Original Research Article

Spectrum of genetics variations, association,path coefficient analysis ingreen gram (*Vigna radiata* L. wilzeck)

Authors' contributions

This work was carried out in collaboration among all authors. Authors MHV and RK did the conceptualization of research work and designing of experiments. Authors MHV, RK and IRD did the execution of field/lab experiments and data collection. Authors MHV, RK, IRD, AVG and AKK did the analysis of data and interpretation. Authors MHV, RK and IRD did the preparation of manuscript. All authors read and approved the final manuscript.

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ABSTRACT

The high protein content and ability of *Vigna radiata* L. Wilczek, sometimes known as the mung bean, to fix nitrogen in the soil make it a highly significant pulse crop.The most challenging feature, seed yield is greatly influenced by the environment and other factors. This interpretation states that the study's goal was to evaluate the relationships between 22 distinct genotypes of mung beans in terms of yield and yield-attributing traits. Research on variations in genetics identified that there was a fair level of diversity among the 22 genotypes. Secondary brancheshad the highest PCV and GCV, followed by grain yield. The characters, 50% flowering, days to reproductive phase, days to maturity, plant height (cm), pods per plant, length of the pod, seeds per pod, primary branches, secondary branches, clusters per plant, grain yield (g), 100 seed weight (g) had shown high heritability combined with genetic advance as percent mean.Pod length, cluster per plant, primary branches, seeds per pod, and 100 seed weightpod lengthwereshown as a highly significant and positive correlation.cluster per plant, plant height, seeds per pod, andreproductive phaseexplained the highest positive direct effect on seed yield, as shown by the analysis of path coefficients. Therefore, to increase the seed yield of green gram, these traits 50% flowering, days to reproductive phase, days to maturity, plant height (cm), pods per plant, length of the pod, seeds per pod, primary branches, secondary branches, clusters per plant, grain yield (g), 100 seed weight (g) must be focused on in developing a breeding strategy.

Keywords: Genetic variability; Heritability;GCV; PCV; Correlation; Path analysis.

1. INTRODUCTION

One of the most significant legumes for food in South and Southeast Asia is the greengram[*Vigna radiata* (L.) Wilczek].It is India's third-most significant pulse crop[1]. Madhya Pradesh, Maharashtra, Uttar Pradesh, Andhra Pradesh, Karnataka, and Rajasthan are the primary regions where it is grown.The green gram is a semi-erect or upright annual herbaceous plant. The flower grows in axillary racemes with diadelphous stamens and an ovary with a long-bearded style. The leaves are trifoliate with long petioles, stipules with basal appendage, stipules minute, and leaflets entirely oval[2]. Due to the claimed health benefits and growing popularity of Indian ethnic dishes, domestic consumption of greengram has surged recently[3]. Protein has a fair amount of lysine, an amino acid deficient in cereal grains.greengram seeds include a variety of vitamins and minerals, including ascorbic acid, thiamine, riboflavin, niacin, pantothenic acid, and vitamin A. Other minerals include calcium, iron, magnesium, phosphorus, and potassium[4].This crop was regarded as a tough pulse crop that thrives in hot, dry climates. After harvest, the crop's cultivation provides 30 to 40 kg N/ha to the soil, increasing its fertility. As a result, roughly 25% less nitrogen needs to be applied to the next crop, which is often a cereal[5].

Genetic variety is useful in selecting the best yield qualities for hybridization or selection[6].An effective breeding program must begin with a survey of genetic variability, including heritability, genotypic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV)[7]. Correlation research can be used to determine the degree of interdependence between significant plant features, which is useful for choosing the right genotype. The majority of plant breeding initiatives focus on increasing yield, a complex trait that depends on numerous other traits that are further related to one another.

Consequently, the correlation study can be deemed inadequate. Finding the appropriate plant varieties for successful plant breeding projects requires determining the correlation and path coefficient between yield and yield criteria. Path analysis was done to determine how much the causal components, directly and indirectly, influenced the effective component. With these considerations in mind, the current study aims to screen greengram germplasm accessions, investigate the high-yield potential and quality traits, and examine genetic variation, heritability, genetic advance, correlation, and yield-related trait path analysis. When choosing a breeding program, heritability knowledge combined with genetic advancement is helpful. Finding optimal procedures for selecting quantitative qualities and comprehending the relationship between yield and contributing characters depend heavily on the correlation coefficient[8].

It should be observed, still that a relationship does not always provide clear insights into the unique effects that each character has on the dependent character[9,10]. "Understandably, identifying the traits that genuinely influence seed yield would need a route analysis.Thus, path analysis is employed to quantify the impacts of attributes, both direct and indirect[11].The study aims to solve the problem of identifying the particular characteristics that affect seed yield in interactions between different features. It draws attention to how standard methods fail to give exact information about the effects of each individual. To provide a more thorough knowledge of the variables influencing seed production, the researchers propose to employ path analysis to quantify both the direct and indirect effects of qualities on seed production.

2. MATERIALS AND METHODS

In *Kharif* 2023, twenty-twogenotypes of mung beans were used in the experiment, which used a Randomized Block Design with three replications at the Genetics and Plant Breeding (GPB) farm, School of Agriculture,LPU, Phagwara, Punjab. With a gap of 30 cm x 10 cm both between and within rows, each row measured 2 m. The research is located 243 meters

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above mean sea level at latitude 31º 19'32" N and longitude 75º 34'45'" E.During the trial, every other suggested package of procedures was adhered to for healthy crop growth, and the genotypes were harvested as soon as the pods reached maturity. For data collection, ten randomly chosen plants were chosen from each genotype in each replication.Every suggested practice in the package was adhered to.ANOVA, or Analysis of variance, was used to examine each of the 12 characters that were being examined. The study of variance includes genotypic and phenotypic coefficients of variation [12]and heritability was all performed using standard statistical procedures [13]. The Falconer formula was used to compute the correlations between genotype and phenotype.The path coefficient study was conducted using therecommended methodology [14]. The characters in the present study *viz*., days to 50% flowering(DF), days to reproductive phase (DP), days to maturity (DM), plant height (PH), number of pods per plant (NPPP), length of the pod (LP), number of seeds per pod (NSPP), number of primary branches (NPB), number of secondary branches (NSB), number of clusters per plant (NCPP), grain yield (GY), 100 seed weight (HSW).

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Table 1. Details of the Genotypes are given below

Sr. No	Genotypes	Source
1.	MASCO - 44	KVK, TELENGANA, RUDROOR
2.	COGG - 1276	KVK, TELENGANA, RUDROOR
3.	MH - 934	KVK, TELENGANA, RUDROOR
4.	JLM - 1748	KVK, TELENGANA, RUDROOR
5.	BANSI BHOOG	KVK, TELENGANA, RUDROOR
6.	GM – 6	KVK, TELENGANA, RUDROOR
7.	ML -818	KVK, TELENGANA, RUDROOR
8.	SML -115	KVK, TELENGANA, RUDROOR
9.	PUSA BAISAKHI	KVK, TELENGANA, RUDROOR
10.	EML - 668	KVK, TELENGANA, RUDROOR
11.	MGG – 295	KVK, TELENGANA, RUDROOR
12.	RAJENDRAN G-65	KVK, TELENGANA, RUDROOR
13.	VIRAT GOLD	ARS, SRI GANGANAGAR
14.	BANSI MOONG	ARS, SRI GANGANAGAR
15.	MOONG TILAK	ARS, SRI GANGANAGAR
16.	TILAK GOLD	ARS, SRI GANGANAGAR
17.	LGG-407	KVK, ANDRA PRADESH, GARIKAPADU
18.	PUSA – 105	KVK, ANDRA PRADESH, GARIKAPADU
19.	WGG – 42	KVK, ANDRA PRADESH, GARIKAPADU
20.	LGG - 460	KVK, ANDRA PRADESH, GARIKAPADU
21.	PDM – 54	KVK, ANDRA PRADESH, GARIKAPADU
22.	TM - 962	KVK, ANDRA PRADESH, GARIKAPADU

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3. RESULTS AND DISCUSSION

At the 0.01 level of significance, the analysis of variance showed that there was a significant difference across all genotypes, demonstrating the existence of genetic variability (Table 3). All of the features under study have their estimated variance components and broad-sense heritability displayed in (Table 4).

3.1 PCV AND GCV

The trait secondary branches had the highest PCV (26.941) and GCV (26.771); the number of seeds per pod had the highest PCV (15.942) and GCV (15.764); the grain yield had the highest PCV (15.679) and GCV (14.928). The lowest GCV (3.003) and PCV (3.498) values are indicated by the number of days before 50% blooming. For each of the 12 traitsexamined in this study, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV). This illustrates how a trait's expression is influenced by its surroundings. Characters with low magnitude GCV and PCV were those with days to 50% flowering, days to maturity, days to reproductive phase, and plant height; characters with moderate magnitude GCV and PCV values were those with pods per plant and pod length.The identical outcomes were observed[15,16].

3.2 Heritability

All of the traits in the current investigation exhibited the highest heritability, whichis number of secondary branches (0.987), number of seeds per pod (0.977), number of pods per plant (0.929), number of clusters per plant (0.918), 100 seed weight (0.917), grain yield (0.906), days to reproductive phase (0.886), days to maturity (0.875), number of primary branches (0.863), length of the pod (0.837), days to 50% flowering (0.737), plant height (0.621) shown in below (Table 4). The outcomes lined upfor grain yield and number of pods per plant [17]. The traits number of secondary branches, number of seeds per pod, number of pods per plant, number of clusters per plant, 100 seed weight,grain yield, days to reproductive phase, days to maturity, number of primary branches, length of the pod, showed a high heritability combined with high genetic advance as percent mean. The yield might be increased by choosing these characters directly.similar findings were obtainedin green gram [18, 19]. Moderate genetic advance as a percentmeanand high heritability wasshown bynumber of pods per plant and, length of the pod. days to 50% flowering, plant height. However, plant height and days to 50% flowering showed high heritability.

3.3 Correlation Studies

Studying the relationships between seed yield and its constituents as well as between the constituents is necessary for genetically improving seed yield while seed yield is a polygenic and complex characteristic that depends on several factors that contribute to yield.The directly observed characteristics are the focus of the phenotypic correlation. In this work, 22 genotypes of mung beans were examined to evaluate the genotypic and phenotypic correlations in every pair of character combinations that could exist.Since the environment's influence on a trait's expression is hidden by phenotypic correlation coefficients, genotypic correlation coefficients are thought to have high estimations[20]. The calculated correlation coefficient values between the various character pairings under consideration are displayed inTable 5. A useful method for elucidating the strength and scope of the relationships between significant plant characteristics is correlation coefficient analysis, which also offers

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fundamental standards for selection in field trials based on yield and its constituent parts[21]. To take full advantage of the genetic variability observed in green gram for seed production, it is essential to understand the inheritance patterns of grain yield and its closely related components[22].

Genotypic correlation of the components characters with grain yield: Grain yield showed a positive and highly significant correlation withlength of the pod (0.7270), number of seeds per pod (0.6906), number of primary branches (0.7760), number of clusters per plant and 100 seed weight, positive and significant correlation with plant height (0.3778), and number of pods per plant, while the negative and non-significant correlation with days to 50% flowering (-0.3405), days to reproductive phase (-0.0712), and days to maturity (-0.1513).Similar findings were observed[6, 23, 24].

Phenotypic correlation of the components characters with grain yield: Grain yield showed a positive and highly significant correlation with the length of the pod (0.48), number of seeds per pod (0.60), number of primary branches (0.53), number of clusters per plant (0.45), and 100 seed weight (0.63), positive and significant correlation with number of pods per plant (0.35), while negative and non-significant correlation with days to 50% flowering (-0.18), days to reproductive phase (-0.03), days to maturity (-0.12).Similar findings were observed[6, 25, 26, 27].The degree of correlation that is shown between characteristics depends on how they relate to one another as well as how genes that cause variation are separated.Some genes may result in a positive association by increasing both attributes, whereas other genes may cause a negative correlation by decreasing one and increasing the other.The competition between features for shared antecedents, which are limited, leads to negative correlations. Positive correlations, on the other hand, result from variations in the genes that supply precursors[6,28].

3.4 Path Analysis

Any breeding program's effectiveness in selecting features mostly rests on understanding the relationships between traits.The relationship between any two variables is simply identified by the correlation coefficient; it is not revealed. To determine the relative importance of the causal variables involved, the correlation coefficient can be divided into direct and indirect effects using the Path Coefficient Analysis[6,29]. Consequently, path coefficient analysis takes into account both the direct and indirect impacts by dividing the correlation coefficient between the variables[30].This helps determine how much a change in one variable will affect a change in another. Eleven characteristics were considered independent characters (causes) in the path coefficient analysis, with seed yield per plant acting as the dependent character (effect).Path coefficient analysis was performed to identify features with major direct and indirect influences on grain yield, and the results were used to define the phenotypic correlation values (Table 6).The factor with the highest positive direct impact onthe yield was recorded by the number of clusters per plant (0.546), plant height (0.277), number of seeds per pod (0.257), and reproductive phase (0.250). It's interesting to note that these traits likewise showed a strong positive link with yield; as a result, they ought to be taken into consideration as crucial selection factors for increasing green gram production. While, days to maturity (-0.988),number of pods per plant (-045), and 100 seed weight (-0.301)resulting a direct decrease in the number of seeds produced per plant.Similar findings were observed [6, 31, 32].

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Table 2. Mean performance of genotypes for twelve characters in greengram

Sr.no	Genotypes	DF	RP	DM	PH	NPPP	LP	NSPP	NPB	NSB	NCPP	HSW	GY
1	MASCO - 44	40.66	47.93	73.22	47.60	35.51	8.21	8.53	4.44	12.07	7.99	4.50	7.92
2	COGG - 1276	42.99	47.63	74.30	52.92	37.08	7.74	8.10	5.31	11.40	7.73	5.52	8.32
3	MH - 934	40.66	47.95	71.72	51.35	38.47	8.70	10.54	5.66	12.39	9.77	6.78	10.66
4	JLM - 1748	43.99	48.61	73.61	48.74	36.22	7.54	11.32	5.87	12.15	8.60	7.53	10.46
5	BANSI BHOOG	40.32	50.56	75.74	51.46	36.56	8.75	8.40	6.00	11.62	8.75	7.39	10.33
6	GM – 6	44.66	48.66	71.77	49.73	35.84	6.60	7.42	4.90	13.70	8.74	6.29	7.43
7	ML -818	44.32	52.78	74.76	46.11	36.22	7.05	7.33	5.16	10.76	7.92	6.29	8.01
8	SML -115	41.99	52.02	75.36	47.58	41.64	7.68	6.79	4.46	14.96	8.84	5.18	8.42
9	PUSA BAISAKHI	40.99	47.74	70.49	51.32	36.63	8.39	8.82	5.43	14.58	8.91	5.69	8.59
10	EML - 668	41.99	49.00	70.64	51.72	42.29	7.29	9.08	4.65	12.24	10.03	5.26	8.09
11	MGG – 295	41.66	49.83	67.28	50.99	35.34	7.20	9.34	5.02	15.46	6.50	5.45	7.88
12	RAJENDRAN G-65	41.66	47.74	72.73	51.74	39.61	7.96	11.10	6.82	13.09	9.55	7.06	10.29
13	VIRAT GOLD	39.66	46.37	67.97	51.51	38.28	9.25	8.49	6.64	14.55	9.66	7.13	10.83
14	BANSI MOONG	41.32	46.91	70.79	51.27	35.68	8.48	10.61	6.12	12.10	9.37	7.24	10.72
15	MOONG TILAK	44.32	49.14	71.71	48.72	44.08	8.46	9.68	5.92	12.96	8.91	7.79	12.14
16	TILAK GOLD	41.90	49.41	65.17	49.03	38.40	6.93	9.66	4.81	5.22	7.63	5.83	8.50
17	LGG-407	40.95	47.22	63.55	50.99	37.30	7.73	10.42	5.20	6.48	7.09	6.90	9.43
18	PUSA – 105	41.04	47.55	66.08	51.32	37.67	7.83	11.00	5.73	11.72	9.17	7.07	10.77
19	WGG – 42	41.66	41.59	72.62	50.65	32.57	7.03	8.27	6.17	10.35	7.93	6.52	7.86
20	LGG - 460	43.99	48.40	72.83	49.35	35.04	7.75	5.93	4.42	4.27	6.42	6.22	7.18
21	PDM – 54	42.99	47.77	72.77	46.00	38.22	8.09	8.88	5.60	7.09	8.00	5.35	7.39
22	TM - 962	40.66	47.63	67.30	50.99	41.84	8.01	9.36	5.57	10.85	7.64	6.07	8.88

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Table3. Analysis of variance for seed yield and its components in green gram

Sr. No	Characters	Mean sum of squares		
		Replication	Genotype	Error
1	Days to 50% flowering	1.44	6.476**	1.705
2	Days to reproductive phase	0.62	14.06**	1.601
3	Days to maturity	2.772	34.66**	4.319
4	Plant height (cm)	0.107	10.933**	4.141
5	No. of pods per plant	2.286	22.617**	1.595
6	Length of the pod (cm)	0.0028	1.341**	0.217
7	No. of seeds per pod	0.035	6.248**	0.138
8	No. of primary branches	0.378	1.410**	0.193
9	No. of secondary branches	0.132	28.109**	0.353
10	No. of clusters per plant	0.0374	3.086**	0.254
11	Grain yield (g)	0.059	6.100**	0.569
12	100 seed weight (g)	0.045	2.397**	0.198

*and** denotes significance at 5% and 1% level of probability respectively.

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Table4.Genetic parameters of variation for seed yield and its components in green gram

Trait	DF	RP	DM	PH	NPPP	LP	NSPP	NPB	NSB	NCPP	HSW	GY

		Range						
Sr. No	**characters**	**Min.**	**Max.**	**Mean**	**GCV**	**PCV**	**h^2**	**GA%**
1	Days to 50% flowering	39.65	44.65	42.01	3.003	3.498	0.737	5.313
2	Days to reproductive phase	46.37	52.78	48.29	4.221	4.483	0.886	8.186
3	Days to maturity	63.55	75.74	71.02	4.479	4.787	0.875	8.633
4	Plant height (cm)	46	52.91	50.04	3.006	3.814	0.621	4.881
5	No. of pods per plant	32.57	44.08	37.74	7.01	7.272	0.929	13.923
6	Length of the pod (cm)	6.59	9.24	7.84	7.777	8.5	0.837	14.659
7	No. of seeds per pod	5.93	11.09	9.04	15.764	15.942	0.977	32.114
8	No. of primary branches	4.42	6.82	5.44	11.691	12.585	0.863	22.373
9	No. of secondary branches	5.21	15.46	11.36	26.771	26.941	0.987	54.801
10	No. of clusters per plant	6.41	10.03	8.41	11.549	12.057	0.918	22.791
11	Grain yield (g)	7.18	12.14	9.09	14.928	15.679	0.906	29.279
12	100 seed weight (g)	4.5	7.79	6.32	13.55	14.149	0.917	26.73

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DF	**1.0000**	0.3913*	0.4577*	-0.6235**	-0.0424	-0.6225**	-0.3784*	-0.3398	-0.2214	-0.2850	0.0642	-0.3405
RP		**1.0000**	0.2650	-0.5169**	0.3729*	-0.1545	-0.2534	-0.4942**	0.1333	-0.0230	-0.1826	-0.0712
DM			**1.0000**	-0.3574*	-0.1301	0.0787	-0.4734*	-0.0303	0.2432	0.2067	-0.0783	-0.1513
PH				**1.0000**	-0.0726	0.3098	0.4139*	0.5447**	0.3085	0.3093	0.3905*	0.3778*
NPPP					**1.0000**	0.2758	0.1775	0.0187	0.1839	0.4361*	0.0528	0.3803*
LP						**1.0000**	0.2603	0.5801**	0.2327	0.4615*	0.3986*	0.7270**
NSPP							**1.0000**	0.5836**	0.1088	0.3702*	0.4947**	0.6906**
NPB								**1.0000**	0.2876	0.4896**	0.7947**	0.7760**
NSB									**1.0000**	0.5590**	0.0331	0.3208
NCCP										**1.0000**	0.3157	0.6375**
HSW											**1.0000**	0.9095**
GY												**1.0000**

Table 5. Genotypic correlation coefficient among characters in greengram

*and** denotes significance at 5% and 1% level of probability respectively.

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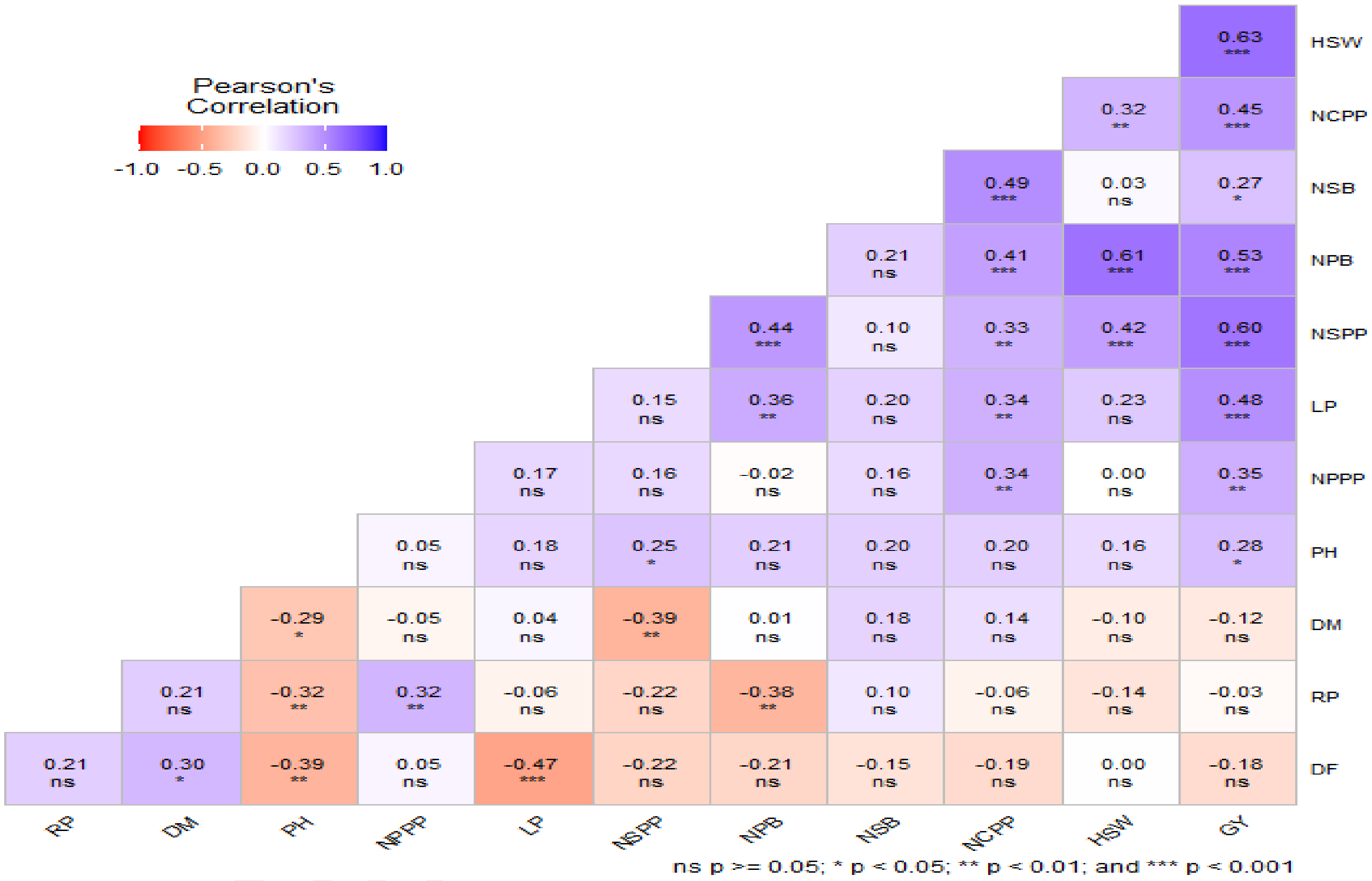

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fig. 1: Phenotypic correlation coefficient

Trait	DF	RP	DM	PH	NPPP	LP	NSPP	NPB	NSB	NCPP	HSW	GY

DF	**1.4259**	0.5580	0.6526	-0.8891	-0.0605	-0.8876	-0.5396	-0.4845	-0.3157	-0.4064	0.0915	-0.3405
RP	0.0981	**0.2506**	0.0664	-0.1295	0.0934	-0.0387	-0.0635	-0.1238	0.0334	-0.0058	-0.0457	-0.0712
DM	-0.4524	-0.2620	**-0.9884**	0.3533	0.1285	-0.0778	0.4679	0.0300	-0.2404	-0.2043	0.0774	-0.1513
PH	-0.1728	-0.1433	-0.0991	**0.2772**	-0.0201	0.0859	0.1147	0.1510	0.0855	0.0857	0.1083	0.3778
NPPP	0.0194	-0.1708	0.0596	0.0333	**-0.4579**	-0.1263	-0.0813	-0.0086	-0.0842	-0.1997	-0.0242	0.3803
LP	-0.9043	-0.2245	0.1144	0.4501	0.4007	**1.4528**	0.3781	0.8428	0.3381	0.6705	0.5792	0.7270
NSPP	-0.0976	-0.0654	-0.1221	0.1068	0.0458	0.0671	**0.2579**	0.1505	0.0281	0.0955	0.1276	0.6906
NPB	-0.0514	-0.0747	-0.0046	0.0824	0.0028	0.0877	0.0882	**0.1512**	0.0435	0.0740	0.1202	0.7760
NSB	-0.0303	0.0183	0.0333	0.0423	0.0252	0.0319	0.0149	0.0394	**0.1370**	0.0766	0.0045	0.3208
NCCP	-0.1557	-0.0126	0.1130	0.1690	0.2383	0.2522	0.2023	0.2676	0.3055	**0.5465**	0.1725	0.6375
HSW	-0.0194	0.0551	0.0236	-0.1178	-0.0159	-0.1202	-0.1492	-0.2397	-0.0100	-0.0952	**-0.3016**	0.9095

Table 6. Genotypic path coefficient showing direct and indirect effects of different contributing characters on grain yield per plant ingreengram

R SQUARE = 1.0465 RESIDUAL EFFECT = SQRT (-1 1.0465)

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Trait	DF	RP	DM	PH	NPPP	LP	NSPP	NPB	NSB	NCPP	HSW	GY
DF	**-0.0860**	-0.0267	-0.0331	0.0425	0.0003	0.0474	0.0264	0.0242	0.0162	0.0205	-0.0029	-0.2682
RP	-0.0037	**-0.0118**	-0.0029	0.0049	-0.0041	0.0014	0.0028	0.0053	-0.0014	0.0005	0.0019	-0.0544
DM	0.0153	0.0097	**0.0396**	-0.0126	-0.0040	0.0024	-0.0174	-0.0004	0.0087	0.0071	-0.0033	-0.1384
PH	0.0233	0.0196	0.0150	**-0.0472**	0.0007	-0.0114	-0.0155	-0.0176	-0.0119	-0.0119	-0.0128	0.3232
NPPP	-0.0007	0.0671	-0.0193	-0.0030	**0.1914**	0.0443	0.0331	0.0019	0.0332	0.0766	0.0064	0.3671
LP	-0.1643	-0.0346	0.0184	0.0717	0.0690	**0.2981**	0.0644	0.1453	0.0648	0.1220	0.0974	0.6238
NSPP	-0.0984	-0.0767	-0.1411	0.1052	0.0554	0.0691	**0.3202**	0.1698	0.0340	0.1133	0.1492	0.6545
NPB	0.0597	0.0943	0.0021	-0.0788	-0.0021	-0.1032	-0.1122	**-0.2116**	-0.0545	-0.0969	-0.1523	0.6775
NSB	-0.0341	0.0220	0.0399	0.0455	0.0315	0.0394	0.0193	0.0467	**0.1813**	0.0969	0.0057	0.2999
NCCP	-0.0033	-0.0005	0.0025	0.0035	0.0055	0.0056	0.0049	0.0063	0.0073	**0.0137**	0.0043	0.5650
HSW	0.0239	-0.1167	-0.0594	0.1916	0.0236	0.2306	0.3287	0.5077	0.0222	0.2231	**0.7054**	0.7991

Table7. Phenotypic path coefficient showing direct and indirect effects of different contributing characters on grain yield per plant in greengram

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R SQUARE = 0.9512 RESIDUAL EFFECT = 0.220

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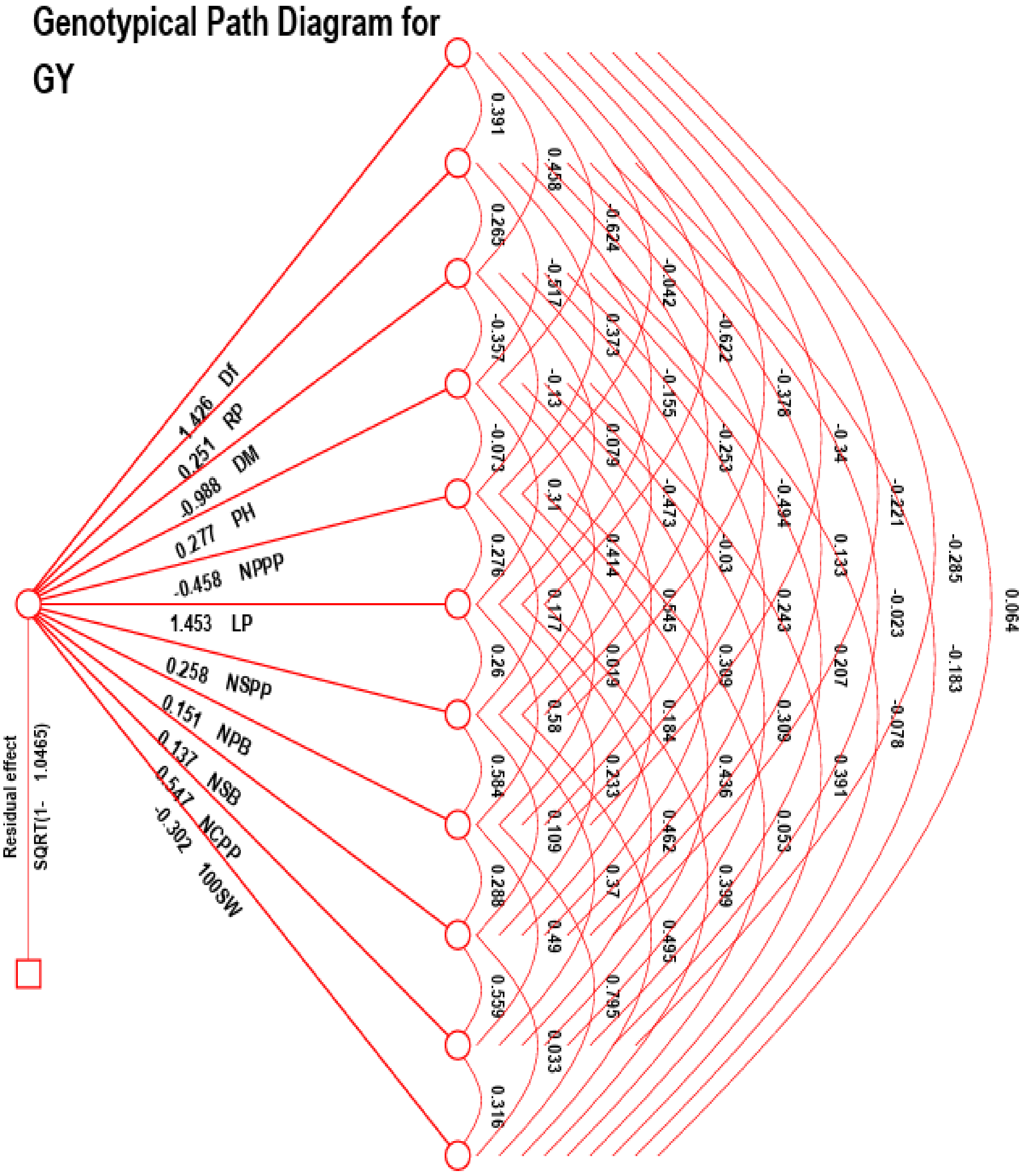

fig.2: Genotypical path diagram for grain yield

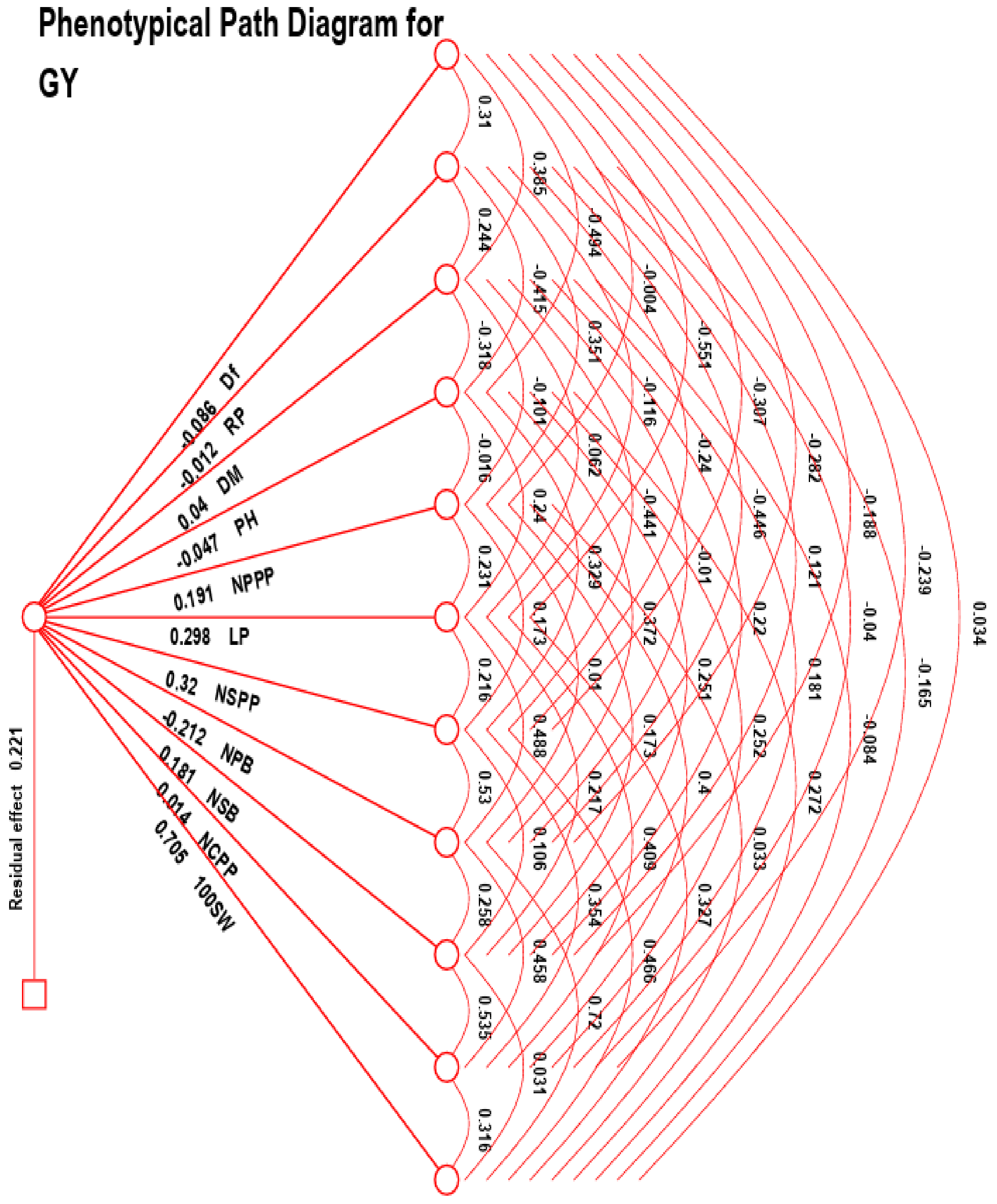

fig.3:Phenotypical path diagram for grain yield

4. CONCLUSION

Understanding how different yield characteristics are interconnected helps improve various other traits directly and indirectly, ultimately enhancing the targeted trait. By examining the correlation between yield and its contributing factors, such as the number of clusters per plant, number of seeds per pod, and plant height, we can determine their impact on seed yield per plant. This analysis reveals that these factors days to 50% flowering, days to reproductive phase, plant height,length of the pod, number of seeds per pod, number of primary branches, number of secondary branches, and number of clustersper plant, have favorable direct effects on seed yield per plant and positive correlations, making them suitable candidates for selection to boost green gram seed yield.

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