www.ThePharmaJournal.com

The Pharma Innovation

Chinta Revathi
Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh, India

Gaibriyal M Lal
Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh, India

Genetic variability and character association for yield and yield component characters in greengram (*Vigna radiata* L. Wilczek)

Chinta Revathi and Gaibriyal M Lal

Abstract
The current investigation involved in the assessment of 20 Greengram genotypes, including a check, during the kharif season of 2022. The study adopted a Randomized Block Design (RBD) with three replications and gathered data on 13 different traits to explore variability, heritability, genetic advancement, correlations, and path analysis. Analysis of variance revealed that the germplasm exhibited significant genetic variability for most of the assessed traits. Regarding grain yield and its components, it was evident that LGG-450 performed exceptionally well, followed closely by VBN-3 and AMULYA. Upon closer examination of variability coefficients, it became apparent that Phenotypic Coefficient of Variation (PCV) exceeded Genotypic Coefficient of Variation (GCV), implying the influence of environmental factors on the expression of the studied traits. Notably, high to moderate GCV and PCV estimates were observed for clusters per plant, biological yield, and economic yield. Furthermore, the study found high heritability estimates for clusters per plant, economic yield, biological yield, and pods per plant. In contrast, traits such as days to 50% pod setting, days to maturity, and days to 50% flowering showed low genetic advance estimates, suggesting their limited responsiveness to selective breeding. The correlation analysis revealed significant positive associations between grain yield per plant and various other traits, including plant height, primary branches per plant, clusters per plant, pods per plant, biological yield, and seed index. Additionally, path analysis, conducted at both phenotypic and genotypic levels. It is identified that plant height, biological yield, harvest index, and seed index are directly influenced on yield. Consequently, these traits were recognized as efficient and promising targets for direct selection to enhance Greengram productivity within the study's experimental materials.

Keywords: Genetic variability, PCV, GCV, correlation, path analysis

Introduction

In Green gram, scientifically known as *Vigna radiata* (L.) Wilczek, is a significant pulse legume characterized by its small, cylindrical shape and bright green skin. It is a diploid crop with a genome size of 579 Mb and a self-pollination mechanism (2n=2x=2). Ranked as the third most important pulse crop in Asia, following chickpea and pigeonpea, it holds a vital place in agriculture. India is a global leader in Mungbean cultivation, producing 24.48 lakh tonnes across 46.07 lakh hectares of land with a productivity rate of 531 kg/ha, as reported in the Annual report for 2021-2022.

Pulses, including green gram, play a crucial role in meeting the protein needs of the human diet, particularly for those with limited resources. They are often referred to as "poor people's meat" due to their affordability and serve as a primary source of essential amino acids for the vegetarian population in India. Green gram is well-regarded for its nutritional value, boasting a rich content of proteins, fats, vitamins, and various minerals. Its popularity for consumption arises from its ease of digestibility and minimal flatulence production.

Farmers typically cultivate green gram as a secondary crop, often intercropped with other plants on marginal lands, often without the use of additional fertilizers. The remaining green gram foliage after pod harvesting can either be used as livestock feed or ploughed back into the soil as green manure, enriching it with organic matter. However, there are challenges associated with green gram cultivation, including frequent droughts in low rainfall areas, poor availability of quality seeds, and a limited genetic base. Many genes responsible for desirable agronomic traits, especially high yield, have been lost over time due to the crop's historical cultivation in harsh conditions or primitive agriculture. To address these challenges and enhance yield, understanding the variability of various traits is essential. The success of breeding programs relies on the availability of genetic variability within the crop species and

Corresponding Author:
Chinta Revathi
Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh, India

the efficiency of selection techniques. Genetic variability plays a pivotal role in selecting elite parents for hybridization programs and is the foundation for effective selection.

Therefore, this study aimed to assess the extent of variability, heritability, genetic advancement, correlations, and path analysis using 20 genotypes of green gram. Correlation and path coefficient analysis offer insights into the significance of various yield components and aid in formulating appropriate selection strategies. These investigations on available germplasm under specific environmental conditions are crucial for harnessing germplasm resources effectively to develop superior green gram varieties.

Materials and Methods
The current investigation was conducted at the Field Experimentation Centre within the Department of Genetics and Plant Breeding at SHUATS, Allahabad, Uttar Pradesh, during the Kharif season of 2022. The experiment employed a Randomized Block Design and featured 20 different Genotypes, each replicated three times. These genotypes were randomly distributed across 60 plots, and the total experimental area spanned 131.5 square meters, with each plot measuring 1 x 1 meter. The spacing between rows was set at 30 centimeters, with a plant-to-plant distance of 10 centimeters. For data collection, five competitive plants were tagged within each replication, and observations were made at various stages of crop growth. Thirteen different characteristics were recorded, including parameters such as days to 50% flowering, plant height, days to 50% pod setting, the number of primary branches per plant, days to maturity, the number of clusters per plant, the number of pods per plant, pod length, the number of seeds per pod, biological yield, 100 seed index (%), harvest index, and seed yield per plant (in grams).

Mean values were computed, and the data underwent analysis of variance following the method recommended by Panse and Sukhatme. Coefficients of variation and heritability (in broad sense) were estimated in accordance with the guidelines outlined by Burton and Devane in 1953 [5]. Genetic advance estimates were derived using the formula proposed by Lush in 1949 [12] and Johnson et al. in 1955 [10]. Correlation coefficient analysis was conducted based on the method provided by Al-Jibouri et al. in 1958 [3], while path analysis followed the approach suggested by Dewey and Lu in 1959 [6].

Results and Discussions
Analysis of variance revealed significant variations among the genotypes across all the traits. This suggests ample opportunities for selecting promising lines from the existing germplasm for traits related to yield and yield components. The genotypes exhibiting the highest economic yield or seed yield per plant, based on the mean values, were LGG-450, Amulya, Shakti, and Pusa Baisakhi.

Table-1 presents the genotypic and phenotypic coefficient of variation, heritability, and genetic advance as percentages over the mean for each trait. Notably, the Phenotypic Coefficient of Variation (PCV) exceeded the corresponding Genotypic Coefficient of Variation (GCV) for all traits, indicating the influence of the environment.

The GCV values ranged from the highest for clusters per plant (34.857), biological yield (32.653), economic yield (30.912), and pods per plant (25.611), to moderate estimates for primary branches per plant (18.751), seeds per pod (13.097), and pod length (10.742). In contrast, lower GCV values were

recorded for plant height (8.907), seed index (6.495), days to 50% flowering (4.306), harvest index (6.062), days to 50% pod setting (1.657), and days to maturity (1.523). As for the Phenotypic Coefficient of Variation (PCV), it was notably high for clusters per plant (36.014) and biological yield (34.192), followed by economic yield (32.159) and pods per plant (27.14). Moderate PCV estimates were recorded for primary branches per plant (19.754), seeds per pod (16.275), pod length (12.553), plant height (11.652), and seed index (10.553). Conversely, lower PCV values were observed for days to 50% flowering (7.595), harvest index (6.062), days to 50% pod setting (2.773), and days to maturity (2.618).The study found that both high phenotypic and genotypic coefficients of variation were prominent for clusters per plant, biological yield, economic yield, and pods per plant. These findings align with previous research by Makeen et al. (2007) [13], and Saxena et al. (2014) [21].

In the current study, the traits displayed varying levels of heritability, with the highest heritability observed for clusters per plant at 93.673 and the lowest for harvest index at 31.996. The high heritability values for these traits suggest that they are less affected by environmental factors, making them suitable for straight forward selection methods based on observed phenotypes. Specifically, heritability estimates were notably high for clusters per plant (93.673), economic yield (92.394), biological yield (91.2), and pods per plant (89.052). These findings suggest that these traits are influenced primarily by additive genetic factors, and improvements can be achieved through individual plant selection. These results align with previous studies conducted by Reddy et al. (2003) [19], and Makeen et al. (2007) [13]. High heritability, in conjunction with significant genetic advance, can be valuable for selection purposes. Clusters per plant (93.673) exhibit high heritability, indicating that these traits are likely influenced by additive gene effects. However, it's worth noting that traits with high heritability estimates but moderate to low genetic advance, such as days to 50% flowering and days to maturity, are more strongly impacted by environmental factors, making direct selection for these traits less effective.

Correlation analysis
Table 2 presents the results of correlation coefficient analysis for various qualitative traits of greengram. Plant height, primary branches per plant, clusters per plant, pods per plant, and seed index displayed positive and statistically significant associations with economic yield or grain yield per plant at both the phenotypic and genotypic levels. These findings are consistent with previous studies conducted by Ahmed et al. (2014) [2], and Muralidhara et al. (2016) [14]. In contrast, days to maturity exhibited a negative and statistically significant correlation with grain yield per plant, a pattern observed in studies by Reddy et al. (2011) [19], and Tejber et al. (2009) [22]. Days to 50% flowering displayed a negative correlation with seed yield per plant, although this correlation was not statistically significant, which aligns with the findings of Garje et al. (2014) [9].

Furthermore, there was a positive association between plant height and primary branches per plant. Primary branches per plant demonstrated a positive and statistically significant correlation with clusters per plant. Pods per plant exhibited a positive and statistically significant correlation with pod length at both the phenotypic and genotypic levels.

Path Coefficient analysis
Table 3 displays the outcomes of Path Coefficient analysis for various qualitative traits of green gram. This analysis revealed that, at the genotypic level, days to maturity, plant height, primary branches per plant, seed index, the number of seeds per pod, biological yield, economic yield, seed index, and harvest index exerted a direct positive influence on seed yield. Meanwhile, at the phenotypic level, days to 50% flowering, days to pod setting, plant height, the number of clusters per plant, the number of pods per plant, pod length, seed index, economic yield, biological yield, and harvest index displayed a direct positive impact on seed yield per plant.

Plant height, biological yield, harvest index, and seed index exhibited direct positive effects on both phenotypic and genotypic levels, aligning with similar findings reported by Alom *et al.* (2015) [4] and Rathor *et al.* (2015) [17]. Additionally, primary branches per plant displayed a positive indirect effect on economic yield at the phenotypic level, consistent with the results reported by Eswaran *et al.* (2015) [7]. At the genotypic level, primary branches per plant directly contributed to seed yield, a trend also observed in the study conducted by Rupaldhoot *et al.* (2017) [16]. Selecting for these traits is likely to enhance the efficiency of breeding programs aimed at improving yield.

Table 1: Estimates of genetic parameters for different quantitative characters in Greengram

| S. No.	Characters	GCV	PCV	Heritability (h^2)	Genetic Advancement (5%)	Genetic Adv as % of Mean (5%)
1	Days to 50% flowering	4.306	7.595	32.151	1.318	5.03
2	Days to 50% pod setting	1.657	2.773	35.717	1.172	2.04
3	Days to maturity	1.523	2.618	33.848	1.253	1.826
4	Plant height	8.907	11.652	58.438	10.085	14.027
5	Primary branches per plant	18.751	19.754	90.1	2.226	36.665
6	Clusters per plant	34.857	36.014	93.673	5.715	69.496
7	Pods per plant	25.611	27.14	89.052	4.358	49.788
8	Pod length	10.742	12.553	73.227	1.36	18.936
9	Seeds per pod	13.097	16.275	64.762	2.323	21.713
10	Economic yield	30.912	32.159	92.394	2.731	61.208
11	Biological yield	32.653	34.192	91.2	5.823	64.237
12	Harvest Index	3.429	6.062	31.996	2.036	3.995
13	Seed Index	6.495	10.553	37.887	5.678	8.236
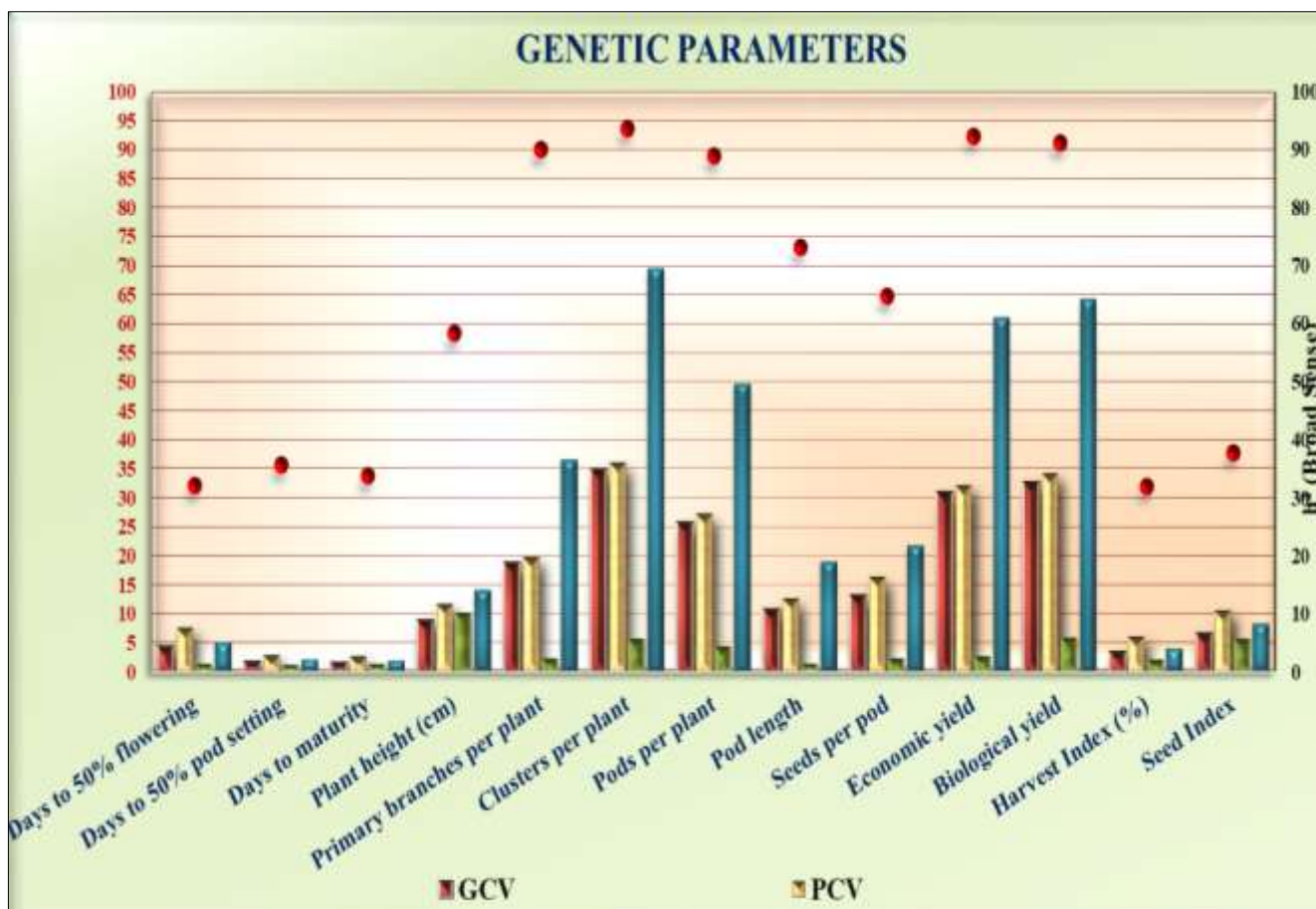
Fig 1: Histogram depicting Genotypic and Phenotypic Coefficient of Variation for different characters in Greengram

Table 2: Correlation coefficient analysis

Traits		Days to 50% flowering	Days to 50% pod setting	Days to maturity	Plant height	Primary branches per plant	Clusters per plant	Pods per plant	Pod length	Seeds per pod	Biological yield	Harvest index	Seed index	Economic yield per plant
Days to 50% flowering	P	1.0000	-0.1280	0.262*	0.0794	-0.1840	0.1106	0.0295	0.1258	0.0959	-0.1259	0.2019	-0.0393	-0.0736
	G	1.0000	-0.363*	-0.1377	0.308*	-0.1942	0.1614	0.0864	0.302*	0.2227	-0.256*	0.442**	-0.1807	-0.1415
Days to 50% pod setting	P		1.0000	0.419**	-0.0136	0.0632	-0.0039	0.0316	-0.0766	-0.0382	-0.1120	0.0495	0.267*	-0.0308
	G		1.0000	0.761**	-0.339*	0.2066	-0.1083	0.1167	-0.0145	0.0019	-0.1132	-0.1400	0.675**	-0.1399
Days to maturity	P			1.0000	-0.1898	-0.2423	-0.0976	-0.2525	-0.0577	0.0596	-0.349*	0.0428	-0.0003	-0.370*
	G			1.0000	-0.474**	-0.324*	-0.2395	-0.416**	-0.1464	0.0177	-0.791**	0.0035	-0.0420	-0.721**
Plant height	P				1.0000	0.599**	0.558**	0.298*	0.0911	0.1130	0.630**	-0.272*	0.308*	0.680**
	G				1.0000	0.788**	0.666**	0.416**	0.1447	0.1811	0.841**	-0.591**	0.298*	0.802**
Primary branches per plant	P					1.0000	0.498**	0.1833	-0.1616	-0.1528	0.668**	-0.339*	0.264*	0.627**
	G					1.0000	0.553**	0.1965	-0.1694	-0.1647	0.721**	-0.552**	0.402*	0.686**
Clusters per plant	P						1.0000	0.0329	-0.1693	-0.0698	0.643**	-0.1296	0.0819	0.676**
	G						1.0000	0.0495	-0.1589	-0.0696	0.671**	-0.257*	0.1839	0.674**
Pods per plant	P							1.0000	0.457**	0.410*	0.363*	0.0594	0.438**	0.423**
	G							1.0000	0.483**	0.447**	0.369*	0.1511	0.746**	0.445**
Pod length	P								1.0000	0.764**	0.1817	0.1516	0.290*	0.2095
	G								1.0000	0.809**	0.1601	0.2384	0.488**	0.2367
Seeds per pod	P									1.0000	0.1056	0.0999	0.1396	0.1378
	G									1.0000	0.0705	-0.0689	0.276*	0.1180
Biological yield	P										1.0000	-0.1869	0.320*	0.956**
	G										1.0000	-0.340*	0.580**	0.815**
Harvest index	P											1.0000	0.0121	-0.0572
	G											1.0000	0.2414	-0.1790
Seed index	P												1.0000	0.366*
	G												1.0000	0.646**
Economic yield per plant	P													1.0000
	G													1.0000

*significance at 5%
**significance at 1%

Table 3: Path Coefficient Analysis

| Traits		Days to 50% flowering	Days to 50% pod setting	Days to maturity	Plant height	Primary branches per plant	Clusters per plant	Pods per plant	Pod length	Seeds per pod	Biological yield	Harvest index	Seed index	Economic yield per plant
Days to 50% flowering	P	0.0079	-0.0010	0.0021	0.0006	-0.0015	0.0009	0.0002	0.0010	0.0008	-0.0010	0.0016	-0.0003	-0.0736
	G	-0.2686	0.0974	0.0370	-0.0827	0.0522	-0.0433	-0.0232	-0.0811	-0.0598	0.0686	-0.1186	0.0485	-0.1415
Days to 50% pod setting	P	-0.0123	0.0964	0.0404	-0.0013	0.0061	-0.0004	0.0030	-0.0074	-0.0037	-0.0108	0.0048	0.0258	-0.0308
	G	0.1356	-0.3739	-0.2847	0.1266	-0.0773	0.0405	-0.0436	0.0054	-0.0007	0.0423	0.0524	-0.2525	-0.1399
Days to maturity	P	-0.0261	-0.0418	-0.0997	0.0189	0.0241	0.0097	0.0252	0.0058	-0.0059	0.0348	-0.0043	0.0000	-0.370*
	G	-0.0344	0.1902	0.2498	-0.1184	-0.0809	-0.0598	-0.1038	-0.0366	0.0044	-0.1976	0.0009	-0.0105	-0.721**
Plant height	P	0.0102	-0.0017	-0.0244	0.1284	0.0768	0.0717	0.0383	0.0117	0.0145	0.0808	-0.0349	0.0395	0.680**
	G	0.1074	-0.1181	-0.1654	0.3488	0.2747	0.2322	0.1452	0.0505	0.0632	0.2932	-0.2062	0.1041	0.802**
Primary branches per plant	P	0.0074	-0.0026	0.0098	-0.0241	-0.0403	-0.0201	-0.0074	0.0065	0.0062	-0.0269	0.0137	-0.0106	0.627**
	G	-0.0309	0.0329	-0.0515	0.1253	0.1591	0.0880	0.0313	-0.0270	-0.0262	0.1147	-0.0878	0.0640	0.686**
Clusters per plant	P	0.0127	-0.0004	-0.0112	0.0641	0.0571	0.1147	0.0038	-0.0194	-0.0080	0.0737	-0.0149	0.0094	0.676**
	G	-0.0003	0.0002	0.0004	-0.0011	-0.0009	-0.0017	-0.0001	0.0003	0.0001	-0.0011	0.0004	-0.0003	0.674**
Pods per plant	P	0.0013	0.0014	-0.0108	0.0128	0.0078	0.0014	0.0428	0.0196	0.0176	0.0155	0.0025	0.0187	0.423**
	G	-0.0096	-0.0130	0.0464	-0.0464	-0.0219	-0.0055	-0.1116	-0.0539	-0.0499	-0.0412	-0.0169	-0.0832	0.445**
Pod length	P	0.0028	-0.0017	-0.0013	0.0020	-0.0036	-0.0038	0.0103	0.0224	0.0172	0.0041	0.0034	0.0065	0.2095
	G	-0.0325	0.0016	0.0157	-0.0156	0.0182	0.0171	-0.0520	-0.1076	-0.0871	-0.0172	-0.0256	-0.0525	0.2367
Seeds per pod	P	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	-0.0001	-0.0001	0.0000	0.0000	0.0000	0.1378
	G	0.0397	0.0003	0.0032	0.0323	-0.0294	-0.0124	0.0798	0.1445	0.1785	0.0126	-0.0123	0.0493	0.1180
Biological yield	P	-0.1011	-0.0900	-0.2804	0.5056	0.5362	0.5161	0.2916	0.1459	0.0848	0.8030	-0.1501	0.2572	0.956**
	G	-0.1814	-0.0804	-0.5617	0.5967	0.5117	0.4760	0.2619	0.1136	0.0500	0.7099	-0.2412	0.4120	0.815**
Harvest index	P	0.0244	0.0060	0.0052	-0.0329	-0.0409	-0.0157	0.0072	0.0183	0.0121	-0.0226	0.1208	0.0015	-0.0572
	G	0.1817	-0.0576	0.0015	-0.2432	-0.2271	-0.1057	0.0622	0.0981	-0.0283	-0.1398	0.4114	0.0993	-0.1790
Seed index	P	-0.0007	0.0048	0.0000	0.0055	0.0047	0.0015	0.0078	0.0052	0.0025	0.0057	0.0002	0.0179	0.366*
	G	-0.0483	0.1806	-0.0112	0.0798	0.1076	0.0492	0.1994	0.1305	0.0739	0.1552	0.0646	0.2675	0.646**
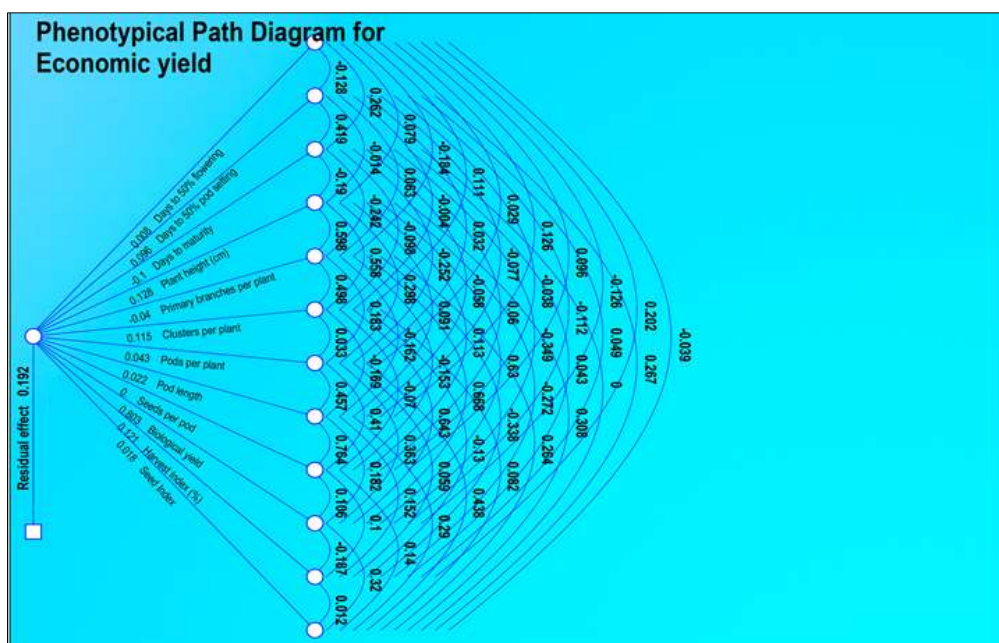
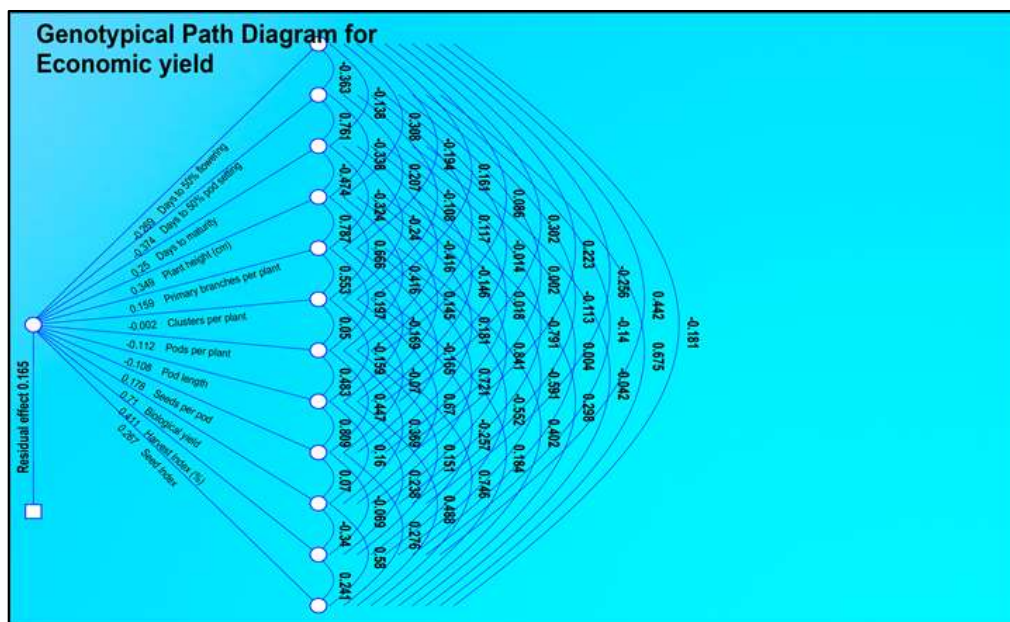**Fig 2:** Phenotypical Path diagram for grain yield per plant

Fig 3: Genotypical Path diagram for grain yield per plant

Conclusion
Based on the findings of this study involving 20 different green gram genotypes, it can be concluded that LGG-450 outperformed the others in terms of grain yield per plant, followed closely by VBN-3 and AMULYA. LGG-450 also exhibited the shortest time to maturity, while VBN-3 had the highest number of pods per plant. Several key traits demonstrated high values for Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), heritability, and genetic advance as a percentage of the mean. Notably, clusters per plant, biological yield, and economic yield displayed these high values, indicating their potential importance for crop improvement. Furthermore, grain yield per plant exhibited significant positive correlations with plant height, primary branches per plant, clusters per plant, pods per plant, biological yield, and seed index. Plant height, biological yield, harvest index, and seed index were identified as having a direct positive impact on grain yield per plant at both

phenotypic and genotypic levels. These traits should be given special consideration in the selection process for crop improvement.

References
1. Annual report. Directorate of pulses development; c2021-22
2. Ahmad HB, Rauf S, Rafiq CM, Mohsin AU, Shahbaz U, Sajjad M. Genetic variability for yield contributing traits in mung bean (*Vigna radiate* L.). J glob. Agric. Soc. Sci. 2014;2(2):52-54.
3. Bouri HAA, Miller PA, Robinson HF. Genotypic and environmental variance in upland cotton of interspecific origin. Journal of Agronomy. 1958;50:633-635.
4. Alom KM, Rashid MH, Biswas M. Genetic Variability, Correlation and Path Analysis in Mungbean (*Vigna radiata* L). Journal of Environmental Science and Natural

Resources. 2015;7(1):131-138.

5. Burton GW, De Vane EH. Estimating heritability in tall fescue (*Fastuca arundinaceae*) from replicated clonal material. Agron J. 1953;45:478-481.

6. Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agron J. 1959;51(9):515-518.

7. Eswaran R, Senthilkumar N. Correlation Path analysis in greengram [*Vigna radiata* (L.) Wilczek] for drought stress Plant Archives. 2015;15(1):247-249.

8. Fisher RA. The correlation between relative on the supposition of Mendalian Inheritance. Trance Royal Society, Edinburg. 1918;52:399-403.

9. Garje UA, Bhailume MS, Deepak R. Nagawade, Sachin D. Parhe Genetic association and path coefficient analysis in green gram [*Vigna radiata* (L.) Wilczek] Journal of Food Legumes. 2014;27(2):151-154.

10. Johnson JL, Robinson HF, Comstock RS. Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 1955;47:314-318.

11. Goyal L, Intwala CG, Modha KG, Vishwas R Acharya Association and diversity analysis for yield attributing traits in advance generation of green gram (*Vigna radiata* (L.) Wilczek) International Journal of Chemical Studies. 2021;9(1):1934-1939.

12. Lush JL. Heritability of quantitative characters in farm animals. Hereditas. 1949;35:356-375.

13. Makeen K, Garard A, Arif J, Singh AK. Genetic variability and correlations studies on yield and its components in mungbean (*Vigna radiata* (L.) Wilczek). Journal of Agronomy. 2007;6(1):216-218.

14. Muralidhara YS, Sanjeev BG, Shanthala J. Genetic Variability, Correlation and Path Coefficient Analysis of Seed Yield Components in Green Gram Advances in life sciences. 2016;5(3):1085-1091.

15. Panse VG, Sukhatme PV. Statistical Methods for Agricultural workers. Indian council of Agricultural Research, New Delhi; c1978.

16. Yadav R, Ram JB, Suresh BG, Lavanya GR. Studies on genetic variability, character association for yield and yield components in green gram (*Vigna radiata* L. Wilczek) Journal of Pharmacognosy and Phytochemistry. 2017;6(4):1988-1991.

17. Rathor P, Singh A, Imran M, Ali K, Fatma R. Character association and Path Analysis for Yield and Yield Component Traits in Mungbean [*Vigna radiata* (L.) Wilczek]. Indian Research Journal of Genetics and Biotechnology. 2015;7(01):93.

18. Reddy KD, Venkateswarlu O, Obaiah MC, Siva Jyothi GL. Studies on genetic variability, character association and path co-efficient analysis in Greengram [*Vigna radiata*. (L.) Wilczek]. Legume Research. 2011;34(3):202-206.

19. Reddy VLN, Reddisekhar M, Reddy KR, Reddy KH. Genetic variability for yield and its components in mungbean, [*Vigna radiata* (L.) Wilczek]. Legume Research. 2003;26(4):300-302.1852.

20. Dhoot R. Modha KG, Kumar D, Dhoot M. Correlations and Path Analysis Studies on Yield and its Components in Mungbean (*Vigna radiata* (L.) Wilczek) Int. J Curr. Microbiol. App. Sci. 2017;6(5):370-378.

21. Saxena RR, Singh PK, Saxena RR. Correlation and path analysis in Mungbean cultivars (*Vigna radiata* (L.)

Wilczek). Journal of Inter Academicia. 2007;11(2):143-148.

22. Singh T, Amitesh S, Alie FA. Morpho-physiological traits as selection criteria for yield improvement in Mungbean [*Vigna radiata* (L.) Wilczek]. Legume Research. 2009;32(1):36-40.