Study of Genetic variability and path analysis for yield in Greengram (*Vigna radiata* L. Wilczek)

Abstract

The current study was conducted in order to estimate thegenetic variability, Correlation and pathanalysis for yield and yield contributing traitsassessed 31 genotypes of green gram during Zaid season 2023. The experiment followed a Randomized Block Design (RBD) with 3 replications. Data were collected from 5 randomly selected plants from each genotypein each replication, among 13 different traitsseed index had highest genotypic and phenotypic coefficient of variance followed by number of pod per plant, while least GCV and PCV was recorded for days to maturity. High heritability was shown by plant height followed by number of seeds per pod. Seed index and harvest index had highly significant positive genotypic correlationwith seed yields per plant. Whiledays to maturity and days to 50% pod setting was recorded as highly significant negative genotypic correlation with seed yields per plant. Plant height followed by primary branches per plant, biological yield seed index and harvest index was recorded as positive direct effect on seed yield per plant at both genotypic and phenotypic levels while days to maturity followed by clusters per plant, pods per plant and pod length was recorded as negative direct effect on seed yield per plant at both genotypic and phenotypic levels. All the traits showed a strong and positive association with seed yield, proving that these traits actually correlate with one another. Therefore, identifying high yielding genotypes from highly segregating populations would be made easier with the use of direct selection for these traits.

Keywords: *Greengram,Variability,Heritability, Correlation,Path coefficient analysis*

Introduction

“Greengram [*Vigna radiata (L.) Wilczek*] is commonly known as mungbean.It is traditional pulse crop that is grown all across India. It belongs to the Leguminosae family's Papilionaceae subfamily and is a diploid species with the chromosome number 2n=2x=22. Its scientific name is *Vigna radiata (L.) Wilczek*. Greengarmoriginated in South Asia (India), and *Vigna radiata var*. *sublobata* is most likely its progenitor. It may be grown using a range of crop rotation techniques because of its short growing season, wide range of adaptability, low water requirements, and photo insensitivity.The total covered area by mungbean in India is 15.93 lac ha (39.38 lac acres) during 2023-24 and the production was 3.74 million tonnes during 2022-23(source: www.agricoop.nic.in).The majority of countries in Southeast Asia, including Nepal, Sri Lanka, Bangladesh, India, and Pakistan, are growers of greengrams” [1,2].

“Greengram is one of the most important sources of amino acids like lysine, arginine, and leucine, valine, which is high in vitamin B, and tryptophan besides other pulses. Sprouts of greengram contain E and C vitamins.Greengram is protein rich (24 grams per 100 grams), about 2.5 times more thancereals. It's also richsource of carbohydrates (60 gm per 100 gm), minerals (3gm/100gm), fat (1 gm per 100 gm) and Fiber (1gm/100gm). Mungbean seeds contain calcium 124 mg per 100 gm, phosphorus 326 mg per 100 gm, 1.3% fat, 7.3% iron per 100 grams, 4.1 percent Fiber, and the calorific value is 334 kcal.Pulses (Dals)are the main sources of protein the daily diet of majority of the India’s population due to their vegetarian eating habits” [3,4]. “Correlation measurementbetween other characteristics and yield are helpful in choosing desirable plant types in developing an efficient breeding strategy. Correlation coefficients measure the degree of association between two variables, either at the genotypic or phenotypic level. These coefficients form the basis for selection in breeding programs by providing information about the inherent relationships among various traits.Path coefficient analysis is an important statistical technique that partitions the correlation coefficients into direct and indirect effects of independent variables on a dependent variable. This analysis helps breeders understand the relative importance of each trait in influencing the dependent variable, such as grain yield” [5-8].

Given the aforementioned details, the current study was conducted to evaluate genetic variability and path analysis for yield attributing traits among the genotypes of mungbean.

MATERIALS AND METHODS

The present investigation was carried out at the Central Research Farm [CRF] Department of Genetics and Plant Breeding, SHUATS, Prayagraj. Thecrop period was Zaid 2023. The soil type of experimental block was sandy loam with pH 7.5. The experimental material is comprised of 30 genotypes along with 1 check variety (samrat). Three replications of a randomized complete block design were used for the experiment. In three replications with 30 × 10 cm inter and intra- row spacing in 1 × 1 m plots. For this mungbean, recommended agronomical and plant protection practice were followed. In order to select the best yielding genotype in the agro climatic conditions of Prayagraj region observation were recorded for various quantitative traits includingPlant height(cm), Days to 50% Flowering, Days to 50% pod setting, days to maturity and seed index(%), harvest index (%) were recorded on plot basis, while for traits like plant height, primary branch count, number of pods, biological yield, seed yield, and others three plants were chosen at random and the harvest index was recorded. Thereafter the phenotypic quantitate traits were compared with high yielding check varieties for varietal selection. During the study, used genotype werementioned in (Table 1).

Table 1: List of 31 Genotypes of Greengram used in the experiment.

Sl. No	Genotypes	Sl. No	Genotypes
01	IC-332327	**16**	IC-76414
02	IC-249567	**17**	IC-76569
03	IC-39294	**18**	IC-76599
04	IC-305291	**19**	IC-333090
05	IC-119006	**20**	IC-11604
06	IC-119048	**21**	IC-76464
07	IC-39280	**22**	IC-119005
08	IC-332181	**23**	IC-43600
09	IC-305241	**24**	IC-9887
10	IC-119027	**25**	IC-249656
11	IC-121224	**26**	IC-121220
12	IC-121221	**27**	IC-282079
13	IC-76378	**28**	IC-22456
14	IC-76418	**29**	IC-103979
15	IC-11468	**30**	IC-38995
31.	Samarat (Check)		

2.1 Statistical Analysis

2.1.1 Genetic Analysis

Range,mean ($\bar{X}$), standard deviation (SD), Standard error of Mean [S.E. (±)],Coefficient of variance (CV. %).

Range = Largest value - smallest value

S.D. = $\sqrt{Varian}$; S.D. = √MSe (S.D. = Standard Deviation; MSe = Error mean square)

SE m (±) =$\sqrt{\ MSe\ /r}$ (MSe = Error mean square and r = Number of replications)

CV (%) = $\sqrt{\ (MSe/\ \bar{X}}$)X 100 (CV = Coefficient of variation and $\bar{X}$ = Population mean)

2.1.2 Genetic variability

Phenotypic coefficient of variation (PCV) and Genotypic coefficient of variation (GCV) was calculated as per formula prearranged by Singhand Chaudhary (1977)

Genotypic coefficient of variation (GCV) GCV (%) = $\sqrt{\sigma^2 g}\ \bar{X}$ X 100

Phenotypic coefficient of variation (PCV) PCV (%) = $\sqrt{\sigma^2 p}\ \bar{X}$ X 100

(Where, $\bar{X}$ = General mean σ^2 g and σ^2 p = Genotypic variance and phenotypic variance respectively)

Heritability in the broad sense (h2) as suggested by Burton and Devane(1953)

Heritability (h2) % = (σ2 g / σ2 p) X 100

(Where, σ 2 g = Genotypic variance ;σ 2 p = Phenotypic variance)

Genetic advance (GA) as per the method described by Johnson et al. (1955)

G. A. = κ X h^2 (b) X σp

Genetic advance as percent of mean (GAM) = $G.A.\ \bar{X}$ X 100

Where,

h 2 = Heritability in broad sense

κ = Selection differential. It is a constant for a given selection intensity. It is taken as 2.06 at 5% selection intensity in the present investigation.

σp = Phenotypic standard deviation, $\bar{X}$ = General mean of character

2.1.3 Correlation coefficient analysis (r)

The correlation coefficients were determined by the degree of a character's relationship with yield as well as among the variables that contributed to yield.The formula was used to calculate the genotypic and phenotypic correlations coefficient[10].

2.1.4 Path coefficient analysis

The concept initiallygiven by Wright[20] and later developed by Dewey and Lu[7] were used to perform path coefficient analysis in order to figure out the indirect and direct impacts of the various characters on yield.

RESULTS AND DISCUSSION

3.1 Variability Studies:

The 2 way ANOVA implies that compared all the characters (Table 2) that the mean sums of squares due to genotypes were significant for all the traits under study viz., days to 50% flowering, days to 50 % pod setting, days to maturity, plant height,no of primary branches, no of clusters per plant ,no of pods per plant, no of seeds per pod, pod length (cm), biological yield (g), seed index (g), harvest index (%), seed yield per plant (g). “This substantial variability provides a good prospect for improving traits of interest in mungbean breedingprogrammes. These findings suggest that selection based on these traits can result in significant improvements, as there is a considerable degree of variability across all the characters” [5] [18].

Genetic parameters of yield and their components are given in Table 3. Results showed that percentage of PCV was higher than the percentage of GCV for all the traits under study (High = >20%). High genotypic and phenotypic coefficient of variance were recorded for seed index (32.54, 35.91) Similarly, the moderate estimates of GCV and PCV were recorded no of pods per plant (17.18, 19.52) followed by biological yield (16.49, 19.12) respectively. While the least estimate of GCV and PCV was recorded for days to maturity, days to 50 % pod setting, days to 50 % flowering, pod length. These results agreed with the finding in Mungbean under similar conditions[4] [12].

High estimates of heritability in broad sense were recorded for Plant height (93.84) followed by no of seeds per pod (87.57), seed index (85.66), seed yield per plant (84.68), harvest index (82.14), numbers of pod per plant (77.48),and biological yield (74.38). Moderate estimates of heritability in broad sense were recorded for no. of clusters per plant (58.05) and low heritability were recorded for days to 50 % flowering (29.23). These results were in close conformity with the findings reported moderate heritability for pods per plant and bunches per plant [6] [8] [11].

“The higher genetic advance as % of Mean was recorded for seed index (63.17) followed by harvest index (60.75) and plant height (44.59). Moderate estimate of genetic advance was recorded for number of pods per pod (34.88) and no pod per plant (31.56) low estimate of genetic advance as percentage of mean was recorded for days to 50 % Flowering (2.48) days to maturity (3.42), showed similarity under similar conditions”[1] [19].

Source	Degree of freedom	Days to 50% Flowering	Days to 50 % pod setting	Days to maturity	Plant Height (cm)	No of Primary Branches	No of Clusters per Plant	No of Pods per plant	No of seeds per pod	Pod length (cm)	Biological yield (g)	Seed Index (g)	Harvest Index (%)	Seed yield per plant (g)
Replication	2	21.62	6.33	3.41	1.81	0.39	1.89	13.25	5.78	0.14	0.29	186.73	324.65	1.31
Treatment	30	8.49*	7.92*	10.45**	289.23**	0.69**	7.38**	39.73**	10.63**	0.65**	0.96**	498.68**	494.28**	7.08**
Error	60	3.79	1.59	2.14	6.19	0.16	1.43	3.51	0.48	0.19	0.1	26.35	33.41	0.4

Table 2. Analysis of Variance (ANOVA) for all characters in greengram

***,* Significant at 1% and 5% level of significance respectively*

Table 3. Parameters of genetic variability for grain yield and its attributing traits

Characters	General Mean	Range		PCV (%)	GCV (%)	Heritability h2 (%)	GA as % of mean @5 %
		MIN	MAX				
Days to 50% flowering	49.09	45	52	4.72	2.55	29.23	2.84
Days to 50% pod setting	58.37	55.67	62	3.3	2.49	57.04	3.87
Days to Maturity	75.29	72.17	79.33	2.94	2.21	56.44	3.42
Plant height (cm)	43.47	27.78	64.58	23.06	22.34	93.84	44.59
Number of primary branches	2.98	2.2	4.2	19.53	14.11	52.22	21.01
Number of clusters per plant	7.83	5.04	11.27	23.59	17.97	58.05	28.21

Number of pods per plant	20.22	14	28.8	19.52	17.18	77.48	31.56
Number of seeds per pod	10.17	7.07	14.33	19.33	18.09	87.57	34.88
Pod length (cm)	6.87	6.23	8.27	8.49	5.69	44.96	7.86
Biological yield (g)	21.25	11.47	29.67	19.12	16.49	74.38	29.29
Seed Index	3.25	2.31	4.7	35.8	33.13	85.66	63.17
Harvest Index	37.87	18.25	63.19	35.91	32.54	82.14	60.75
Seed yield per plant	6.89	4.53	10.73	23.54	21.66	84.68	41.06

3.2 Correlation Coefficient Analysis

“A technique for finding features that influence significant dependent characteristics, such seed yield, is correlation coefficient and path analysis. These tools aid in the development of selection criteria for concurrently enhancing multiple characters and economic output” [17].

Highly significant positive genotypic correlation (Table 4) of seed yield per plant was recorded with seed index (0.639) followed by harvest index (0.613), number of seed per pod (0.544) and plant height (0.314) and Number of clusters per plant (0.246), whereas it exhibited significant negative correlation with days to maturity (-0.1359), days to 50% pod setting(-0.1359) and days to 50% flowering(-0.0981). While highly significant positive phenotypic correlation (Table 5) of seed yield per plant was recorded with seed index (0.675),and followed by harvest index (0.611), number of seed per pod (0.601), number of clusters per plant (0.373), Plant height (0.311). Whereas it exhibited significant negative correlation with days to 50% pod setting (-0.1263), biological yield (-0.0756), days to maturity (-0.0652) [2] [13] [14].

3.3 Path - Coefficient Analysis

The correlation coefficient indicates only the interrelationship of the characteristics irrespective of cause and effect, it becomes more meaningful when the correlation coefficients are partitioned into components of direct and indirect effects through path analysis. All the 12characteristics that were employed in correlation studies were considered independent variables for path analysis, with seed yield serving as the dependent variable(Tables 6,7) and (Fig1,2).

Each component's associations with other parameters had an effect on the yield both directly and indirectly. At both the genotypic and phenotypic levels, all of the features had positive direct influences on the amount of seed produced per plant: plant height (0.0948,0.0829), number of primary branches per plant (0.0357,0.029), biological yield (0.8438,0.877), seed index (0.2114,0.2385), and harvest index (1.2186,1.198). Conversely, at both the genotypic and phenotypic levels, negative direct influences on the number of seeds produced per plant were noted for all features by Day to maturity (-0.0084, -0.0803), Number of clusters per plant (-0.0917, -0.0002), Number of pods per plant (-0.1341, -0.0656), and Pod length (-0.0421, -0.0832)[3] [14] [15].

Days to 50% flowering (0.008,0.0067), Days to 50% pod setting (0.0094,0.0045), Days to maturity (0.0077,0.0026), Plant height (0.0032,0.0042), Number of clusters per plant (0.0145,0.0123), Number of pods per plant (0.0044,0.0033), and Pod length (0.0061,0.0037) were the positive indirect effects of the number of primary branches per plant, respectively, at both genotypic and phenotypic levels. Days to maturity (0.0049, 0.0162), number of primary branches per plant (0.0084, 0.0120), number of clusters per plant (0.0162, 0.019), and number of seeds per pod (0.0269, 0.0131) were among the indirect effects of plant height that were found to be positively correlated. Harvest index (0.0092,0.0139), Seedindex (0.0308,0.035), and Pod length (0.0038,0.0073) [9] [16].

Table 4. Correlationcoefficientbetweenyieldanditsattributingtraitsin31greengramgenotypesatgenotypiclevel

Genotypic Correlation Matrix

Characters	Days to 50% flowering	Days to 50% pod setting	Days to Maturity	Plant height (cm)	Number of primary branches	Number of clusters per plant	Number of pods per plant	Number of seeds per pod	Pod length (cm)	Biological yield (g)	Seed Index	Harvest Index	Seed yield per plant
Days to 50% flowering	**1**	0.505**	0.274*	0.0529	0.224*	0.0881	-0.0542	-0.0882	-0.1199	0.0638	-0.0364	-0.1606	-0.0981
Days to 50% pod setting		**1**	0.481**	-0.0474	0.262*	0.250*	0.263*	-0.1219	0.0375	0.0549	-0.0471	-0.1011	-0.1359
Days to Maturity			**1**	0.0519	0.216*	0.1237	0.0513	-0.294*	-0.1333	0.179	-0.0197	-0.234*	-0.1359
Plant height (cm)				**1**	0.0891	0.1711	-0.0946	0.283*	0.0397	0.0434	0.324*	0.0968	0.314*
Number of primary branches					**1**	0.407**	0.1233	0.1133	0.1699	-0.0223	0.0492	0.0668	0.0581
Number of clusters per plant						**1**	0.360**	0.254*	0.231*	0.0428	0.323*	0.218*	0.246*
Number of pods per plant							**1**	0.0573	0.0705	-0.1571	0.1967	0.336**	0.1366
Number of seeds per pod								**1**	0.265*	-0.0149	0.604**	0.376**	0.544**
Pod length (cm)									**1**	0.250*	0.260*	-0.0018	0.1913
Biological yield (g)										**1**	0.0786	-0.727**	-0.0147
Seed Index											**1**	0.334*	0.639**
Harvest Index												**1**	0.613**
Seed yield per plant													**1**

*5% level of significance, **1% level of significance

Table 5. Correlation coefficient between yield and its attributing traits in 31 greengram genotypes at phenotypic level

Characters	Days to 50% flowering	Days to 50% pod setting	Days to Maturity	Plant height (cm)	Number of primary branches	Number of clusters per plant	Number of pods per plant	Number of seeds per pod	Pod length (cm)	Biological yield (g)	Seed Index	Harvest Index	Seed yield per plant
Days to 50% flowering	**1**	0.594**	0.241*	-0.0434	0.231*	0.253*	0.164	-0.1028	-0.1148	-0.0901	0.0587	0.0918	0.0341
Days to 50% pod setting		**1**	0.439**	-0.1164	0.156	0.214*	0.263*	-0.291*	-0.0528	-0.1194	-0.08	0.0343	-0.1263
Days to Maturity			**1**	0.1951	0.0881	0.1713	0.0857	-0.363**	-0.2035	-0.1185	0.0753	0.0665	-0.0652
Plant height (cm)				**1**	0.1442	0.229*	0.0198	0.1583	0.0883	-0.0673	0.422**	0.1675	0.311*
Number of primary branches					**1**	0.424**	0.1135	-0.0112	0.1281	0.0676	0.0934	-0.0552	0.0338
Number of clusters per plant						**1**	0.373**	0.1865	0.1116	0.0146	0.415**	0.220*	0.373**
Number of pods per plant							**1**	-0.0007	0.0149	-0.260*	0.302*	0.404**	0.266*
Number of seeds per pod								**1**	0.299*	0.085	0.512**	0.284*	0.601**
Pod length (cm)									**1**	0.1989	0.281*	-0.0428	0.1488
Biological yield (g)										**1**	-0.0931	-0.783**	-0.0756
Seed Index											**1**	0.420**	0.675**
Harvest Index												**1**	0.611**
Seed yield per plant													**1**

*5% level of significance, **1% level of significance

Table 6. Direct and Indirect effects of yield attributing traits on seed yield at genotypic level

Genotypic Path Matrix													
Characters	**Days to 50% flowering**	**Days to 50% pod setting**	**Days to Maturity**	**Plant height (cm)**	**Number of primary branches**	**Number of clusters per plant**	**Number of pods per plant**	**Number of seeds per pod**	**Pod length (cm)**	**Biological yield (g)**	**Seed Index**	**Harvest Index**	**Seed yield per plant**
Days to 50% flowering	**0.0416**	0.021	0.0114	0.0022	0.0093	0.0037	-0.0023	-0.0037	-0.005	0.0027	-0.0015	-0.0067	-0.0981
Days to 50% pod setting	-0.0068	**-0.0134**	-0.0064	0.0006	-0.0035	-0.0033	-0.0035	0.0016	-0.0005	-0.0007	0.0006	0.0014	-0.1359
Days to Maturity	-0.0023	-0.004	**-0.0084**	-0.0004	-0.0018	-0.001	-0.0004	0.0025	0.0011	-0.0015	0.0002	0.002	-0.1359
Plant height (cm)	0.005	-0.0045	0.0049	**0.0948**	0.0084	0.0162	-0.009	0.0269	0.0038	0.0041	0.0308	0.0092	0.314*
Number of primary branches	0.008	0.0094	0.0077	0.0032	**0.0357**	0.0145	0.0044	0.004	0.0061	-0.0008	0.0018	0.0024	0.0581
Number of clusters per plant	-0.0081	-0.0229	-0.0113	-0.0157	-0.0373	**-0.0917**	-0.033	-0.0233	-0.0212	-0.0039	-0.0296	-0.02	0.246*
Number of pods per plant	0.0073	-0.0352	-0.0069	0.0127	-0.0165	-0.0483	**-0.1341**	-0.0077	-0.0095	0.0211	-0.0264	-0.045	0.1366
Number of seeds per pod	0.0016	0.0022	0.0053	-0.0051	-0.0021	-0.0046	-0.001	**-0.0182**	-0.0048	0.0003	-0.011	-0.0068	0.544**
Pod length (cm)	0.005	-0.0016	0.0056	-0.0017	-0.0071	-0.0097	-0.003	-0.0112	**-0.0421**	-0.0105	-0.0109	0.0001	0.1913
Biological yield (g)	0.0538	0.0463	0.151	0.0366	-0.0188	0.0361	-0.1325	-0.0126	0.2106	**0.8438**	0.0664	-0.6132	-0.0147
Seed Index	-0.0077	-0.01	-0.0042	0.0686	0.0104	0.0683	0.0416	0.1277	0.055	0.0166	**0.2114**	0.0707	0.639**
Harvest Index	-0.1957	-0.1232	-0.2847	0.1179	0.0814	0.2657	0.4094	0.4581	-0.0022	-0.8857	0.4073	**1.2186**	0.613**

*5% level of significance, **1% level of significance

Table 7. Direct and Indirect effects of yield attributing traits on seed yield at phenotypic level

Phenotypic Path Matrix												
Characters	**Days to 50% flowering**	**Days to 50% pod setting**	**Days to Maturity**	**Plant height (cm)**	**Number of primary branches**	**Number of clusters per plant**	**Number of pods per plant**	**Number of seeds per pod**	**Pod length (cm)**	**Biological yield (g)**	**Seed Index**	**Harvest Index**	**Seed yield per plant**
Days to 50% flowering	**-0.0046**	-0.0027	-0.0011	0.0002	-0.0011	-0.0012	-0.0007	0.0005	0.0005	0.0004	-0.0003	-0.0004	0.0341
Days to 50% pod setting	0.0168	**0.0283**	0.0124	-0.0033	0.0044	0.0061	0.0075	-0.0082	-0.0015	-0.0034	-0.0023	0.001	-0.1263
Days to Maturity	-0.0194	-0.0352	**-0.0803**	-0.0157	-0.0071	-0.0137	-0.0069	0.0291	0.0163	0.0095	-0.006	-0.0053	-0.0652
Plant height (cm)	-0.0036	-0.0097	0.0162	**0.0829**	0.012	0.019	0.0016	0.0131	0.0073	-0.0056	0.035	0.0139	0.311*
Number of primary branches	0.0067	0.0045	0.0026	0.0042	**0.029**	0.0123	0.0033	-0.0003	0.0037	0.002	0.0027	-0.0016	0.0338
Number of clusters per plant	-0.0001	0	0	0	-0.0001	**-0.0002**	-0.0001	0	0	0	-0.0001	0	0.373**
Number of pods per plant	-0.0108	-0.0173	-0.0056	-0.0013	-0.0074	-0.0245	**-0.0656**	0	-0.001	0.0171	-0.0198	-0.0265	0.266*
Number of seeds per pod	-0.0056	-0.016	-0.0199	0.0087	-0.0006	0.0102	0	**0.0548**	0.0164	0.0047	0.0281	0.0156	0.601**
Pod length (cm)	0.0096	0.0044	0.0169	-0.0073	-0.0107	-0.0093	-0.0012	-0.0249	**-0.0832**	-0.0166	-0.0234	0.0036	0.1488
Biological yield (g)	-0.079	-0.1047	-0.1039	-0.0591	0.0593	0.0128	-0.2281	0.0745	0.1744	**0.877**	-0.0816	-0.687	-0.0756
Seed Index	0.014	-0.0191	0.018	0.1007	0.0223	0.0989	0.0721	0.1222	0.0671	-0.0222	**0.2385**	0.1003	0.675**
Harvest Index	0.11	0.0411	0.0796	0.2006	-0.0662	0.263	0.484	0.3404	-0.0512	-0.9385	0.5036	**1.198**	0.611**

**5% level of significance, **1% level of significance*

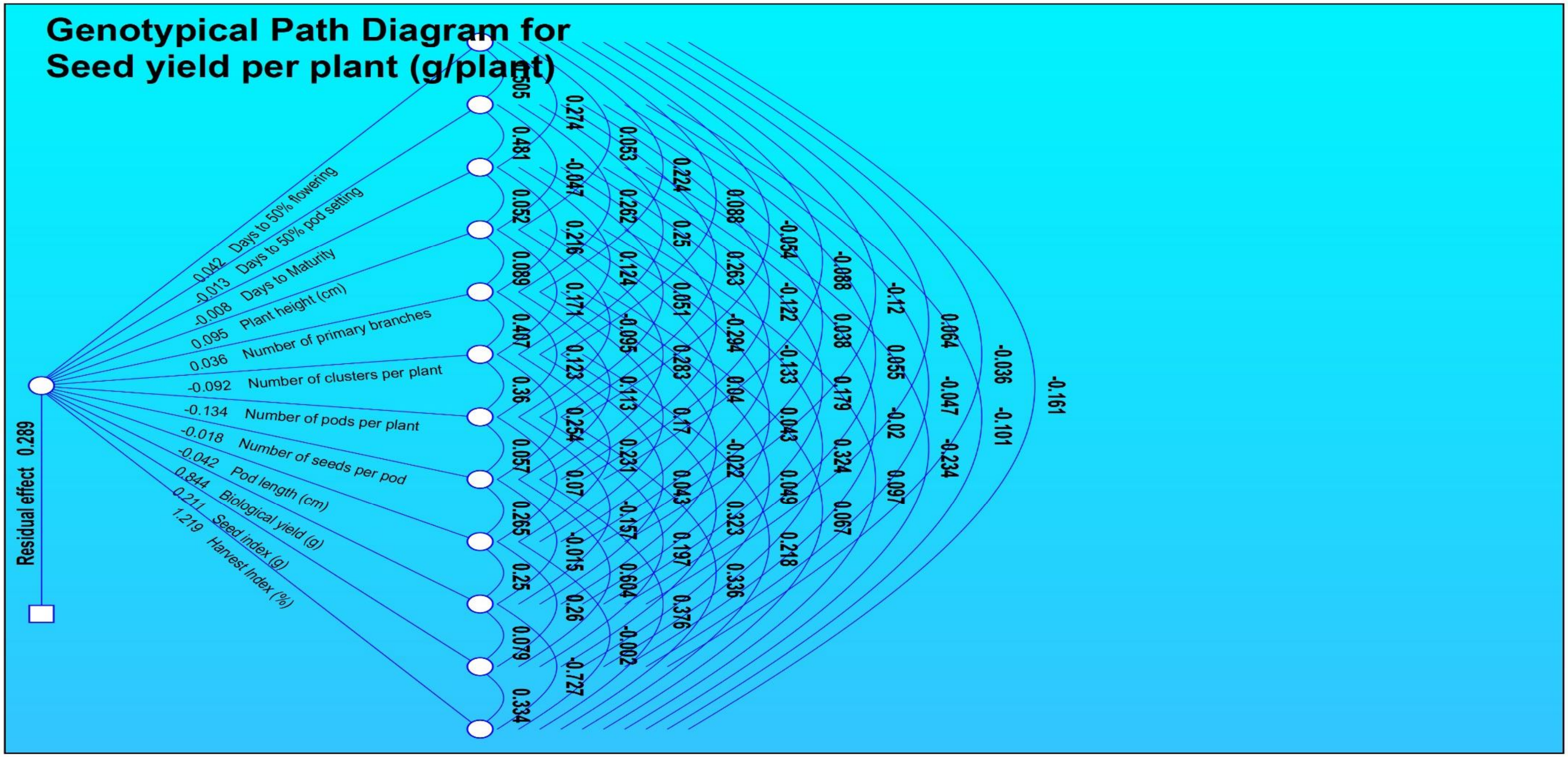

Fig 1. Genotypic path diagram for seed yield per plant

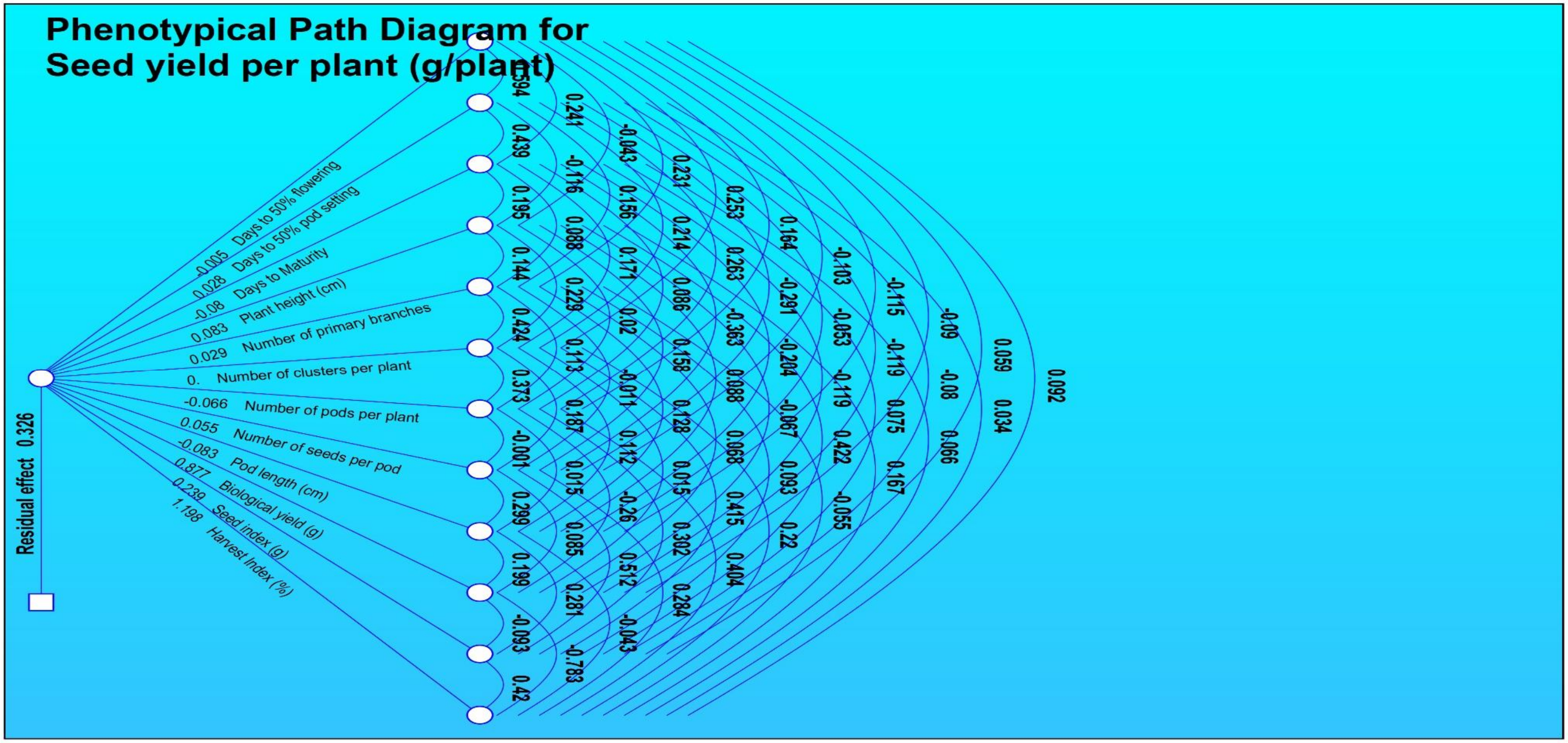

Fig 2. Phenotypic path diagram for seed yield per plan

Conclusion

In light of the results of present investigation it is concluded that among 30 genotypes of green gram on the basis of mean performance 3 genotypes were found to be superior for seed yield per plant over check variety Samrat viz., IC-76569, IC-121220 and IC-119006. It is also concluded that analysis of variance showed significant variation among different genotypes for all characters studied. In the current investigation, traits such as harvest index, plant height, and seed index exhibited high heritability estimates along with substantial genetic advance as a percentage of the mean and high genotypic coefficient of variation (GCV). Similarly, the number of seeds per pod, number of pods per plant, and seed index displayed high heritability with moderate GCV and notable genetic advance as a percentage of the mean. Positive and significant correlation was observed for number of clusters per plant, plant height, number of seeds per pod, seed index and harvest index with seed yield per plant at genotypic level. At genotypic level the highest positive direct effects on seed yield at genotypic level was depicted by harvest index, seed index, biological yield, number of primary branches per plant, days to 50% flowering and plant height. This indicated that seed yield was mainly a product of direct and indirect effects of above attributing characters and priority should be given to these characters during selection for improvement in mungbean.

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Option 1:

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

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Details of the AI usage are given below:

1.

2.

3.

References:

1. Anand, G., Anandhi, K., &Paulpandi, V. K. (n.d.). Genetic variability, correlation, and path analysis for yield and yield components in F6 families of Greengram *(Vigna radiata (L.) Wilczek)* under rainfed conditions.*Electronic Journal of Plant Breeding, ISSN 0975-928X, Vol 7 no 2.*
2. Azam, M. G., Hossain, M. A., Alam, M. S., Rahman, K. S., & Hossain, M. (2018). Genetic variability, heritability, and correlation, path analysis in mungbean (*Vigna radiata* (L.) Wilczek). *Bangladesh Journal of Agricultural Research*, 43(3), 407-416.
3. Bhutia, P., Lal, M., & Thomas, N. (2016). Studies on genetic variability, correlation, and path analysis in green gram (*Vigna radiata* (L.) Wilczek) germplasm. *International Journal of Agriculture Science*, 8(51), 2267-2272.
4. Burton, G. W., &Devane, E. H. (1953). Estimating heritability in tall fescue (Festuca arundinacea). *Agronomy Journal*, 45(10), 478-481.
5. Chaudhary, P. L., Kumar, B., & Kumar, R. (2023). Analysis of heterosis and heterobeltiosis for earliness, yield and its contributing traits in okra (*Abelmoschus esculentus* L. Moench). *International Journal of Plant & Soil Science, 35*(11), 84-98.
6. Dadepeer, Peerajade, Kumar, R. L. R., &Salimath, P. M. (2009). Genetic variability and character association in local green gram genotypes. *Environment and Ecology, 27*(1), 165-169.
7. Dewey, D. R., & Lu, K. H. (1959). A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*, 51(9), 515-518.
8. Dhananjay, Ramakant, Singh, B. N., & Singh, G. (2009). Studies on genetic variability, correlations and path coefficients analysis in mung bean. *Crop Research Hisar, 38*(1/3), 176-178.
9. Engel RH. The importance of legumes as a protein source in Asian diet. Proceeding of first international mungbean symposium, Taiwan. 1978;35-39.
10. Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimation of genetic and environmental variability in soybean. *Agronomy Journal*, 47(7), 314-318.
11. Kamleshwar, K., Yogendra, P., Mishra, B., Pandey, S., & Kumar, R. (2013). Study on genetic variability, correlation and path analysis with grain yield and yield attributing traits in green gram [*Vigna radiata* (L.) Wilczek]. *The Bioscan, 8*(4), 1551-1555.

12. Khanpara, M. D., Vachhani, J. H., Jivani, L. L., Jethava, A. S., &Vaghasia, P. M. (2012). Correlation and path coefficient analysis in green gram [*Vigna radiata* (L.) Wilczek]. *Asian Journal of Bio Science, 7*(1), 34-38.
13. Kumar, A., Sharma, N. K., Kumar, R., Sanadya, S. K., & Sahoo, S. (2018). Correlation and path analysis for seed yield and components traits in mungbean under arid environment. *International Journal of Chemical Studies*, 6(4), 1679-1681.
14. Muthuswamy, A., Jamunarani, M., & Ramakrishnan, P. (2019). Genetic variability, character association, and path analysis studies in mungbean (*Vigna radiata* (L.) Wilczek). *International Journal of Current Microbiology and Applied Sciences*, 8(4), 1136-1146.
15. Nikhil, A., Gaibriyal, M. L., Lavanya, G. R., &Yajavathi, C. (2022). Study of correlation and path analysis in greengram [*Vigna radiata* (L.) Wilczek] for yield and yield attributing traits. *International Journal of Plant & Soil Science, 34*(23), 2483.
16. Singh C, Singh P, Singh R. Modern Techniques of Raising Field Crops. *Oxford & IBH Publishing Co. Pvt. Ltd.,* New Delhi. 2015;386.
17. Singh, R. K., & Chaudhary, B. D. (1977). *Biometrical methods in quantitative genetic analysis*. New Delhi: Kalyani Publishers.
18. Srivastava, R. L., & Singh, G. (2012). Genetic variability, correlation and path analysis in mungbean (*Vigna radiata* (L.) Wilczek). *Indian Journal of Life Sciences, 2*(1), 61-65.
19. Udayasri, S., Lavanya, G. R., & Lal, G. M. (2022). Estimation of variability and genetic divergence in greengram (*Vigna radiata* (L.) Wilczek) for yield characters. *International Journal of Plant & Soil Science, 34*(23), 31560.
20. Wright S. (1921). Correlation and causation. Journal of Agriculture Research, 20, 557-587.