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Genetic variability, correlation and path analysis in clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.]

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Abstract

Genetic variability & trait association analysis were studied for yield and its attributing traits in thirty diverse clusterbean genotypes under rainfed conditions. The analysis of variance revealed, highly significance difference among the genotypes for all the studied traits. Traits viz., days to flowering, number of pod per plant and seed yield per plant exerted high GCV and PCV values, respectively. High heritability with high genetic advance as per cent of mean recorded in six traits viz., days to flowering, days to maturity, number of branch per plant, number of pod per plant, gum content and seed yield per plant, respectively. Under rainfed conditions number of pod per plant, number of seed per pod and test weight were significantly positively correlated with seed yield per plant. Number of pod per plant showed highest positive direct effect towards the seed yield per plant followed by days to flowering and number of seed per pod. Based on mean performance, genotypes GG 1907, GG 2108, GG 2109, GG 2111 and GG 2114 were superior for all the characters under study along with yield. For indirect selection in yield, pod per plant and number of seed per pod can be considered for future breeding strategies.

Keywords: Genotype, genetic variability, correlation, path analysis

Introduction

Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] ($2n=2x=14$) is hardy and drought resilient leguminous crop commonly known as guar, belongs to the family Fabaceae, sub family papilionaceae and tribe galegae. Africa is probably the center of origin of *Cyamopsis*. In India, guar is being grown since ancient times. It has been established as a high-valued cash crop mainly cultivated in the arid and semi-arid regions during *kharif* and summer season. Vavilov (1951) [37] has suggested that India as a geographic centre of variability for guar, although it is not found to exist as wild in this region. Hymowitz (1972) [17] hypothesized clusterbean is considered to be originated by domestication of the African wild species *Cyamopsis senegalensis*, which appear to be the ancestor of the *Cyamopsis tetragonoloba*. The domestication process could have been taken place in the dry areas of the north western region of the Indo-Pakistan Subcontinent. It was cultivated as a minor crop in India during ancient times as a vegetable and feed for cattle (Hymowitz and Matlock, 1963) [18]. The word “guar” represents a derivation from the Sanskrit word “Gaaahar” which means cow food or fodder of livestock (Bhosle and Kothekar, 2010) [7]. Guar has been used as an alternative source for galactomannan (Anderson, 1949) [4]. Further, studies done on milling the guar seeds for gum production and application in the manufacturing of paper revealed the beneficial effects of guar gum on paper processing. This information helped in the adoption of guar gum in the different manufacturing process.

Clusterbean is completely self-pollinated crop because of its cleistogamous nature. The extent of out crossing has been recorded to vary from 0.3 to 7.9 per cent (Chaudhary and Singh., 1986; Ahlawat *et al.*, 2012) [12, 1]. The style is short and slender while stigma is head-shaped (Menon *et al.*, 1968; Ahlawat *et al.*, 2012) [26, 1]. It is grown in almost all states of India, but the major concentration is in arid and semiarid regions of north western states of Rajasthan, Gujarat, Haryana, Punjab, Uttar Pradesh, Madhya Pradesh and Tamil Nadu (Rai and Dharmatti, 2013) [31]. In, Gujarat, it is mainly grown in Banaskantha, Mahesana, Ahmedabad, Anand, Kheda, Gandhinagar and Kutch districts. The cultivated area under guar in Gujarat was 1.23 lakh ha with a production of 0.86 lakh tonnes and productivity of 699.4 kg/ha (Anonymous, 2021) [5]. Clusterbean is potential vegetable cum industrial crop grown for its tender pods for vegetable and endosperm gum *i.e.*, galactomannan (22-33%) (Gresta *et al.*, 2013) [16] and guar meal (Singh *et al.*, 2014) [36].

Guar seeds are mainly used for extraction of gum (30-35%) having good binding properties and high demand in food, petroleum, pharmaceutical and paper industries. Guar enrich the soil productiveness by fixing atmospheric nitrogen for its own necessities and also for the succeeding crop (Bewal *et al.*, 2009) [6].

The knowledge of genetic variability in the available germplasm is a pre-requisite for effective selection of superior genotypes. Therefore, there is need for identification or development of clusterbean genotypes suited for vegetable, fodder and gum purpose. The knowledge of nature and magnitude for genetic variability, heritability and genetic advance over mean for pod yield and component characters are useful for an effective selection programme. Therefore, it becomes necessary to partition the observed phenotypic expression of the plant into the genetic makeup of the plant and the environment in which it is growing. Therefore, it becomes necessary to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance (Chatale, 2015) [11].

The correlation analysis is a biometrical technique to find out the nature and degree of association between various morphological traits indicating yield. It could be effectively exploited to formulate selection strategies for improving yield and quality. Correlation study does not reveal the direct and indirect contribution of individual character towards yield. In order to have clearer picture of yield components for effective selection programme, it would be desirable to consider the relative magnitude of various characters contributing towards yield. The path coefficient technique developed by Wright (1921) [38] helps in estimating direct and indirect contribution of various components in building-up the correlation towards yield. On the basis of these studies, the quantum importance of individual characters is marked to facilitate the selection programme in clusterbean. Considering the importance of variability & character association in crop improvement programme the present study is formulated.

Materials and Method

The present investigation was carried out with thirty diverse clusterbean genotypes (Table 1) received from Pulses Research Station, Sardarkrushinagar and evaluated with four replications in Randomized Block Design (RBD) during *kharif* 2020-21 at Agronomy Instructional Farm, S. D. Agricultural University, Sardarkrushinagar, Gujarat. The centre is situated 24°-19' North latitude and 72°-19' East latitude with an elevation of 154.52 meter above the mean sea level and represents the North Gujarat Agro-climatic region. General view of experimental site is depicted in Fig 1. Climatic conditions during the experimental period are presented in Table 2 and Fig 2. Observations from five randomly selected plants of each genotype in each replication were recorded on nine quantitative traits [days to flowering, plant height (cm), number of branch per plant, number of pod per plant, pod length (cm), days to maturity, number of seed per pod, test weight (g) and seed yield per plant (g)] and two biochemical characters [gum content (%) and protein content (%)]. Each genotype was represented by single row of 4.0 m length. The inter and intra row distances were 45 cm and 15 cm, respectively. Observations were recorded and its averages were made on randomly selected 5 tagged plants for different

yield attributing traits. The mean performance of each genotype for all traits were subjected to statistical analysis. The analysis was carried out by adopting genetic parameters of variability, estimation of heritability and genetic advance were computed as per Johnson *et al.* (1955) [19]. Correlation studies are conducted as per Panse and Sukhatame (1978) [29] whereas, construction of Path coefficient analysis suggested by Dewey and Lu (1959) [14]. The formula suggested by Burton (1952) [10] was employed to calculate phenotypic and genotypic coefficient of variation.

Genotypic coefficient of variation (GCV)

$$\text{GCV (\%)} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

Where,

σ_p^2, σ_g^2 = Phenotypic and genotypic variance, respectively and
 \bar{X} = Mean value of character

Phenotypic Coefficient of Variation (PCV) and genotypic coefficient of variation (GCV) were classified as suggested by Shivasubramanian and Menon (1973) [35] as follows:

< 10% = Low
 10-20% = Moderate
 > 20% = High

Heritability (Broad sense)

It is the proportion of phenotypic variability that is due to genetic reasons. It was computed in per cent using the formula given by Allard (1960) [3].

$$h_{(b)}^2 (\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

$h^2(b)$ = Heritability (broad sense).

σ_g^2 = Genotypic variance.

σ_p^2 = Phenotypic variance.

Heritability percentage was categorized as demonstrated by Robinson *et al.* (1949).

< 30% = Low
 30-60% = Moderate
 > 60% = High

Genetic advance as percentage of mean

The expected genetic advance (GA) was calculated for each character by adopting the procedure as suggested by Allard (1960) [3].

$$\text{GA} = K \times \frac{\sigma_g^2}{\sigma_p^2} \times \sigma_p$$

Where,

K = Standardized selection differential.

(K = 5% selection intensity coefficient).

σ_p = Phenotypic variance.

$\frac{\sigma_g^2}{\sigma_p^2}$ = Heritability in broad sense,

The genetic advance expressed as per cent of mean was estimated as under.

$$GA (\% \text{ of mean}) = \frac{GA}{\bar{X}} \times 100$$

Where,

GA = Expected genetic advance.

\bar{X} = Mean value of the character.

The genetic advance as per cent was categorized as demonstrated by Johnson *et al.* (1955) [19].

< 10% = Low

10-20% = Moderate

> 20% = High

Results and Discussion

For any breeding programme the main important parameter is genetic variability which provides the basis for future hybridization & selection programme.

Analysis of variance

The analysis of variance for all the eleven characters in thirty genotypes was carried out in a randomized block design. The results obtained are presented in Table 3. The result revealed highly significant difference for all the traits *viz.*, days to flowering, days to maturity, plant height, number of branch per plant, number of pod per plant, number of seed per pod, test weight, gum content, protein content and seed yield per plant which indicated the existence of tremendous variability in the experimental material under study and there may be a scope for improvement of these traits through selection. Similar results were reported by Boghara *et al.* (2016) [9] and Makwana *et al.* (2021) [23].

Variability parameter for clusterbean genotypes

The highest GCV (%) and PCV (%) was recorded for seed yield per plant (40.38 and 42.99) followed by number of pod per plant (41.68 and 43.37), days to flowering (27.72 and 28.16), respectively (Table 4), indicating high variability present in the population and simple selection would be desirable for improving these characters. Similar results were reported by Santhosha *et al.* (2017) [34], Meghana *et al.* (2019) [25] and Makwana *et al.* (2021) [23]. The degree of inheritance of particular traits from parents to offspring is provided by heritability. In present investigation high heritability coupled with high genetic advance as per cent of mean were recorded for six traits *viz.*, days to flowering (96.89 and 56.21), days to maturity (94.88 and 33.42), number of branch per plant (76.24 and 34.93), number of pod per plant (92.37 and 82.53), gum content (97.26 and 25.66) and seed yield per plant (88.25 and 78.14) respectively, which may be due to additive gene effects indicating better scope for the improvement by effective selection. Similar results were also reported by Makwana *et al.* (2021) [23], Meghana *et al.* (2019) [25], Patel *et al.* (2018) [30], Bishnoi and Prakash (2020) [8], Kumar and Ram (2015) [21] and Choyal *et al.* (2018) [13].

Top performing genotypes for yield and its component traits

Based on mean performance, GG 1910, GG 2113, GG 2104, GG 2105 and GG 2106 genotypes depicted earliness in

flowering, GG 2112, GG 2108, GG 2113, GG 2111 and GG 2114 genotypes depicted earliness in maturity. GG 2103, GG 1, GG 2, GG 1902 and GG 2106 genotypes were dwarf, GG 1907, GG 1909, GAUG 1305, GG 2101 and GG 2112 genotypes depicted maximum number of branch per plant, GG 1913, GG 2111, GG 2109, GG 1907 and GG 2104 genotypes recorded maximum number of pod per plant, GG 1905, GG 2112, GG 2104, GG 1907 and GG 2114 genotypes recorded highest pod length, GG 2, GG 2107, GG 2101, GG 2109 and GG 2114 genotypes recorded maximum number of seed per pod, GG 2110, GG 1901, GG 1913, GG 2109 and GG 2 genotypes observed high test weight, GG 2111, GG 2109, GG 2114, GG 2 and GG 1902 genotypes recorded highest gum content, GG 2114, GG 1909, GG 2105, GG 2 and GG 1903 recorded highest protein content and GG 1913, GG 2109, GG 1907, GG 2104 and GG 2111 observed highest seed yield per plant. Genotypes specific to particular trait can be allocating in breeding programme to develop ideal variety.

Phenotypic (r_p) and Genotypic (r_g) correlation

Correlation studies provides the information about degree and direction of trait association with grain yield which is useful for selection of elite genotypes from population. Genotypic and phenotypic correlation coefficient among seed yield per plant and its contributing traits are presented in Table 6. For all traits genotypic correlation values are higher than phenotypic correlation values which indicates little influence of environment. Under rainfed conditions number of pod per plant ($r_p = 0.88^{**}$ and $r_g = 0.94^{**}$), number of seed per pod ($r_p = 0.19^*$ and $r_g = 0.20$) and test weight ($r_p = 0.32^{**}$ and $r_g = 0.44^*$) were positively correlated with seed yield per plant. Thus, improvement in such characters also leads to increment in seed yield per plant of clusterbean genotypes. Kumar and Ram (2015) [21], Boghara *et al.* (2016) [9], Reddy *et al.* (2018) [32], Patel *et al.* (2018) [30], Panchta and Khatri (2017) [28] and Manivannan *et al.* (2017) [24] also reported similar results.

Path analysis

Path analysis breaks correlation between traits into their direct and indirect effects on the economic product, permitting a critical examination of specific trait contributing individually and collectively to produce the total effect. It also helps to measure the relative importance of each trait. Path analysis, in this study was carried out using the estimates of genotypic coefficients. The analysis of correlation coefficient together with information on path coefficient helps in identification of suitable character for proper weightage to be given to each trait during selection. Such an analysis of genotypes under study provided precise indication of the trait that may contribute towards increased total seed yield and also outlined the possible directions to be followed in the future breeding programme for improvement in these traits. The estimates of direct and indirect effects of various traits on total seed yield per plant are presented in Table 7 and fig 3. Number of pod per plant (1.34) showed highest positive direct effect towards the seed yield per plant followed by days to flowering (0.89) and number of seed per pod (0.55). Therefore, this character should be considered during selection program. Results in accordance were observed by Kumar *et al.* (2019) [20], Reddy *et al.* (2018) [32] and Elshiekh *et al.* (2012) [15].



Fig 1: General view of experimental site

Table 1: List of genotypes

Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes
1.	GG 1	11.	GG 1908	21.	GG 2105
2.	GG 2	12.	GG 1909	22.	GG 2106
3.	GAUG 1305	13.	GG 1910	23.	GG 2107
4.	GG 1901	14.	GG 1911	24.	GG 2108
5.	GG 1902	15.	GG 1912	25.	GG 2109
6.	GG 1903	16.	GG 1913	26.	GG 2110
7.	GG 1904	17.	GG 2101	27.	GG 2111
8.	GG 1905	18.	GG 2102	28.	GG 2112
9.	GG 1906	19.	GG 2103	29.	GG 2113
10.	GG 1907	20.	GG 2104	30.	GG 2114

All the genotypes were obtained from Pulses Research Station Sardarkrushinagar

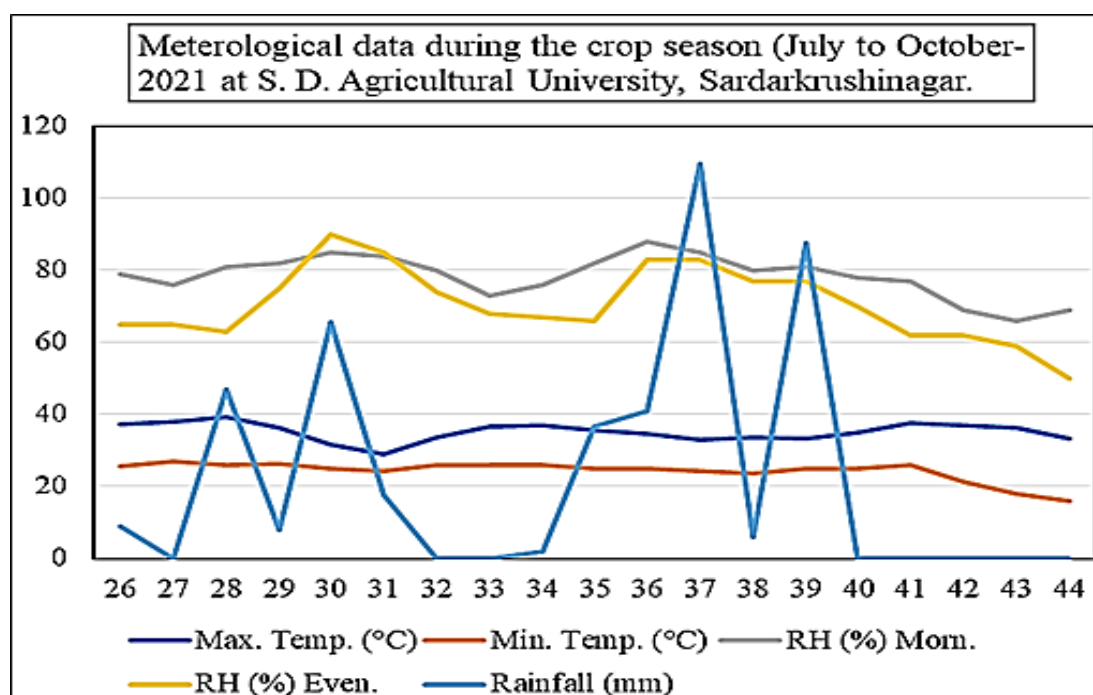


Fig 2: Meteorological data during the crop season

Table 2: Weekly meteorological data recorded during the crop season (July-2021 to october-2021)

Month and year	Std. Weeks	Temperature (°C)		Relative Humidity (%)		Rain fall (mm)
		Max.	Min.	Morn.	Even.	
July 2021	26	37.2	25.6	79	65	9.0
	27	38.0	26.8	76	65	0.0
	28	39.1	26.0	81	63	47.0
	29	36.1	26.2	82	75	8.0
	30	31.6	24.8	85	90	65.5
August 2021	31	29.0	24.3	84	85	17.5
	32	33.5	25.9	80	74	0.0
	33	36.5	25.7	73	68	0.0
	34	36.9	26.0	76	67	2.0
September 2021	35	35.6	24.7	82	66	36.5
	36	34.4	24.9	88	83	41.0
	37	32.9	24.2	85	83	109.5
	38	33.5	23.6	80	77	6.0
	39	33.1	24.9	81	77	87.5
October 2021	40	34.7	25.0	78	70	0.0
	41	37.4	25.8	77	62	0.0
	42	36.9	21.1	69	62	0.0
	43	36.2	18.0	66	59	0.0
	44	33.3	15.9	69	50	0.0

Source: Agricultural Meteorology Department, C. P. College of Agriculture, Sardarkrushinagar.

Table 3: Analysis of variance

Sr. No.	Characters
	Degree of Freedom:
1.	Days to flowering
2.	Days to maturity
3.	Plant height (cm)
4.	Number of branch per plant
5.	Number of pods per plant
6.	Pod length (cm)
7.	Number of seed per pod
8.	Test weight (g)
9.	Gum content (%)
10.	Protein content (%)
11.	Seed yield per plant (g)

Table 4: Variability parameter for clusterbean genotypes

Sr. No.	Characters	GCV (%)	PCV (%)	$h^2_{(b.s)}$ (%)	GA as (%) of mean
1.	Days to flowering	27.72	28.16	96.89	56.21
2.	Days to maturity	16.66	17.10	94.88	33.42
3.	Plant height (cm)	11.75	14.74	63.55	19.30
4.	Number of branch per plant	19.42	22.24	76.24	34.93
5.	Number of pod per plant	41.68	43.37	92.37	82.53
6.	Pod length (cm)	4.07	10.36	15.46	3.30
7.	Number of seed per pod	9.32	13.15	50.30	13.62
8.	Test weight (g)	8.70	12.76	46.47	12.21
9.	Gum content (%)	12.63	12.81	97.26	25.66
10.	Protein content (%)	2.25	2.60	75.16	4.02
11.	Seed yield per plant	40.38	42.99	88.25	78.14

Source: Agricultural Meteorology Department, C.P. College of Agriculture, Sardarkrushinagar.

Table 5: Top performing genotypes for yield and its component traits

Characters	Top 5 genotypes
Days to flowering	GG 2113, GG 2104, GG 1910, GG 2105, GG 2106.
Days to maturity	GG 2112, GG 2113, GG 2108, GG 2111, GG 2114.
Plant height (cm)	GG 2103, GG 1902, GG 2, GG 2106, GG 1.
Number of branch per plant	GG 1907, GG 1909, GG 2101, GG 2112, GAUG 1305.
Number of pod per plant	GG 1913, GG 2111, GG 1907, GG 2104, GG 2109.
Pod length (cm)	GG 1905, GG 2112, GG 2104, GG 2114, GG 1907.
Number of seed per pod	GG 2109, GG 2107, GG 2114, GG 2101, GG 2.
Test weight (g)	GG 2110, GG 1901, GG 1913, GG 2109, GG 2.
Gum content (%)	GG 2111, GG 2109, GG 2114, GG 1902, GG 2.
Protein content (%)	GG 2114, GG 1909, GG 2105, GG 1903, GG 2.
Seed yield per plant (g)	GG 1913, GG 2109, GG 1907, GG 2111, GG 2104.

Table 6: Phenotypic (r_p) and Genotypic (r_g) correlation

		DF	DM	PH	NBPP	NPPP	PL	NSPP	TW	GC	PC	SYPP
DF	r_p	1.00	0.78**	-0.40**	0.07	-0.29**	0.04	-0.12	0.20*	0.00	-0.11	-0.20*
	r_g	1.00	0.80**	-0.48**	0.09	-0.30	0.09	-0.20	0.30	0.01	-0.14	-0.22
DM	r_p		1.00	-0.52**	0.14	-0.20*	0.05	-0.23**	0.06	-0.26**	-0.07	-0.21*
	r_g		1.00	-0.66**	0.16	-0.20	0.05	-0.38**	0.11	-0.28	-0.09	-0.23
PH	r_p			1.00	0.10	0.24**	-0.21*	0.02	-0.15	0.29**	-0.09	0.17
	r_g			1.00	0.12	0.35	-0.16	0.05	-0.21	0.38*	-0.10	0.27
NBPP	r_p				1.00	-0.08	0.16	-0.04	-0.04	0.02	-0.10	-0.10
	r_g				1.00	-0.09	0.15	0.02	-0.17	0.02	-0.09	-0.13
NPPP	r_p					1.00	-0.00	-0.01	0.11	0.12	-0.22*	0.88**
	r_g					1.00	0.10	0.02	0.16	0.12	-0.30	0.94**
PL	r_p						1.00	-0.01	-0.04	-0.12	0.00	0.08
	r_g						1.00	0.17	-0.21	-0.26	-0.10	0.04
NSPP	r_p							1.00	-0.00	0.41**	0.07	0.19*
	r_g							1.00	0.10	0.59**	0.08	0.20
TW	r_p								1.00	0.07	0.05	0.32**
	r_g								1.00	0.07	0.15	0.44*
GC	r_p									1.00	0.15	0.17
	r_g									1.00	0.16	0.19
PC	r_p										1.00	-0.14
	r_g										1.00	-0.19
SYPP	r_p											1.00
	r_g											1.00

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

DF=Days to flowering, DM=Days to maturity, PH=Plant height, NBPP=Number of branch per plant, NPPP=number of pod per plant, PL=Pod length, NSPP=number of seed per pod, TW=Test weight, GC=Gum content, PC=Protein content, SYPP=Seed yield per plant.

Table 7: Direct and Indirect effects

	DF	DM	PH	NBPP	NPPP	PL	NSPP	TW	GC	PC	r_g (SYPP)
DF	0.89	-0.48	0.01	0.01	-0.41	-0.04	-0.11	-0.04	-0.01	-0.05	-0.22
DM	0.71	-0.60	0.02	0.01	-0.27	-0.02	-0.21	-0.01	0.17	-0.03	-0.23
PH	-0.43	0.40	-0.03	0.01	0.47	0.07	0.03	0.02	-0.24	-0.03	0.27
NBPP	0.08	-0.09	0.00	0.09	-0.12	-0.07	0.01	0.02	-0.01	-0.03	-0.13
NPPP	-0.27	0.12	-0.01	-0.01	1.34	-0.04	0.01	-0.02	-0.08	-0.10	0.94**
PL	0.08	-0.03	0.00	0.01	0.13	-0.43	0.09	0.03	0.16	-0.01	0.04
NSPP	-0.18	0.23	0.00	0.00	0.03	-0.07	0.55	-0.01	-0.37	0.03	0.20
TW	0.27	-0.07	0.01	-0.01	0.22	0.09	0.06	-0.12	-0.04	0.05	0.44*
GC	0.01	0.17	-0.01	0.00	0.17	0.11	0.32	-0.01	-0.63	0.06	0.19
PC	-0.12	0.05	0.00	-0.01	-0.40	0.01	0.04	-0.02	-0.10	0.35	-0.19

Where,

(Residual effect = -0.037)

DF=Days to flowering, DM=Days to maturity, PH=Plant height, NBPP=Number of branch per plant, NPPP=number of pod per plant, PL=Pod length, NSPP=number of seed per pod, TW=Test weight, GC=Gum content, PC=Protein content, SYPP=Seed yield per plant.

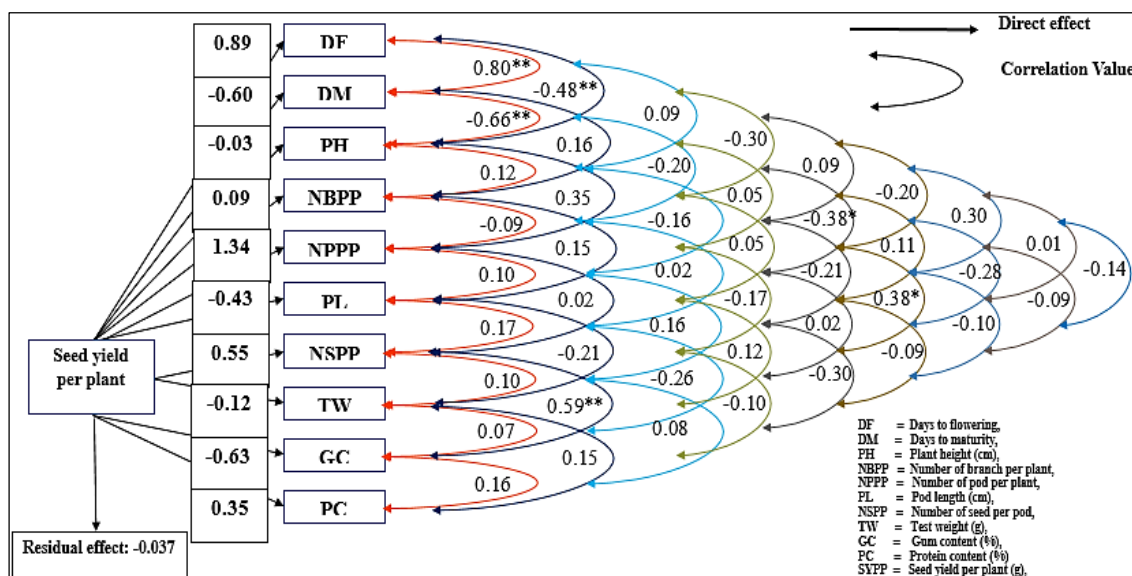


Fig 3: Genotypic path diagram for seed yield per plant in clusterbean

Conclusion

The traits likes, days to flowering, number of pod per plant and seed yield per plant exerted high genotypic and phenotypic coefficients of variation indicating high variability present in the population and simple selection would be desirable for improving these characters. High heritability values coupled with high genetic advance were recorded for days to flowering, days to maturity, number of branch per plant, number of pod per plant, test weight and seed yield per plant indicating that these traits are governed by additive gene effects and direct selection for these traits would be more effective for desired genetic improvement.

Correlation between seed yield per plant with number of seed per pod, number of pod per plant and test weight was found positive and significant and therefore selection for these traits can directly be followed for yield improvement in clusterbean. From path analysis we concluded that the traits viz., days to flowering, number of pod per plant and number of seed per pod exhibited highest positive effect on seed yield per plant and each trait must be given preference in selecting of superior high yielding genotypes.

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