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CORRELATION AND PATH COEFFICIENT ANALYSIS OF YIELD COMPONENTS IN MUNG BEAN (*PHASEOLUS AUREUS* ROXB.)

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Abstract

The present study was undertaken to determine the correlations and path coefficient between plant yield and its component traits in mutants of mung bean, ***Phaseolus aureus*** Roxb. Estimates of mean, genotypic and phenotypic coefficients of variation, broad-sense heritability, genetic advance, correlation coefficients and path analysis revealed that the mean values of different quantitative characters increased in almost all the mutants. High estimates of genetic parameters were recorded in number of fertile branches, number of pods and total plant yield followed by plant height and then pod length, 100-seed weight and seeds per pod. Correlation coefficients at genotypic and phenotypic level showed more or less similar trends, and, in general, the genotypic values were higher than the corresponding phenotypic values. Positive genotypic correlations were shown by number of fertile branches and number of pods whereas at phenotypic level, plant yield also showed positive correlation. Path coefficient analysis revealed that the number of pods gave high positive direct effect on plant yield. Though number of fertile branches showed negative direct effect on plant yield but it was nullified by its high indirect effects via number of pods, pod length and seeds per pod. Therefore, in mung bean, number of fertile branches and number of pods should be given greater weightage while formulating selection indices.

Key words: Path coefficient analysis; yield components; mung bean; genetic advance.

Introduction

During the past few years, intensive research work has been initiated to improve yield as well as the quality of pulses. Grain yield in mung bean is a complex entity determined by the interplay of a number of attributes. Adequate knowledge of interrelation of factors influencing such complex character is essential

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for designing an effective plant breeding programme. Studies of correlations of agronomic and morphological characters are helpful in the identification of the components of a complex character such as yield but they do not provide precise information on the relative importance of direct and indirect influences of each of the componential characters (Larik, 1978). If the number of variables are more, it becomes essential to measure the contribution of the various variables to the observed correlation and partition the correlation coefficient into components of direct and indirect effects. The technique of path coefficient analysis developed by Wright (1921) has been extensively used by conventional breeders (Gupta and Singh, 1969; Singh and Malhotra, 1970; Giriraj and Vijaya Kumar, 1974; Singh *et al.*, 1980; Malik *et al.*, 1983) and most probably is being employed here for the first time in mung bean by a mutation breeder. The present paper elucidates the interrelationship of factors influencing grain yield of the mutants isolated in M3 generation through path coefficient analysis.

Materials and Methods

The material was originated from the gamma rays, ethyl methane sulphonate (EMS) and hydrazine hydrate (HZ) in the var. G-65 (released at Punjab Agricultural University, Ludhiana, India) of mung bean, ***Phaseolus aureus*** Roxb. Eight mutants classified on the basis of grain yield in M3 generation, were grown in a randomized complete block design with three replications. The plant to plant and interrow distances were 30 cm and 60 cm, respectively. The data were collected on 10 randomly selected plants from each replication to study the following seven quantitative characters: (1) plant height, (2) number of fertile branches, (3) number of pods, (4) pod length, (5) seeds per pod, (6) 100-seed weight and (7) plant yield. Analysis of variance and covariance was carried out on a T.D.C.-12 computer of Osmania University. The broad-sense heritability (h^2), genotypic and phenotypic coefficients of variation and correlation coefficients were estimated following the methods of Singh and Chowdhury (1977). The genotypic correlation coefficients were partitioned into path coefficients using the technique outlined by Dewey and Lu (1959). The expected genetic advance was calculated according to the modified formula (see Khan, 1983).

$$G_s = k \cdot \delta_p \cdot h^2$$

where δ_p = phenotypic standard deviation of the mean performance of mutant populations; h^2 = broad-sense heritability and $k = 2.64$ constant for 1% selection intensity.

Results

The different quantitative characters were analysed for the evaluation of mean values, genetic parameters, correlations (phenotypic and genotypic). The correlation coefficients were partitioned into components of direct and indirect effects through path coefficient analysis.

Mean Values

The mean values estimated for the different characters are presented in Table 1. These values are significantly (P≥0.01) increased for the traits, plant height, number of fertile branches and pods and also 100-seed weight. However, pod length and seeds per pod showed non-significant increase as well as decrease. Plant yield increased more at 30 kR (20.59 g.) followed by 0.3% EMS (17.91 g.) and then 0.2% EMS (16.90 g.), 0.4% EMS (16.82 g.), 0.03% HZ (16.35 g.), respectively. It was 12.63 g. in the control population.

Genetic Parameters

The data on phenotypic coefficients of variation, genotypic coefficients of variation, heritability and genetic advance are presented in Table 2. Highest phenotypic and genotypic coefficients of variation showed by the number of branches, number of pods and plant yield followed by plant height and 100-seed weight and then pod length and seeds per pod. Heritability estimates ranged from 11.18% for seeds per

Table 1. *Mean values ($\bar{X}$) and standard error of mean ($SE_{\bar{x}}$) of seven quantitative characters in different mutants*

S. No.	Strain number	Strain/ treatment/ origin	Plant height (cm)	Number of branches	Number of pods	Pod length (cm)	Seeds per pod	100-Seed weight (g)	Plant yield (g)
1.	G-65	G-65 (Control)	39.13 ±0.39	4.23 ±0.12	42.23 ±2.13	6.24 ±0.03	11.03 ±0.13	3.20 ±0.03	12.63 ±0.81
2.	G-IH-137	0.4%EMS/6h	46.90** ±0.62	7.28** ±0.35	59.59** ±2.36	6.15 ±0.32	11.48** ±0.13	3.43** ±0.05	16.82** ±0.76
3.	G-IH-127	0.3%EMS/6h	43.10** ±0.72	6.87** ±0.28	63.03** ±2.35	6.41 ±0.07	11.34* ±0.15	3.46** ±0.05	17.91** ±0.69
4.	G-IH-121	30kR of gamma-rays	48.47** ±1.15	9.41** ±0.68	73.88** ±5.38	6.99** ±0.04	11.62* ±0.10	3.41** ±0.06	20.59** ±1.55
5.	G-IH-216	0.2%EMS/6h	44.71** ±0.49	6.95** ±0.19	62.46** ±1.70	6.75** ±0.04	11.69** ±0.07	3.41** ±0.02	16.90** ±0.50
6.	G-IH-143	0.03%HZ/6h	52.30** ±0.90	7.39** ±0.43	55.04** ±2.24	6.56** ±0.06	11.20 ±0.15	3.37** ±0.04	14.18 ±0.65
7.	G-IH-127	0.03%HZ/6h	46.95** ±1.57	8.57** ±0.45	64.45** ±3.27	6.44 ±0 20	11.26 ±0.11	3.53** ±0.05	16.35* ±0.89
8.	G-IH-121	0.03%HZ/6h	45.80** ±1.29	7.52** ±0.33	55.92** ±2.32	6.61** ±0.08	11.41** ±0.14	3.55** ±0.03	14.82* ±0.67
9.	G-IH-145	0.03%HZ/6h	50.73** ±1.64	8.82** ±0.45	55.33** ±3.21	6.62** ±0.08	11.37 ±0.17	3.51** ±0.05	14.69* ±0.95

*,** Significant at 5% and 1% level, respectively.

Table 2. *Estimates of phenotypic and genotypic coefficients of variation, broad-sense heritability* (h^2) *and expected genetic advance* (*Gs*) *of seven quantitative characters*

Characters	CV(p) (%)	CV(g) (%)	h^2 (%)	Gs (% of $\bar{X}$)
Plant height	58.06	45.75	62.00	18.63
No. of branches	163.11	136.56	70.09	44.87
No. of pods	128.06	104.53	66.63	43.75
Pod lenghth	27.78	18.68	45.27	11.09
Seeds per pod	20.30	6.77	11.18	1.86
100-Seed weight	42.18	18.95	20.17	3.37
Plant yield	143.41	114.66	63.92	46.74

CV(p)=Phenotypic coefficient of variation,
CV(g)=Genotypic coefficient of vairation

pod to 70.09% for number of branches. Plant height, number of pods and plant yield also gave higher values of heritability. Altogether a different trend was noticed for the values of expected genetic advance. The lowest value was recorded in seeds per pod (1.86%) and highest for plant yield (46.74%). Number of branches and number of pods also gave higher values.

Correlation Coefficients

The genotypic and phenotypic correlation coefficients between plant yield and its components as well as among the six components *inter se* are presented in Table 3. Plant height showed positive correlations with number of fertile branches, pod length and seeds per pod. On the other hand, plant yield and 100-seed weight gave negative correlation with plant height. Number of fertile branches were positively correlated with number of pods, pod length, 100-seed weight and plant

Table 3. *Genotypic* (*above diagnoal*) *and phenotypic* (*below diagonal*) *correlation coefficients between seven quantitative characters*

Characters	1	2	3	4	5	6	7
1. Plant height	1.0000	0.2616	−0.8975**	0.4401*	0.3780*	−0.3707*	−0.9956**
2. No. of branches	0.2098	1.0000	0.6229*	0.5308*	−0.0555	0.0495	0.5161**
3. No. of pods	0.0495	0.4549*	1.0000	−0.7859**	−0.7942**	−0.2415	0.9471**
4. Pod length	0.0855	0.0276	0.7288**	1.0000	0.3674*	0.1285	−0.9348**
5. Seeds per pod	0.1413	−0.2407	−0.2579	0.7667**	1.0000	−0.7060**	−0.8977**
6. 100-Seed weight	−0.0134	0.1251	0.0101	0.1083	−0.1836	1.0000	−0.9353**
7. Plant yield	−0.2813	0.3289*	0.9469**	−0.5011*	−0.3843**	0.8571**	1.0000

*,** Significant at 5% and 1% level, respectively.

yield and negatively with seeds per pod. Positive correlation was exhibited by the number of pods and the total plant yield. Likewise, correlation coefficients were positive for pod length on seeds per pod and 100-seed weight and negative with plant yield. However, seeds per pod displayed negative correlations with 100-seed weight and plant yield.

Path Coefficient Analysis

The estimates of direct and indirect effects of the six attributes on plant yield are presented in Table 4. The path coefficient analysis showed that the direct effect of the number of pods on plant yield was high and positive. The positive correlation between number of fertile branches and total plant yield was obtained largely by its indirect effect via number of pods, pod length and number of seeds per pod. The high positive correlation exhibited by the number of pods and plant yield partially due to its indirect effects via plant hight, seeds per pod and 100-seed weight. On the other hand, pod length, seeds per pod and 100-seed weight showed the highest negative direct effects on plant yield.

Table 4. *Correlations and path coefficients showing direct and indirect effects of six components on plant yield in mung bean (genotypic correlation with plant yield)*

Characters	1	2	3	4	5	6	Genotypic correlation with plant yield
1. Plant height	<u>−0.1772</u>	−0.5499	−1.5833	1.3036	−0.9797	0.9965	−0.9900
2. No. of branches	−0.0461	<u>−2.1150</u>	1.0907	1.5703	0.1547	−0.1347	0.5199
3. No. of pods	0.1594	−1.3113	<u>1.7593</u>	−2.3406	2.0368	0.6464	0.9500
4. Pod length	−0.0779	−1.1209	−1.3898	<u>−2.9628</u>	−0.9539	−0.3501	−0.9298
5. Seeds per pod	−0.0673	0.1269	−1.3898	1.0962	<u>−2.5782</u>	1.9122	−0.9000
6. 100-Seed weight	0.0655	−0.1057	−0.4222	0.3852	1.8305	<u>−2.6932</u>	−0.9399

Underlined figures denote direct effects.

The direct and indirect effects of the six attributes on plant yield are depicted in Fig. 1. Though the number of branches showed highly negative direct effect on plant yield, its correlation was positive owing to its high indirect effects via number of pods, pod length and seeds per pod. Seeds per pod and 100-seed weight gave negative association with plant yield, through the indirect effects via number of branches, pod length and 100-seed weight and plant height, pod length and seeds per pod, respectively, are positive.

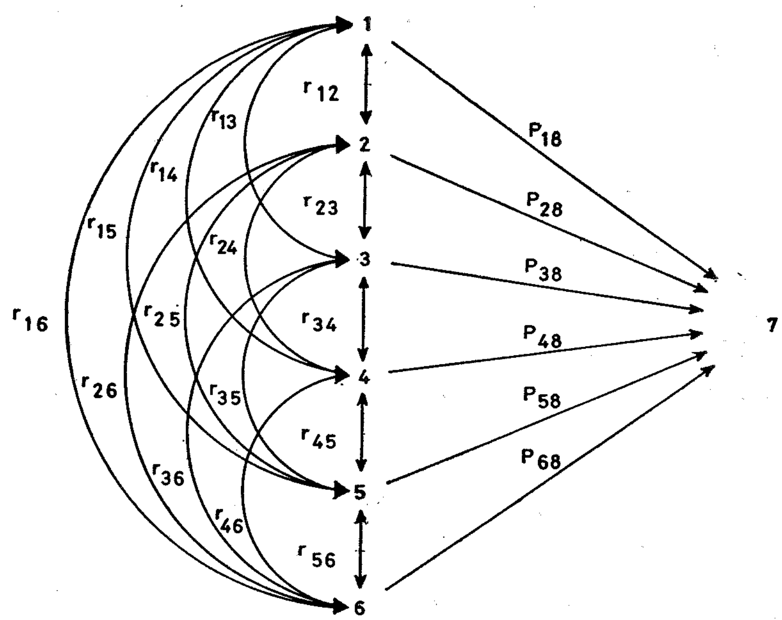

Fig. 1. Path diagram showing direct and indirect effects. Unidirectional arrows represent path coefficients (direct effects), bidirectional arrows represent correlation coefficients as follows: (1) Plant height, (2) Number of fertile branches, (3) Number of pods, (4) Pod length, (5) Seeds per pods, (6) 100-Seed weight, and (7) Plant yield.

Discussion

The phenotypic and genotypic correlation coefficients between all possible combinations of seven quantitative characters revealed that plant yield exhibited a positive correlation with number of fertile branches and pods per plant. These findinings are in agreement with those of Singh and Malhotra (1970) and Malik *et al.* (1983). From these associations it is inferred that lines with high yield potential tend to bear more number of pods and pod bearing branches per plant. Hence, greater weightage should be given to these traits while constructing selection indices for the improvement of yield and its genetic architecture in mung bean.

Genotypic correlations were, in general, higher than phenotypic correlations. These results were in agreement with the observations of Singh and Chowdhury (1983). The high values of genotypic correlations indicate a strong inherent association that would result in higher response in respect to yield than would have been expected when selection is made for these components. Genotypic coefficient of variation would be more useful for assessing the variability, since, it depends upon the heritable portion of variability (Allard, 1970). The high genotypic coefficient of variation exhibited by plant height, number of fertile branches, number of pods and total plant yield indicated that these traits are genotypically predominant. High estimates of phenotypic coefficient of variation were observed in these traits only. Johnson *et al.* (1955) have reported that heritability estimates along with genetic advance will be more useful than heritability value alone in selecting best individuals. Burton (1952) suggested that genotypic coefficient of variation together with high heritability estimates would give better picture to the extent of genetic advance to be expected by selection. In the present study, number of fertile branches, number of pods and plant yield showed high genetic advance in conjunction with high heritability and genotypic coefficients of variations. Similar results have been reported by Parmasivan and Rajasekharan (1980) in green gram. Low genotypic coefficients of variation, heritability and genetic advance manifested by pod length, seeds per pod and 100-seed weight, suggest that these characters cannot be relied upon for the purpose of selection.

The path analysis showed that the number of pods exhibited high positive direct effects on plant yield. The direct effect of number of branches on plant yield was highly negative; nevertheless, much of this influence was nullified by its high positive indirect effects via number of pods, pod length and seeds per pod. Pod length, seeds per pod and 100-seed weight depicted negative direct effects on plant yield, but indirect effects of seeds per pod via pod length and 100-seed weight were high and positive and for 100-seed weight via seeds per pod were high and positive. The high positive genotypic correlation of number of branches and pods and plant yield indicated that if the other variables held constant, an increase in pod number and branches might increase seed yield per plant.

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綠豆產量構成因子之相關與路徑係數分析

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本研究測定綠豆突變種之產量與構成因子各性狀之相關與路徑係數。平均值估值，變異性之基因型與表現型係數，廣義遺傳率，遺傳進數（genetic advance），相關係數與路徑分析顯示出幾乎所有突變種中各數量性狀之平均值均增加。結實枝數，結莢數與總產量表現高遺傳常數估值，次爲株高，最低爲莢長，百粒重與每莢種子數。基因型相關係數與表現型相關係數有相似趨勢，而基因型係數值大體上略大於對應之表現型係數值。表現正基因型相關的有結實枝數和結莢數；與表現型呈正相關者爲植株產量。路徑係數分析顯示結莢數對產量有正向直接效應。雖然結實枝數對產量呈現負向直接效應，但它被結莢數莢長和每莢種子數之高間接效應抵消。因此，擬定綠豆選種指數時，應加重於結實枝數與結莢數。