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Correlation and path coefficient analysis for yield and its contributing traits in Greengram [*Vigna radiata* (L.) Wilczek]

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Abstract
Current investigation comprised of 40 genotypes, including 2 check varieties, grown at the Instructional Farm of Rajasthan College of Agriculture, Udaipur, using a randomized block design with three replications during the *Kharif* season of 2022. Significant variability among genotypes for various traits was observed, as evidenced by statistically significant mean sum of squares attributed to genotypes. Seed yield per plant exhibited substantial genetic gain as a percentage of the mean, indicating its potential for improvement. Traits with high heritability and substantial genetic gain, such as seed yield per plant and number of pods per plant, are primarily governed by additive gene action. Genotypic correlation coefficients were higher than phenotypic correlations, and significant correlations were observed between seed yield per plant and the number of pods per plant, biological yield per plant, harvest index, 100-seed weight, and number of seeds per pod. Path analysis highlighted the significant positive direct effect of harvest index on seed yield per plant followed by biological yield per plant. Discriminate function analysis showed that among all the traits under study showed the greatest genetic gain and relative efficiency. This outcome strongly suggests that substantial emphasis should be placed on these particular traits during the process of selecting high-yielding genotypes in greengram breeding endeavors. Genotypes G28, G36, G35, G27, and G26 exhibited excellence in yield and key yield-contributing traits, suggesting their potential for future breeding programs.

Keywords: Path coefficient, greengram, correlation, heritability

Introduction
Greengram, scientifically known as *Vigna radiata* (L.) Wilczek, is a crucial and widely cultivated legume in Asia. It holds significant importance as a nutritious food source and is extensively grown and consumed across India (Datta *et al*., 2012) [3]. Greengram, a member of the Fabaceae family, is a self-pollinating legume with a somatic chromosome number of 2n=2x=22. The grain of greengram is a significant protein source, containing 22.51% protein content (Kochhar and Hira, 1997) [5].

Greengram holds the third position among pulses, following chickpea and pigeon pea, in terms of both cultivation area and production (Dhopre *et al*., 2022) [8]. India stands as the leading global producer and consumer of greengram, contributing to over 70% of the world's total production. In India, the total cultivated land dedicated to greengram encompasses 4.5 million hectares, resulting in a total production of 2.5 million tonnes and a productivity of 548 kg per hectare (Greengram outlook report, 2021). Rajasthan, Maharashtra, Karnataka, Madhya Pradesh, Odisha, and Telangana are the primary states in India known for major greengram production. Among these, Rajasthan stands at the forefront, leading both in terms of production and the extent of land dedicated to greengram cultivation. Greengram is grown across an expansive area of 24.678 lakh hectares in Rajasthan, yielding a total production of 12.23 lakh tonnes and boasting a productivity of 495 kg per hectare (Greengram outlook report, 2021).

The variation observed in the field for phenotypic traits is influenced by both genetic and environmental factors. Environmental variation introduces uncertainty in phenotypic variation, necessitating its partition into genetic and non-genetic components (Prajapati *et al*. 2022 & Prajapati *et al*., 2023) [7, 6]. Interaction effects can also mislead the evaluation of genotypic variation, especially when they are high and non-heritable.

To address this, phenotypic variation is partitioned into heritable and non-heritable fractions using genetic parameters such as Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), heritability, and genetic advance.

Materials and Methods

The study was conducted in *Kharif* season of 2022 at the experimental farm of the Department of Genetics and Plant Breeding, Rajasthan College of Agriculture, MPUAT, Udaipur. A total of 40 greengram genotypes, along with two check varieties, were evaluated using a Randomized Block Design. Each genotype was planted in two rows. Throughout the experiment, all the recommended package of practices for Zone IV A of Rajasthan were followed meticulously to foster the healthy growth of the crops.

Characters studied

The data for all the genotypes were collected by observing five randomly selected plants from each plot in every replication. Traits such as plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, seed yield per plant, biological yield per plant, harvest index, and seed protein content were observed from competitive plants, along with days to 50 percent flowering and days to 75 percent maturity at the plot level.

Statistical analysis

The correlation analysis for genotypes was calculated as per formula proposed by Burton (1952) [2]. The coefficient of variance at two (genotypic and phenotypic level), GCV and PCV was calculated. Path coefficients were analyzed at genotypic and phenotypic levels for seed yield per plant. The path coefficient analysis was carried out as per the method suggested by Dewey and Lu (1959) [4].

Results and Discussion

The genotypic and phenotypic correlation coefficients for twelve characters studied are presented in table 1.The genotypic correlation coefficients displayed greater values compared to the phenotypic correlation coefficients for all the examined traits. Days to 50 percent flowering exhibited significant and positive correlation at genotypic and phenotypic levels with days to 75 percent maturity (rg = 0.878** and rp = 0.659**), while showed significant and negative correlation with seed protein content (rg = -0.324*) at genotypic level. Days to maturity showed significant and positive correlation (rp = 0.29*) only with number of seeds per pod (rp = 0.203*) at phenotypic level. Plant height was significantly and positively correlated with seed protein content (rg = 0.309* and rp = 0.474**) at both genotypic and phenotypic levels. Number of branches per plant showed significant and positive correlation with plant height (rg = 0.435** and rp = 0.393**) at both genotypic and phenotypic level. Pods per plant depicted highly positive and significant correlation at genotypic and phenotypic levels with seed yield per plant (rg = 0.724** and rp = 0.736**) and harvest index (rg = 0.709** and rp = 0.724**). It was negatively and significantly correlated with 100-seed weight (rg = -0.348* and rp = -0.256**) at both genotypic and phenotypic level. Pod length showed positive and significant correlation with days to 50 percent flowering (rp = 0.263**), number of seeds per pod (rp = 0.470), harvest index (rp = 0.196*) and seed protein content (rp = 0.331**) at phenotypic level. Number of seeds per pod was positively and significantly correlated with days to 50 percent flowering (rp = 0.317**), days to 75 percent maturity (rp = 0.203*), pod length (rp = 0.470**), harvest index (rp = 0.319), seed yield per plant (rp = 0.296**) and biological yield per plant (rp = 0.222*) at phenotypic level. It showed negative and significant correlation with number of branches per plant (rg = -0.336* and rp = -0.293**) and seed protein content (rg = -0.468**). 100-seed weight exhibited significant and positive correlation with seed yield per pod (rp = 0.306**), biological yield per plant (rp = 0.224*), harvest index (rp = 0.286**) and seed protein content (rp = 0.359**) at only phenotypic level. At both phenotypic and genotypic levels, seed yield per plant had significant and positive correlation with number of pods per plant (rg = 0.724** and rp = 0.736**), biological yield per plant (rg = 0.431**and rp = 0.461**) and harvest index (rg = 0.939** and rp = 0.940**). It also showed positive and significant correlation with 100-seed weight (rp = 0.306**) and number of seeds per pod (rp = 0.296**) only at phenotypic level. Negative and significant correlation was exhibited by number of branches per plant (rp = -0.189*) at phenotypic level. Biological yield per plant showed positive and significant correlation with seed yield per plant (rg = 0.431** and rp = 0.461**) at both genotypic and phenotypic levels, with days to 50 percent flowering (rp = 0.31**), plant height (rp = 0.424**), number of pods per plant (rp = 0.293**), number of seeds per pod (rp = 0.222*), harvest index (rp = 0.202*) and seed protein content (rp = 0.388**) at only phenotypic level. It exhibited negative and significant correlation with only pod length (rg = -0.735**) at genotypic level.Harvest index showed positive and significant correlation with number of pods per plant (rg = 0.709** and rp = 0.724**) and seed yield per plant (rg = 0.939** and rp = 0.940**) at both phenotypic and genotypic level. It also exhibited positive and significant correlation with pod length (rp = 0.196*) and number of seeds per pod (rp = 0.319**) but only at phenotypic level. Protein content was positively and significantly correlated with plant height (rg = 0.309* and rp = 0.474**), pod length (rp = 0.331**), days to 50 percent flowering (rp = 0.182**), 100-seed weight (rp = 0.359**) and biological yield per plant (rp = 0.388**). It showed negative and significant correlation with days to 50 percent maturity 9rg = -0.324**), days to 75 percent maturity (rg= -0.398** and rp = -0.243**) and pod length (rg = -0.948**).

Path coefficient analysis shows that seed yield per plant served as the dependent variable, while other traits including days to 50 percent flowering, days to 75 percent maturity, plant height, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, biological yield per plant, harvest index, and seed protein content were regarded as independent variables.

Table 1: Genotypic (r_g) and phenotypic (r_p) correlation coefficients between different characters in greengram

Characters	r	100-Seed weight (g)	Biological yield per plant (g)	Number of branches per Plant	Days to 50 percent flowering	Days to 75 percent maturity	Harvest Index (%)	Plant height (cm)	Pod length (cm)	Number of pods per plant	Seed protein content (%)	Number of seeds per Pod	Seed yield per plant (g)
100-Seed weight (g)	r_g r_p		0.067 0.224*	0.124 0.115	-0.121 0.041	-0.179 -0.161	0.228 0.286**	0.029 0.142	-0.408** 0.047	-0.348* -0.256**	0.204 0.359**	-0.256 -0.054	0.263 0.306**
Biological Yield per plant (g)	r_g r_p			-0.017 -0.022	0.067 0.31**	-0.058 -0.058	0.079 0.202*	0.277 0.424**	-0.735** 0.144	0.211 0.293**	-0.095 0.388**	-0.092 0.222*	0.431** 0.461**
Number of branches per Plant	r_g r_p				0.123 0.102	0.086 0.078	-0.201 -0.194*	0.435** 0.393**	0.055 0.019	-0.126 -0.125	0.202 0.115	-0.336* -0.293**	-0.194 -0.189*
Days to 50 percent flowering	r_g r_p					0.878** 0.659**	-0.066 0.057	0.119 0.272**	-0.266 0.263**	-0.059 0.050	-0.324* 0.182*	0.106 0.317**	-0.015 0.079
Days to 75 percent maturity	r_g r_p						-0.149 -0.133	0.152 0.109	-0.057 -0.041	-0.089 -0.082	-0.398** -0.243**	0.281 0.203*	-0.158 -0.142
Harvest Index (%)	r_g r_p							-0.256 -0.137	-0.021 0.196*	0.709** 0.724**	-0.194 0.072	0.234 0.319**	0.939** 0.940**
Plant height (cm)	r_g r_p								-0.559** 0.036	-0.059 0.029	0.309* 0.474**	-0.241 3.00E-04	-0.102 -0.019
Pod length (cm)	r_g r_p									-0.155 0.102	-0.948** 0.331**	0.088 0.470**	-0.129 0.097
Number of pods per plant	r_g r_p										-0.160 0.071	0.003 0.114	0.724** 0.736**
Seed protein content (%)	r_g r_p											-0.468** 0.144	-0.069 0.109
Number of seeds per pod	r_g r_p												0.232 0.296**
Seed yield per Plant (g)	r_g r_p												

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

Table 2: Direct (diagonal) and indirect effects (non-diagonal) of different characters on seed yield per plant (g) in green gram at genotypic level

Characters	100-Seed weight (g)	Biological yield per plant (g)	Number of branches per plant	Days to 50 percent flowering	Days to 75 percent maturity	Harvest Index (%)	Plant height (cm)	Pod length (cm)	Number of pods per plant	Seed protein content (%)	Number of seeds per pod
100-Seed weight (g)	-0.310	0.018	0.007	0.022	-0.019	0.296	0.000	0.090	0.141	-0.019	0.037
Biological yield per plant (g)	-0.021	0.272	-0.001	-0.012	-0.006	0.103	-0.003	0.162	-0.085	0.009	0.013
Number of branches per plant	-0.038	-0.005	0.060	-0.023	0.009	-0.261	-0.004	-0.012	0.051	-0.019	0.048
Days to 50 percent flowering	0.037	0.018	0.007	-0.184	0.095	-0.086	-0.001	0.059	0.024	0.031	-0.015
Days to 75 percent maturity	0.055	-0.016	0.005	-0.161	0.108	-0.195	-0.001	0.013	0.036	0.038	-0.040
Harvest Index (%)	-0.071	0.022	-0.012	0.012	-0.016	1.299	0.002	0.005	-0.287	0.019	-0.034
Plant height (cm)	-0.009	0.075	0.026	-0.022	0.016	-0.333	-0.009	0.124	0.024	-0.030	0.035
Pod length (cm)	0.126	-0.200	0.003	0.049	-0.006	-0.027	0.005	-0.221	0.063	0.091	-0.013
Number of pods per	0.108	0.057	-0.007	0.011	-0.010	0.921	0.001	0.034	-0.405	0.015	0.000

plant											
Seed protein content (%)	-0.063	-0.026	0.012	0.060	-0.043	-0.251	-0.003	0.209	0.065	-0.096	0.067
Number of seeds per pod	0.079	-0.025	-0.020	-0.019	0.030	0.303	0.002	-0.019	-0.001	0.045	-0.144

Residual effect= 0.0224

Conclusion

The genotypic correlation coefficients displayed greater values compared to the phenotypic correlation coefficients for all the examined traits. Seed yield per plant exhibited a significant and positive correlation with the number of pods per plant, biological yield per plant, harvest index, 100-seed weight, and number of seeds per pod. Additionally, a significant and negative correlation between seed yield per plant and the number of branches per plant was also observed in the study.

The analysis of path coefficients revealed that the most prominent positive direct effect on seed yield per plant originated from the harvest index, succeeded by biological yield per plant, days to 75 percent maturity, and number of branches per plant. Conversely, the most notable negative direct effect on seed yield per plant was attributed to the number of pods per plant, followed by 100-seed weight, pod length, days to 50 percent flowering, number of seeds per pod, protein content, and plant height. The residual effect (R = 0.0224) indicated that 97.76 percent of the variability was accounted for by the traits included in the path analysis.

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