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ASSESSMENT OF SEGREGATING GENERATIONS FOR GENETIC VARIABILITY AND YIELD REGULATING TRAITS IN MUNGBEAN

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ABSTRACT

Looking for limited genetic variation, due to homogeneity and homozygosity, F_5 and F_6 populations of thirty five mungbean (*Vigna radiata* L. Wilezek) genotypes were studied to assess genotypic variability and character association considering nineteen nitrogen fixing and yield attributing parameters. Straw protein content (0.306*), nitrogen fixation (0.342*), plant height (0.474*), pod per plant (0.388*), 100 seed weight (0.442*) were found to be major yield factors. Nitrogen fixation had positive and significant correlation with primary branches, seed per pod, yield per plant and straw protein in both the generations. Maximum direct positive effects towards yield were exerted by nitrogen fixing per plant (1.111), seeds per pod (0.423), pods per cluster (0.837), 100-seed weight (0.561) and plant height (0.257). Variability coefficients exhibited approximate similar pattern for both generations indicating stabilization of parameters with generation advance. However, continued recombination was also apparent for GCV and PCV in nodule volume (75.50 and 80.80%), nodule dry weight (43.72 and 48.78%) and nitrogen fixing ability (43.8 and 48.80%) which is probable sign of genetically complex mechanism. The findings will be useful for broadening the genetic base of autogamous crops and establishment of selection criteria for pulse improvement.

INTRODUCTION

Legumes represent the second largest family of higher plants, second only to grasses, in agricultural importance (Kumar *et al.*, 2013). Among legumes, mungbean (*Vigna radiata* (L.) is the third most important annual crop of Asia (Alam *et al.*, 2014), due to high protein content, broad adaptation, lesser agronomical requirement and high ability to increase soil fertility (Makeen *et al.*, 2007; Zaid *et al.*, 2012). Mungbean is rich source of proteins (22-28%), carbohydrates (60-65%), fat (1-1.5%), fibers (3.5-4.5%) and iron (40–70 ppm) for nutritionally balanced cereal-based diets in South and Southeast Asia (Bains *et al.*, 2003; Weinberger, 2005). In India it's grown in 2.53 mha with 0.86 m.t. production and 340 kg/ha productivity (Srivastava and Singh, 2012). This low productivity is the major constraint for large scale production of this crop among marginal farmers.

Presence of limited variation calls for creation of genetic variation among available breeding material to broaden the scope for selection. Moreover, breeding of varieties for different geographical areas is also the main factor affecting crop performance and final yield. Hence, genetic variability and heritability estimation for quantitative characters are important in selecting suitable genotype and reliable yield components (Ullah *et al.*, 2011a). Various applied statistical techniques like correlation, path coefficient and multivariate analysis are used for selection for seed yield traits in breeding programmes (Mohammad *et al.*, 2008; Tejbir *et al.*, 2009; Hussain *et al.*, 2012).Seed yield, being polygenic, is controlled by association of various traits. Therefore, information on association of yield attributes and their direct and indirect effects on seed yield are of great importance (Surek and Baser, 2003; Ilahi *et al.*, 2009). The objectives of this study were to investigate genetic variability in segregating generations and identify the most responsible yield components among accessions.

MATERIALS AND METHODS

Experiment conduction and data recording

The experimental material comprised of 35 advanced breeding lines (F_5 and F_6 generations) of mungbean grown at N. E. Borlaug Crop Research Center, G. B. Pant University of Agriculture and Technology, Pantnagar during *Kharif* 2011 and *Kharif* 2012. Standard agronomic package of practices was followed to raise the crop. The data were recorded for nineteen characters, viz., days to 50 percent flowering, number of root nodules, nodule volume, root length, shoot length, nodule dry weight, days to maturity, plant height, number of primary branches, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, seed yield per plant, harvest index, seed protein, straw protein, nitrogen fixation and yield per plot. Nitrogen content of the plant and seeds were estimated following Micro Kjeldhal method and the crude protein content was calculated using the factor (Nitrogen % x 6.25) and expressed in percent.

Statistical analysis

The data for each trait was statistically analyzed using analysis of variance recommended for randomize complete block design (RCBD). F-test followed by least significant difference

(LSD) test was applied for means analysis. The genetic and environmental variance for each trait was estimated by;

Genetic variance = VG = Genotype Ms - Error Ms

Environmental variance = VE = Error Ms

Phenotypic variance = VP = VG + VE

Heritability (h^2 BS) = VG / VP.

The mean value were used to obtained analysis of variance was carried out as per methodology advocated by Panse and Sukhatme (1967). PCV and GCV were calculated by the formula given by Burton (1952), Heritability in broad sense (h2) by Burton (1952), Burton and De Vane (1953) and genetic advance *i.e.* the expected genetic gain were calculated by using the procedure given by Johnson et al (1955). Correlation coefficient and path coefficient was worked out as method suggested by Al-Jibouri *et al*. (1958); Deway and Lu (1959) respectively.While genetic and phenotypic correlations among the traits were determined by Singh and Chaudhery (2005) method.

RESULTS AND DISCUSSION

Segregation promotes genetic variability

Segregation, by allowing unexpected allelic recombination, increases the variability among population. Variability is measured in terms of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance and heritability. Comparative study of variability measures with advancement of generations revealed that both phenotypic and genotypic variability constants were approximately equal in both F_5 and F_6 generations (Fig. 01) for all the characters, except plant height, pod per plant and nitrogen fixation, suggesting sufficient homogeneity has been achieved for these

Table 1: Direct and indirect effects of characters on plot yield using genotypic correlation matrix in F_5 generations

Character	Indirect effect via correlation with yield per plot	Direct Effect	Days to 50 % Flowering	Nodule no.	Nodule vol	Root length	Shoot length	Nodule dry weight	Maturity	Plant height	Pri. Branches
50 % flowering	-0.001	-0.401		-0.065	-0.092	-0.105	0.159	0.208	0.186	0.116	-0.019
Nodule no.	-0.555**	-0.176	-0.148		-0.229	-0.126	-0.149	0.838	-0.012	0.119	-0.047
Nodule vol	-0.448**	-0.441	-0.083	-0.092		-0.122	0.123	0.526	0.022	0.029	0.089
Root length	0.236	0.997	0.042	0.022	0.054		-0.393	-0.314	0.146	-0.049	-0.458
Shoot length	-0.023	-0.899	0.071	-0.029	0.06	0.436		0.139	0.132	-0.011	0.129
Nodule dry weight	-0.495**	1.012	-0.082	-0.146	-0.229	-0.309	-0.124		-0.034	0.101	0.018
Maturity	0.242	0.366	-0.204	0.006	-0.027	0.398	-0.323	-0.093		0.109	-0.136
Plant height	-0.004	0.257	-0.182	-0.082	-0.049	-0.19	0.04	0.4	0.156		0.004
Pri. Branches	0.297	-0.869	-0.009	-0.009	0.045	0.525	0.134	-0.021	0.057	-0.001	
Pod per plant	-0.571**	-0.575	-0.003	-0.095	-0.192	-0.103	0.035	0.56	0.071	0.115	-0.17
Pod length	-0.3	-0.867	-0.052	-0.09	-0.125	0.014	0.133	0.521	-0.051	0.148	-0.173
Seed per pod	0.291	0.423	-0.09	-0.062	-0.074	0.183	0.213	0.191	0.073	0.143	-0.484
100 seed weight	-0.509**	0.011	0.027	-0.093	-0.038	-0.037	-0.07	0.656	-0.057	0.12	-0.234
Plant yield	0.196	-0.069	0.028	-0.041	0.023	0.263	0.25	0.191	0.053	0.096	-0.826
HI	-0.386*	0.017	0.006	-0.067	-0.185	-0.225	0.214	0.471	0.173	0.088	0.149
Seed protein	-0.131	-0.556	-0.018	-0.099	-0.103	0.134	-0.037	0.39	-0.009	0.023	0.019
Straw protein	0.395*	-0.897	-0.008	0.063	0.158	0.133	0.117	-0.32	-0.105	-0.022	-0.127
N_2 fixation	0.389*	1.111	-0.025	0.004	0.109	0.25	0.171	-0.081	-0.071	0.035	-0.532

Character	Pod per plant	Pod length	Seed per pod	100 seed weight	Plant yield	HI	Seed protein	Straw protein	N_2 fixation
	-0.005	-0.112	0.095	-0.001	0.005	0	-0.024	-0.017	0.071
50 % flowering	-0.309	-0.443	0.15	0.006	-0.016	0.006	-0.313	0.318	-0.023
Nodule no.	-0.251	-0.247	0.071	0.001	0.004	0.007	-0.13	0.321	-0.275
Nodule vol	0.06	-0.012	0.078	0	-0.018	-0.004	-0.075	-0.119	0.279
Root length	0.023	0.128	-0.1	0.001	0.019	-0.004	-0.023	0.116	-0.212
Shoot length	-0.318	-0.446	0.08	0.007	-0.013	0.008	-0.214	0.284	-0.089
Nodule dry weight	-0.111	0.121	0.084	-0.002	-0.01	0.008	0.014	0.257	-0.214
Maturity	-0.258	-0.5	0.235	0.005	-0.026	0.006	-0.049	0.077	0.152
Plant height	-0.112	-0.173	0.235	0.003	-0.066	-0.003	0.012	-0.131	0.68
Pri. Branches		-0.564	0.158	0.009	-0.038	0.012	-0.097	0.323	-0.019
Pod per plant	-0.374		0.255	0.008	-0.059	0.007	-0.079	0.179	0.306
Pod length	-0.215	-0.524		0.003	-0.074	0.002	-0.023	-0.028	0.635
Seed per pod	-0.513	-0.649	0.121		-0.038	0.005	-0.092	0.236	0.136
100 seed weight	-0.313	-0.741	0.455	0.006		0	-0.002	-0.197	1.02
Plant yield	-0.406	-0.343	0.058	0.003	0		-0.221	0.419	-0.536
HI	-0.1	-0.123	0.018	0.002	0	0.007		0.473	-0.15
Seed protein	0.207	0.173	0.013	-0.003	-0.015	-0.008	0.293		0.744
Straw protein	0.01	-0.239	0.242	0.001	-0.063	-0.008	0.075	-	0.6
N_2 fixation									

characters. However, ample variation does exists among population e.g. in F_5 GCV and PCV was ranged between 0.52 - 73.25% and 1.1-75.79% respectively. Similarly in F_6, it varied between 0.51 - 83.75 (GCV) and 1.12 - 85.82 (PCV). Higher PCV value in comparison to GCV is a suggests that, apparent variation is not entirely due to genotype but due to influence of environment as well (Venkateswarlu, 2001, Dikshit *et al.,* 2002; Reddy *et al.*, 2003; 2013 and Tejbir *et al.*, 2009).

High heritability estimates coupled with high genetic advance was observed for nodule number, plant height and pod per plant, indicating the preponderance of additive and fixable genetic variance (Begum *et al.*, 2013; Hozayn *et al.*, 2013); suggesting that this trait may be subjected to any selection scheme to develop the stable genotypes and selection pressure may be exercised in early generation. High heritability coupled with moderate genetic advance for number of nodule volume, shoot length, primary branches and pod length as well as high heritability coupled with low genetic advance indicating the presence of additive as well as non-additive gene action (Parameswarappa, 2005; Kodanda *et al.*, 2009 and 2011). For these traits improvement can be made opting the two to three cycles of recurrent selection followed by pedigree or single seed descent methods of breeding (Dadepeer *et al.*, 2009; Dhananjay *et al.*, 2009 and Rahim *et al.*, 2010).

Identifying yield regulating traits

The concept of secondary selection was evolved for quantitative traits to explore the possibility of increasing grain yield by indirect selection of some component traits (Ahmad *et al.*, 2013; Thippani *et al.*, 2013). However, any unfavourable association between the desirable and undesirable characters limits the genetic advance. Therefore, to accurately understand the inter-relationship of contributing characters and seed yield,

Table 2: Direct and indirect effects of characters on plot yield using genotypic correlation matrix in F_6 generations

Character	Indirect effect via correlation with yield per plot	Direct Effect	Days to 50 % flowering	Nodule no.	Nodule vol	Root length	Shoot length	Nodule dry weight	Maturity	Plant height
flowering	0.391*	0.715		0.058	-0.097	0.013	0.001	-0.025	-0.063	0.002
Nodule no.	-0.265	0.673	0.062		-0.183	0.004	-0.001	-0.211	-0.014	0.001
Nodule vol	-0.291	-0.403	0.173	0.306		-0.004	-0.001	-0.15	0.004	0
Root length	0.255	0.069	0.132	0.042	0.023		-0.001	0.017	-0.056	0.001
Shoot length	-0.077	-0.009	-0.051	0.055	-0.029	0.011		-0.039	-0.018	0.001
Nodule dry weight	-0.273	-0.26	0.068	0.545	-0.233	-0.005	-0.001		0	0
Maturity	0.348*	-0.119	0.376	0.08	0.015	0.032	-0.001	0		0.005
Plant height	0.589**	0.005	0.3	0.081	0.007	0.016	-0.001	-0.013	-0.115	
Pri. Branches	0.580**	0.232	0.016	-0.08	0.126	-0.011	-0.002	0.036	-0.046	0.003
Pod per plant	0.651**	0.837	0.047	0.076	0.035	-0.01	-0.002	-0.056	-0.025	0.003
Pod length	-0.17	-0.896	-0.015	0.347	-0.089	-0.046	-0.001	-0.102	0.015	0.001
Seed per pod	0.174	0.19	-0.045	0.19	-0.033	-0.026	-0.002	-0.046	-0.046	0.002
100 seed weight	0.442**	0.561	-0.142	0.077	-0.001	-0.031	0	0.023	0.027	0.001
Plant yield	0.634**	-0.046	0.117	-0.104	0.155	-0.019	-0.002	0.058	-0.051	0.003
HI	-0.107	-0.244	-0.4	-0.048	0.163	-0.015	-0.001	0.027	0.004	-0.002
Seed protein	-0.023	-0.466	0.182	0.459	-0.09	0.023	-0.001	-0.111	-0.001	0
Straw protein	0.29	0.369	0.02	-0.334	0.162	0.008	0.002	0.109	0.027	0
N_2 fixation	0.529**	-0.818	0.166	-0.129	0.121	0.002	-0.001	0.048	-0.038	0.003

Character	Pri. Branches	Pod per plant	Pod length	Seed per pod	100 seed weight	Plant yield	HI	Seed protein	Straw protein	N_2 fixation
50 % flowering	0.005	0.056	0.018	-0.012	-0.111	-0.008	0.136	-0.119	0.01	-0.189
Nodule no.	-0.028	0.095	-0.462	0.054	0.064	0.007	0.017	-0.317	-0.183	0.157
Nodule vol	-0.073	-0.073	-0.198	0.016	0.002	0.018	0.099	-0.104	-0.148	0.246
Root length	-0.037	-0.127	0.599	-0.072	-0.257	0.013	0.055	-0.159	0.043	-0.028
Shoot length	0.06	0.205	-0.066	0.038	0.029	-0.013	-0.016	-0.064	-0.073	-0.097
Nodule dry weight	-0.032	0.179	-0.352	0.034	-0.049	0.01	0.025	-0.198	-0.155	0.15
Maturity	0.09	0.175	0.11	0.073	-0.128	-0.02	0.009	-0.003	-0.083	-0.262
Plant height	0.12	0.495	-0.122	0.081	0.144	-0.029	0.07	-0.02	0.009	-0.442
Pri. Branches		0.797	-0.284	0.159	0.37	-0.057	-0.121	0.026	-0.004	-0.581
Pod per plant	0.221		-0.309	0.139	0.427	-0.044	-0.066	-0.074	0.042	-0.59
Pod length	0.074	0.289		0.146	0.398	-0.015	-0.075	-0.047	-0.178	0.026
Seed per pod	0.194	0.612	-0.688		0.591	-0.046	-0.101	-0.087	-0.073	-0.413
100 seed weight	0.153	0.637	-0.636	0.2		-0.033	-0.092	-0.014	-0.041	-0.246
Plant yield	0.29	0.812	-0.303	0.189	0.402		-0.2	0.05	0.064	-0.781
HI	0.115	0.225	-0.277	0.079	0.212	-0.038		0.09	0.013	-0.01
Seed protein	-0.013	0.134	-0.091	0.036	0.017	0.005	0.047		-0.027	-0.126
Straw protein	-0.003	0.094	0.433	-0.038	-0.062	-0.008	-0.009	0.034		-0.514
N_2 fixation	0.165	0.604	0.028	0.096	0.169	-0.044	-0.003	-0.072	0.232	

Residual are 0.06430

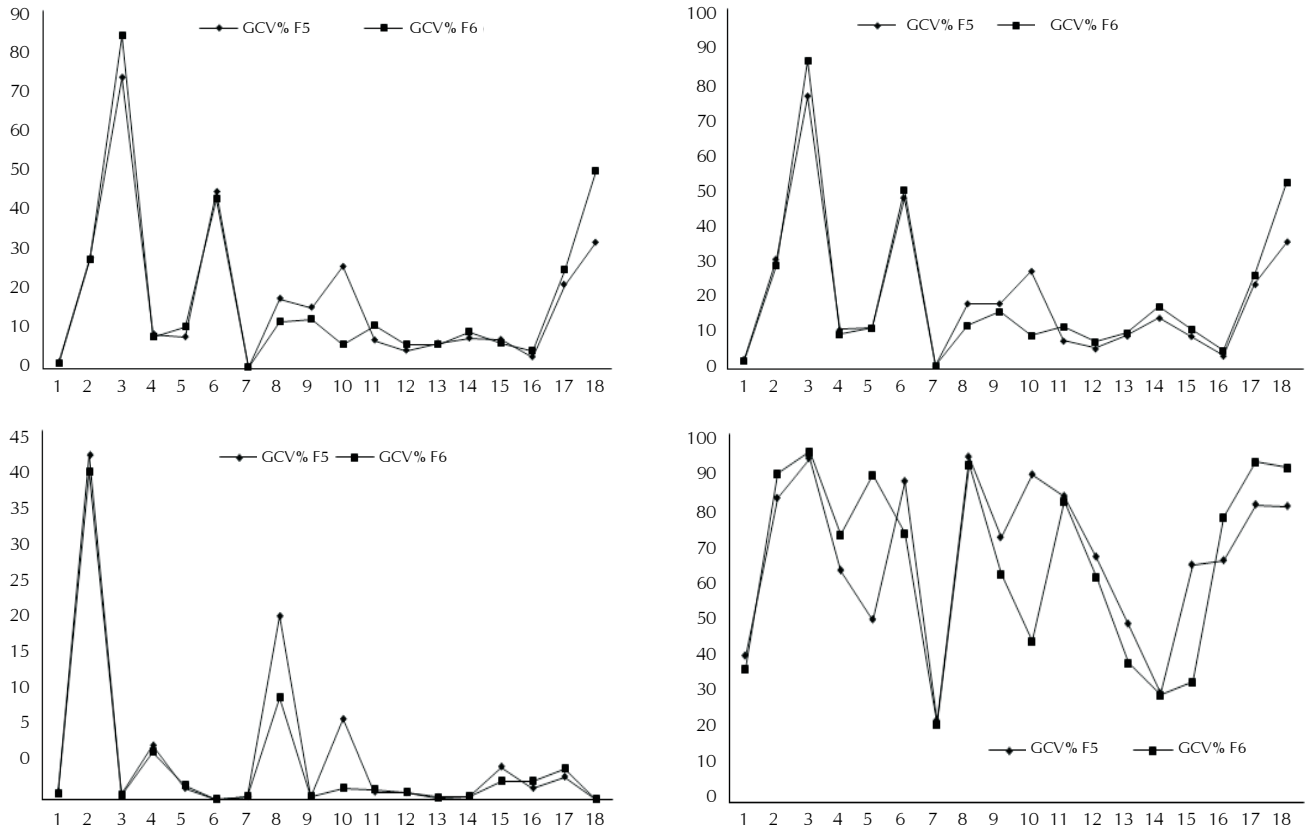

Figure 1: Variability parameters among segregating populations (Y axis - percent GCV, PCV, GA and Heritability respectively; X axis-18 characters under study)

genotypic and phenotypic correlation coefficients were computed from the estimates of variances and co variances for all possible combinations of characters studied. The study revealed greater genotypic correlations than their corresponding phenotypic correlations indicating the preponderance of genetic variance in expression of characters (Kumar *et al.*, 2003; Gul *et al.*, 2008; Tabasum *et al.*, 2010). Seed yield per plant was positive and significantly associated with plant height (0.257), number of primary branches (0.507), pods per plant (0.282), pod length (0.338), seed per pod (0.448), 100 seed weight (0.278) and nitrogen fixation (0.918) (Hakim, 2008; Priya and Reddy, 2008; Rahim *et al.*, 2010; Reddy *et al.*, 2011and Khanpara *et al.*, 2012). So improvement in seed yield is possible by considering above as selection criteria.

Atmospheric nitrogen fixation with root nodule (legheamoglobin component) and soil micro flora were found to be positively associated with primary branches (0.612), seed per pod (0.571) and yield per plant (0.918) (Makeen *et al.*, 2007 and Biradar *et al.*, 2007). Hence to assimilate atmospheric nitrogen, crop plant should have sufficient canopy that will be necessary to produce large number of seeds per plant and to develop healthy root network which will in-turn increase the nitrogen fixation. Seed protein, determinant of nutritive value of legume, is primary function of nodule number, nodule dry weight and nitrogen fixing ability (Prakash, 2006; Birader *et al.*, 2007; Makeen *et al.*, 2007; Verma and Garg, 2007; Shrivastava and Singh, 2012). In our study, seed protein content showed parallel relationship with crop duration (0.298), nodule number (0.563), nodule dry weight (0.386) and harvest index (0.398) in F_5 and nodule number (0.681), nodule dry weight (0.342) and root length (0.426) in F_6. Positive association with crop duration provides an idea about optimum time span requirement to synthesize the polypeptide chain i.e. longer the duration-higher the protein content.The study indicates that the high yielding mungbean genotypes could be obtained by selecting taller or medium plants having higher number of primary branches with higher pods per plant, seed per pod, 100 seed weight, harvest index and nitrogen fixing ability.

Contribution of characters towards grain yield

Genetic control of yield can be indirectly achieved by knowledge of agronomic, morphological and physiological traits (Sharma and Childiyal, 2005; Parameswarappa and Salimath, 2007). Despite, the increase in crop yields over the past decades, morphological and physiological processes underlying this yield enhancement is still not well understood (Lalinia and Manni, 2014). Path coefficient analysis is an effective tool to determine the nature of relationships between seed yield and its contributing components, and to identify those components with significant effects on yield to use as potential selection criteria (Prakash, 2006; Rao *et al.*, 2006; Verma and Garg, 2007). In F_5 populations nitrogen fixing ability exerted direct positive impact on yield per plot (Table 01).

Nodule dry weight, root length, seeds per pod, maturity, plant height, harvest index and 100 seed weight also exhibited similar response, whereas negative direct effect was also registered for root length, straw protein, primary branches, pod per plant and seed protein percentage. Since days to 50 % flowering, nodule number, nodule volume, pod per plant, pod length and seed protein % had negative correlation with yield per plot and hence direct effect of these characters was negative. In contrast, 100 seed weight showed negative correlation with yield per plot but the direct effect on yield per plot was positive. Similarly, plant height showed non-significant negative correlation with yield per plot, the direct effect of this character is positive. The residual factor was 0.28418 observed.

In F_6 generations (Table 02), the direct effect of pod per plant was highest followed by days to 50% flowering, number of nodules, 100 seed weight, nitrogen fixation per plant, primary branches per plant and seed per pod (Sadiq *et al.*, 2006; Nair et al., 2007; Rahim *et al.*, 2010). Nodule volume and nodule dry weight had negative correlation with yield per plot and therefore their direct effect was also negative. Number of nodule was having negative correlation with yield per plot but its direct effect on yield per plot was positive. Yield per plant and nitrogen fixation had positive correlation with yield per plot but their direct effect was negative. The observed residual factor was 0.06430, indicating that factors which have been considered here are sufficient to account variation in yield. On the basis of path analysis the traits like seed yield per plant, plant height, seed per pod, 100 seed weight and harvest index are good selection criteria for improving the yield per plot of mungbean as these have a prominent direct effect. Although some other traits such as nodule characteristics, maturity duration, straw protein and nitrogen fixation may also have good impact on yield, hence selection for these traits will also improve the yield.

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