds and seed yield. Also, P content in seeds showed significant positive genotypic and phenotypic correlation with days to

maturity, 100-seed weight, number of nodules/plant, nodules dry weight, P content in shoot, *P. indica* infection in root and seed yield and negative association with days to 50% flowering. P content in shoot showed significant positive genotypic and phenotypic correlation with plant height, seeds per pod, P content in seeds and *P. indica* infection in root. Very less work has been done on *P. indica* and P in mungbean and such studies could not be traced in the literature. Days to 50% flowering showed negative significant correlation with 100-seeds weight, number of nodules per plant, nodules dry weight, N content in shoot and seeds, P content in seeds and seed yield. Similar results were envisaged by Yucel *et al.* (2006). Days to maturity indicated positive and significant correlation with nodules dry weight and P content in seeds. Similar results have been reported for days to 50% flowering and plant height by Srivastava and Singh (2012). However, negative correlation with number of pods per plant as earlier reported by Srivastava and Singh (2012) and Degefa *et al.* (2014) for seed yield, number of pods/plant, pod length and 100-seed weight.

Seed yield was taken as dependent variable while computing the path coefficient. Number of pods/plant exerted the maximum positive direct effect on seed yield followed number of nodules per plant and number of branches per plant (Table 3). Thus, selection pressure on these traits may lead to an overall increase in seed yield. On the contrary, days to maturity showed maximum negative direct effect on seed yield followed by plant height and 100-seed weight. High positive indirect effect of number of nodules/plant through number of pods/plant was the main cause of positive and significant association with seed yield. Path coefficient analysis revealed the importance of characters such as number of branches, number of nodules/plant and number of pods/plant in selection of superior genotypes for seed yield. Highly significant positive correlation of number of pods/plant, number of

nodules/plant and number of branches per plant with seed yield and their positive direct effect on seed yield indicated true and perfect relationship between them suggesting that direct selection for these traits will be rewarding. Lower residual effect (0.176) revealed that all the traits under study accounted for 82.4% of variability towards seed yield. These results were in partial agreement with earlier findings of Venkateswarlu (2001), Tabasum *et al.* (2010), Yucel *et al.* (2006), Srivastava and Singh (2012) and Garje *et al.* (2014). Therefore, it can be concluded that emphasis should be on number of pods/plant, number of nodules/plant and number of branches per plant for obtaining desired improvement in seed yield.

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Table 2: Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for different characters in mungbean

Characters	DF	DM	PH	BP	PP	SP	100 SW	NP	NW	SW	NS	PS	NG	PG	PI	SY
DF	1.000	0.161	-0.067	0.091	-0.148	-0.262	-0.202	-0.473	-0.565	-0.562	-0.277	-0.184	-0.387	-0.357	-0.149	-0.447
DM	-0.109	1.000	-0.060	0.225	-0.231	-0.526	0.158	0.125	0.250	-0.152	0.246	0.026	-0.008	0.280	-0.073	-0.030
PH	-0.027	-0.025	1.000	-0.414	0.236	0.866	-0.327	0.229	0.411	0.508	0.546	0.359	0.413	0.070	0.230	0.112
BP	0.036	0.113	-0.304**	1.000	0.262	-0.930	0.688	-0.230	-0.062	-0.415	-0.019	-0.173	0.088	-0.054	0.068	0.405
PP	-0.044	-0.181*	0.125	0.204*	1.000	-0.023	0.498	0.365	0.354	0.042	0.293	0.101	0.409	0.200	0.261	0.832
SP	-0.066	-0.051	0.138	-0.322**	-0.011	1.000	-0.683	0.442	0.542	0.563	0.050	0.555	0.100	0.347	0.474	0.008
100 SW	-0.185*	0.110	-0.291**	0.141	0.455**	-0.297**	1.000	0.260	0.331	-0.093	0.124	-0.215	0.439	0.197	0.211	0.689
NP	-0.315**	0.110	0.209*	-0.172	0.309**	0.191*	0.211*	1.000	0.844	0.479	0.283	-0.017	0.455	0.270	0.092	0.616
NW	-0.421**	0.211*	0.398**	-0.047	0.303**	0.188*	0.288**	0.807**	1.000	0.706	0.457	-0.004	0.601	0.338	0.153	0.702
SW	-0.176	0.028	0.227*	-0.106	-0.023	0.148	-0.066	0.211*	0.314**	1.000	0.653	0.015	0.613	-0.111	-0.297	0.190
NS	-0.236**	0.176	0.521**	-0.028	0.264**	-0.019	0.129	0.266**	0.449**	0.231*	1.000	0.158	0.572	0.019	-0.134	0.300
PS	-0.102	0.102	0.319**	-0.133	0.104	0.221*	-0.115	-0.008	0.004	0.006	0.138	1.000	-0.086	0.373	0.509	-0.043
NG	-0.295**	0.002	0.399**	0.087	0.371**	0.048	0.384**	0.426**	0.579**	0.252**	0.552**	-0.082	1.000	0.055	0.058	0.556
PG	-0.279**	0.231*	0.071	-0.007	0.162	0.141	0.182*	0.241**	0.316**	-0.048	0.026	0.299**	0.052	1.000	0.510	0.355
PI	-0.115	-0.048	0.226*	0.048	0.239**	0.187*	0.193*	0.086	0.149	-0.132	-0.131	0.442**	0.058	0.464**	1.000	0.343
SY	-0.318**	-0.037	0.107	0.255**	0.689**	0.025	0.573**	0.526**	0.625**	0.092	0.273**	0.009	0.506**	0.292**	0.316**	1.000

** Significant at p= 0.01 and * Significant at p= 0.05

DF: Days to 50% flowering
 BP: Number of branches per plant
 100SW: 100-seed weight
 SW: Shoot dry weight
 NG: Nitrogen content in seed
 SY: Seed yield per plot

DM: Days to maturity
 PP: Number of pods per plant
 NP: Number of nodule per plant
 NS: Nitrogen content in shoot
 PG: Phosphorus content in seed

PH: Plant height
 SP: Number of seeds per pod
 NW: Nodules dry weight
 PS: Phosphorus content in shoot
 PI: *Piriformospora indica* infection in root

Table 3: Direct (diagonal) and indirect path co-efficients of different traits towards seed yield in mungbean

T R A I T S	Days to 50 % flowering	Days to maturity	Plant ht.	No. of branches / plant	No. of pods / plant	No. of seeds / pod	100-seed wt.	No. of nodules / plant	Nodules dry wt. / plant	Shoot dry wt. / plant	N cont-ent in shoot	P cont-ent in shoot	N cont-ent in grain	P cont-ent in grain	<i>Piriformospora indica</i> infection in roots	Pheno- typic correl- ation with seed yield
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
1	-0.072	-0.178	-0.006	0.005	-0.088	-0.004	0.012	-0.090	-0.045	-0.003	0.001	-0.005	0.012	0.007	-0.008	-0.318**
2	-0.044	-0.290	-0.027	-0.011	-0.092	-0.004	0.014	-0.106	-0.054	-0.003	0.000	-0.004	0.015	0.002	-0.008	-0.037
3	-0.003	-0.052	-0.152	-0.035	0.103	0.019	0.017	0.069	0.034	0.003	-0.003	0.003	-0.005	-0.003	0.014	0.107
4	-0.003	0.023	0.040	0.135	0.064	-0.019	-0.027	-0.060	-0.005	-0.002	0.000	-0.004	-0.003	0.005	0.003	0.255**
5	0.013	0.055	-0.032	0.018	0.486	-0.002	-0.030	0.151	0.048	0.001	-0.001	0.002	-0.015	-0.004	0.013	0.689**
6	0.005	0.018	-0.049	-0.043	-0.020	0.059	0.018	0.042	0.020	0.002	0.000	0.004	-0.002	0.000	0.011	0.025
7	0.013	0.064	0.042	0.059	0.237	-0.017	-0.062	0.060	0.031	-0.001	-0.001	-0.001	-0.011	0.002	0.011	0.573**
8	0.021	0.099	-0.034	-0.026	0.236	0.008	-0.012	0.311	0.086	0.003	-0.002	0.003	-0.017	-0.010	0.007	0.526**
9	0.030	0.146	-0.048	-0.006	0.217	0.011	-0.018	0.249	0.107	0.005	-0.002	0.003	-0.019	-0.006	0.008	0.625**
10	0.013	0.056	-0.029	-0.014	0.037	0.009	0.004	0.067	0.034	0.015	-0.001	0.000	-0.005	-0.002	-0.008	0.092
11	0.018	0.025	-0.074	-0.005	0.125	0.000	-0.007	0.092	0.049	0.003	-0.005	0.002	-0.010	-0.004	-0.007	0.273**
12	0.019	0.062	-0.027	-0.027	0.046	0.013	0.003	0.055	0.016	0.000	-0.001	0.018	-0.007	-0.007	0.026	0.009
13	0.030	0.150	-0.023	0.015	0.250	0.005	-0.022	0.174	0.068	0.003	-0.002	0.004	-0.030	0.000	0.013	0.506**
14	0.015	0.014	-0.014	-0.021	0.058	0.000	0.003	0.090	0.019	0.001	-0.001	0.004	0.000	-0.035	0.004	0.292**
15	0.009	0.037	-0.036	0.006	0.106	0.011	-0.011	0.036	0.015	-0.002	0.001	0.008	-0.007	-0.002	0.061	0.316**

Residual effect = 0.176