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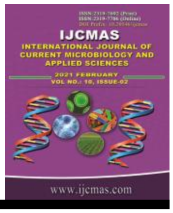

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Correlation and Path Coefficient Estimation in Horsegram [*Macrotyloma uniflorum*(L) Verdcout] Genotypes Collected from Bastar Plateau

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ABSTRACT

Horsegram (*Macrotyloma uniflorum* (L) Verdcout) is a popular pulse among the tribal's of Bastar region, locally known as Hirwa or Harwa. An experiment was accompanied with 56 horsegram genotypes and 1 check Indira kulthi-1 at SGCARS Jagdalpur (C.G.), to assess correlation and path coefficient analysis for 10 quantitative characters. Result obtained from Analysis of variance revealed highly significant differences among the genotypes for all the characters under study. Correlation coefficient analysis revealed significant positive correlation for the traits plant height, primary branches and seeds per pod with seed yield per plant at both phenotypic and genotypic level. Path analysis revealed that on phenotypic class pods per plant exhibited uppermost positive direct effect trailed by primary branches, days to 50% flowering, seeds per pod, plant height and pod length whereas on genotypic class uppermost direct effect was of trait pods per plant trailed by primary branches per plant, seeds per pod, days to 50% flowering and pod length.

Keywords

Horsegram, *Macrotyloma uniflorum*, Correlation coefficient; Path coefficient

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Introduction

Horsegram (*Macrotyloma uniflorum* (L) Verdcout) is an under exploited arid legume crop. Horsegram seeds are rich in protein and consumed in majority by low income section of the society. It is an important component in the dryland crop production system due to its ability to withstand drought with minimum crop management practices. It is commonly known as kulthi, hirwa or harwa in Bastarplateau region. Horsegram [*Macrotyloma uniflorum* (L) Verdcourt] belonging to Family: Leguminosae, Sub-family: Faboidae, Tribe: Phaseoleae, Sub-tribe: Phaseolinae, Genus: *Macrotyloma*, Species: *uniflorum*. *Macrotyloma uniflorum* (L) Verdcourt synonyms are *Dolichosuniflorus* and *Dolichosbiflorus* with chromosome number of 2n=2x=20, 22, 24. Genus *Macrotyloma* consist about twenty five species; most of them are mainly present in Africa. Within *Macrotyloma uniflorum* (L) Verdcout four varieties have been identified *viz*., var. *uniflorum*, *benadirianum*, *stenocarpum* and *verrucosum* (Uma Rani *et al*., 2013). Horsegram is an annual succulent herb, slender, downy, slightly twining branching, springing from the base of the plant, semi-erect, low growing habit with 60-120 cm height; leaves are trifoliate with 2.5 to 5.0 cm in length. Stipules are one cm long and ovate lanceolate. Peduncles are short, bisexuals, bracteate, pedicellate, zygomorphic and complete. Calyx are downy teeth lanceolate, corolla arc light yellow, 5 petals, standard petal longer than wings, stamens diadelphos (9+1), filaments are alternately short and long anthers, introse, uniform diversified. Gynoecium is with superior ovary. Style file from terminal, curved, stigma capitate and hairy. Pods are linear, recurned beaked with 5-7 seeds. Seeds are normal, flattened, 3-6 mm long, black, light red, brown and mottled apperance, testa skinny with small hilum. Horsegram is a self-fertilized crop, matures in 3 to 4.5 months. The tap root produces a branched root system with smooth, rounded nodules. Nodules contain nitrogen fixing bacteria (Kumar and Vittal, 2007). During twelfth plan (2012-2015), the total area under horsegram was 2.32 lakh hectares and production was 1.05 lakh tonnes respectively. With regard of area and production, Karnataka is on the first position on all India basis sharing 26.72% and 25.71% respectively followed by Odisha sharing 19.46% area and 15.48% production and Chhattisgarh is in third position sharing 19.29% area and13.29% production. The highest productivity was noted in the state of Bihar (959 kg/ha) followed by W.B. (796 kg/ha) and Jharkhand (603 kg/ha) (Anon., 2015-16).

In Chhattisgarh during 2017-2018 area, production and productivity under crop was 47.62 ha, 16.37 MT, 344 kg/ha (Anon., 2017-18).

All the varieties developed to date are mainly by single plant selection from locals. There is greater need to increase the yield and quality of this crop by breeding while understanding the genetic makeup of this crop. Hence, it is essential to generate new variability through hybridization. By germplasm exploration superior germplasm's can be identified from these local varieties which can be ultimately used for developing superior lines in breeding programme. Hence looking to the above facts investigation entitled "Correlation and Path coefficient estimation in horsegram [*Macrotyloma uniflorum* (L) Verdcout] genotypes collected from Bastar Plateau" is being carried out with the objective " to study association of characters concerned under study with seed yield per plant".

Materials and Methods

The present experiment entitled "Correlation and Path coefficient estimation in horsegram [*Macrotyloma uniflorum* (L) Verdcout] genotypes collected from Bastar Plateau" was performed at Research cum Instructional Farm, Shaheed Gundadhoor College of Agriculture and Research Station, Kumhrawand, Jagdalpur, (Chhattisgarh) located at N 19°5'35'' longitude E 81°57'37'' latitude and at an altitude ranging from 530 to 850 meters above mean sea level (MSL) with an annual rainfall 1400 mm. The experimental material comprised of 56 horsegram genotypes along with 1 check variety i.e., Indira kulthi-1. The experimental material was planted in a Randomized Complete Block Design with three replications during kharif

2018. Each genotype was planted in three rows of 4×1 m plot having 30×10 cm inter and intra row spacing. The observations were recorded on five randomly selected plants per replication for each accession.

The analysis of variance for different characters was carried out using the mean data through method given by Panse and Sukhatme (1967).

Estimation of Analysis of Variance

The analysis of variance for different characters was carried out using the mean data in order to partition the variability due to different sources by following the method given by Panse and Sukhatme (1967) (Table 1).

Where,

SSB = sum of square of block

MSE = mean sum of square of error

MSB = mean sum of square of block

TSS = total sum of square

MST = mean sum of square of treatment

SSE = sum of square of error

SST = sum of square of treatment

Estimation of correlation coefficient

The correlation coefficients were worked out to determine the degree of association of a character with yield and also among the yield components. Phenotypic and genotypic correlation coefficients were computed by using the formula given by Weber and Morthy (1952).

$$(rp) = \frac{\mathrm{Cov(xy)p} \times 100}{\sigma p_X \times \sigma p_Y}$$

$$(rg) = \frac{\mathrm{Cov(xy)g} \times 100}{\sigma g_X \times \sigma g_Y}$$

Where,

(rp) = Phenotypic correlation coefficient

(rg) = Genotypic correlation coefficient

Cov (xy)p = Phenotypic covariance between the characters ‘x’ and ‘y’

Cov (xy)g = Genotypic covariance between the characters ‘x’ and ‘y’

σp_X and σp_Y = Phenotypic variance of the character ‘x’ and ‘y’ respectively

σg_X and σg_Y= Genotypic variance of the character ‘x’ and ‘y’ respectively

Correlation coefficients were compared against ‘r’ values as given in Fisher and Yates (1963) table at (n-2) degrees of freedom at the probability levels of 0.05 and 0.01 to test their significance.

Estimation of path coefficient

The path analysis was originally developed by Wright (1921) and elaborated by Dewey and Lu (1959). Path coefficient analysis splits the correlation coefficients into the measures of direct and indirect effects of independent variables on dependent variable. If a character y is determined by correlated characters x1, x2 and x3, a path diagram must be formulated. Thus we get a set of simultaneous equations as given below:

r (x1,y) = a + r (x1, x2) b + r (x1, x3) c.

r (x2,y) = b + r (x2, x1) a + r (x2, x3) c.

r (x3,y) = c + r (x3, x1) a + r (x3, x2) b Considering the three factors i.e. x1, x2 and x3, the simultaneous equations given above can be matrix notation as:

rx1y = r x1x1 r x1x1 r x1x1 a

rx2y = r x2x1 r x2x2 r x2x3 b

rx3y = r x3x1 r x3x2 r x3x3 c

Where,

rx1y = Correlation coefficient between character x1 and y.

rx2y = Correlation coefficient between character x2 and y.

rx3y = Correlation coefficient between character x3 and y.

a = Direct effect of character x1 and y.

b = Direct effect of character x2 and y.

c = Direct effect of character x3 and y.

The solution for vector C may be obtained as follows:

A = B.C or

C = B-1A

Where,

B-1 = inverse of matrix B.

After calculating the values of path coefficient i.e. “C” vectors the residual effect can be estimated by the given formula:

R = 1- Σ (rij)

Where,

R = Residual effect.

rij = Correlation coefficient between i^{th} character and j^{th} dependent variable

The results of path coefficient analysis are interpreted as per the following scale suggested by Lenka and Mishra (1973) (Table 2).

Results and Discussion

Analysis of variance

Analysis of variance was worked out on ten polygenic characters including yield and yield attributing traits of fifty seven genotypes.

From the analysis of variance it was observed that mean sum of squares due to genotypes were significant for all characters at 5% level of significance under study thus exhibiting the presence of considerable genetic variability for all the traits in the experimental material. The results found were presented in Table 3.

This finding in authorization with the finding of Chahota *et al.*, (2005), Gupta *et al.*, (2005), Joshi *et al.*, (2007),Ram *et al.*, (2003), Singhal *et al.*, (2010), Durga (2012), Varma *et al.*, (2013), Gomashe *et al.*, (2018) and Priyanka *et al.*, (2019) except for petiole length.

Correlation coefficient analysis

The statistics that measures the index of relationship between two or more variables is known as correlation coefficient. It computes the mutual association between various plant character pairs and defines the component characters on which selection can be depend on for improvement in seed yield.

Through correlation coefficient analysis emphasis can be given for selecting character which is genetically correlated with the dependent character. To know the nature and magnitude of relationship existing between the traits under study correlation coefficient was carried out at phenotypic as well as genotypic levels. Result regarding correlation among various traits had been depicted in table 4.

Seed yield per plant (g)

At phenotypic level seed yield per plant exhibited significant positive correlation with pods per plant (0.980), seeds per pod (0.550), primary branches per plant (0.528) and plant height (0.372).

At genotypic level primary branches per plant (0.775), seeds per pod (0.718) and plant height (0.411) were positively correlated with seed yield per plant.

Days to 50% flowering

Days to maturity was the only character which showed positive and significant association both at phenotypic (0.689) as well as at genotypic (0.740) level whereas primary branches per plant (-0.266) and seeds per pod (0.423) showed significant correlation only at genotypic level with days to 50 per cent flowering.

Days to maturity

Days to maturity showed negative significant correlation with seeds per pod (-0.333), pod length (-0.283) and petiole length (-0.271) at genotypic level.

Plant height (cm)

Plant height was significantly positively correlated with seed yield per plant (0.372) and pods per plant (0.358) at phenotypic level.

However, at genotypic level petiole length (0.427) showed highest association value wit plant height followed by seed yield per plant (0.411), pods per plant (0.393), seeds per pod (0.301) and primary branches per plant (0.266) respectively.

Number of primary branches per plant

Characters seed yield per plant (0.775) showed highest significant positive correlation with primary branches per plant trailed by pods per plant (0.668) and test weight (0.422) at genotypic level.

At phenotypic level seed yield per plant (0.528) and pods per plant (0.468) showed association with the character.

Number of pods per plant

Trait pods per plant showed positive and significant association with seeds per pod at phenotypic (0.548) and also at genotypic (0.668) level while seed yield per plant (0.980) showed association at phenotypic level only.

Petiole length (cm)

Petiole length showed positive significant correlation with plant height (0.427) and seeds per pod (0.260) at genotypic level whereas negative significant correlation with days to maturity (-0.271) respectively.

Pod length (cm)

Pod length showed negative significant correlation with days to maturity (-0.283) at genotypic level indicating early maturity leads to decrease in pod length.

Number of seeds per pod

Trait seeds per pod found to be positive significantly associated with seed yield per plant (0.718), days to 50% flowering (0.423), plant height (0.301), pods per plant (0.668) and petiole length (0.260) while negative correlated with days to maturity (-0.333) at genotypic level. At phenotypic level significant positive correlated with seed yield per plant (0.55) and pods per plant (0.548) respectively.

Test weight

This trait at genotypic level had been found significant positively associated with primary branches per plant (0.422). However, with all other traits test weight had shown negative nonsignificant correlation.

From the above, it is clear that overall value of genotypic correlation was slightly greater than the values of phenotypic correlation, low phenotypic correlations can be explained due to masking or modifying effects of environment on genetic association between characters.

The experimental findings on correlation coefficient analysis has supported by earlier workers *viz*., Lad *et al.*, (1998),Pandya *et al.*, (2002), Roopdevi *et al.*, (2002), Bhadait (2005), Paliwal *et al.*, (2005), Kalia *et al.*, (2007), Prabha *et al.*, (2010), Neelam *et al.*, (2014), Alle *et al.,* (2016) and Priyanka *et al.*, (2019).

Path coefficient analysis

Through correlation coefficient analysis we find association between various characters but it does not tell about the type of association of independent characters with the dependent character.

Path coefficient analysis splits the correlation coefficient into the measures of direct and indirect effects thus it provides information about the direct and indirect contribution of various independent characters on a dependent character.

Hence it helps in determining yield contributing and thus is useful in indirect selection. The direct and indirect effects of various traits with respect to seed yield at phenotypic level are presented in Table 5 and 6 and fig. 1.

Direct effects at phenotypic and genotypic level

Horsegram germplasm under study were exposed to path analysis to estimate the direct and indirect effect of various characters towards seed yield per plant.

Among the nine characters included in the study, six characters showed positive direct effect towards seed yield per plant in which pods per plant (0.9117) had higher positive direct effect followed by primary branches per plant (0.1070), days to 50 per cent flowering (0.0274), seeds per pod (0.0239), plant height (0.0167) and pod length (0.0025) whereas negative direct effect was shown by test weight (-0.0428) followed by days to maturity (-0.0202) and petiole length (-0.0078) respectively at phenotypic level.

At genotypic level highest direct effect towards seed yield per plant was shown by pods per plant (0.6659) followed by primary branches per plant (0.4078), seeds per pod (0.1585), days to 50 per cent flowering (0.0919) and pod length (0.0835) whereas negative direct effect was shown by test weight (-0.1984), petiole length (-0.0401), days to maturity (-0.0132) and plant height (-0.0110) respectively.

The above discussed results on direct effect of characters towards seed yield per plant at genotypic level are confirmed with the findings of earlier workers *viz*.,Yarguntappa (1987), Savithramma (1994), Nagaraja *et al.*, (1999), Prakash and Khanure (2000), Pandya *et al.*, (2002), Raina *et al.*, (2002), Paliwal *et al.*, (2005), Raina *et al.*, (2007), Bhave *et al.*, (2007), Khulbe *et al.*, (2013) and Priyanka *et al.*, (2019)

Table.1 Skeleton of analysis of variance for seed yield and its component traits

Source of Variation	Degree of Freedom	Sum of Square	Mean Sum of Square	F Calculated
Replication	(r − 1)	SSR	MSR	MSR / MSE
Genotypes	(g − 1)	SSG	MSG	MSG / MSE
Error	(r −1)(g − 1)	SSE	MSE	
Total	rg − 1	SS total		

Panse and Sukhatme (1967)

Table.2 Scale of direct and indirect effects

Value of direct and indirect effects	Rate/ Scale
0.00 to 0.09	Negligible
0.10 to 0.19	Low
0.20 to 0.29	Moderate
0.30 to 0.99	High
>1.00	Very high

Lenka and Mishra (1973)

Fig.1 Path diagram for seed yield and its attributing traits in horse gram genotypes

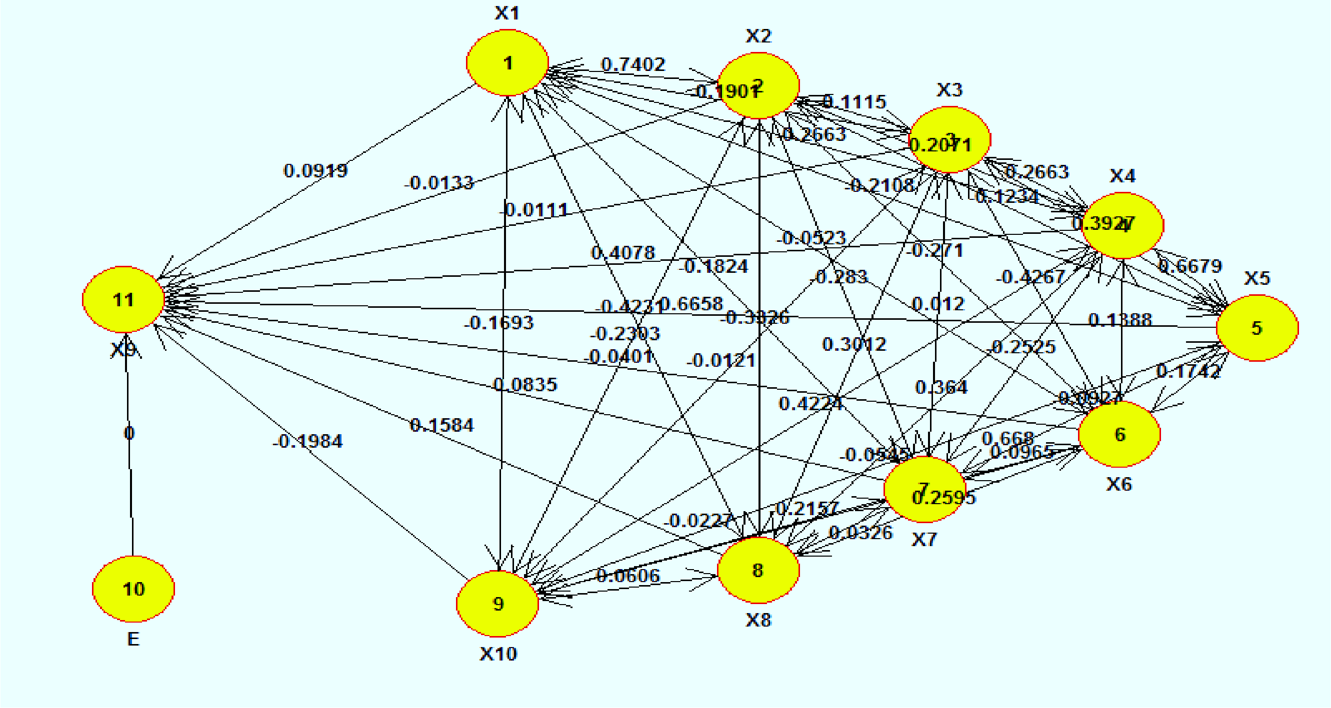

Table.3 Analysis of variance for seed yield and seed yield attributing traits in horse gram germplasm lines

Source of variation	Degree of freedom	DFF	DM	PH (cm)	PBPP	PPP	PeL (cm)	PL (cm)	SPP	SYPP (g)	TW (g)
Replication	2	19.702	10.251	34.014	0.155	8.855	3.25	1.09	1.754	2.029	0.531
Treatment	56	17.076*	58.539*	132.352*	1.449*	160.639*	0.714*	0.892*	1.231*	18.327*	6.412*
Error	112	2.404	2.388	16.605	0.720	2.988	0.401	0.295	0.433	1.023	0.649
S.Em.±	-	0.895	0.892	0.895	0.490	0.998	0.366	0.314	0.380	0.584	0.465
CV (%)	-	3.369	1.770	3.369	12.886	3.652	14.739	12.370	15.123	11.375	3.086
CD (5%)	-	2.512	2.504	2.512	1.375	2.800	1.026	0.880	1.066	1.639	1.305

***Significant at 5%level of significance**

DFF= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height, PBPP= Number of primary branches per plant, PPP= Number of pods per plant, PeL= Petiole length, PL= Pod length, SPP= Number of seeds per pod, SYPP= Seed yield per plant, TW= Test weight.

Table.4 Phenotypic and genotypic correlation coefficient analysis for seed yield and its component traits in horse gram

Characters		DFF	DM	PH	PBPP	PPP	PeL	PL	SPP	TW	SYPP
DFF	P	1	0.689**	-0.219	-0.186	-0.193	-0.114	-0.186	-0.316	-0.136	-0.187
	G	1	0.740**	-0.190	-0.266*	-0.211	-0.052	-0.182	0.423**	-0.169	-0.211
DM	P		1	-0.109	-0.141	-0.115	-0.183	-0.24	-0.245	-0.208	-0.119
	G		1	-0.112	-0.207	-0.123	-0.271*	-0.283*	-0.333*	-0.230	-0.130
PH	P			1	0.230	0.358**	-0.207	0.043	0.22	-0.016	0.372**
	G			1	0.266*	0.393**	0.427**	0.012	0.301*	-0.012	0.411**
PBPP	P				1	0.468**	0.197	-0.081	0.234	0.266	0.528**
	G				1	0.668**	0.139	-0.253	0.364	0.422**	0.775**
PPP	P					1	0.097	-0.078	0.548**	-0.058	0.980**
	G					1	0.174	-0.093	0.668**	-0.055	1.018
PeL	P						1	0.115	0.167	-0.133	0.109
	G						1	0.097	0.260*	-0.216	0.228
PL	P							1	-0.019	-0.011	-0.774
	G							1	0.033	-0.023	-0.088
SPP	P								1	-0.068	0.550**
	G								1	-0.078	0.718**
TW	P									1	-0.600
	G									1	-0.061
SYPP	P										1
	G										1

** Significant at 1% level of significance

*Significant at 5% level of significance

DFF= Days to 50% flowering, DM= Days to maturity, PH= Plant height, PBPP= Primary branches per plant, PPP= Pods per plant, PeL= Petiole length, PL= Pod length, SPP= Seeds per pod, SYPP= Seed yield per plant, TW= Test weight.

Table.5 Phenotypic path coefficient analysis (direct and indirect) for seed yield per plant and its component traits in horse gram

Characters	DFF	DM	PH	PBPP	PPP	PeL	PL	SPP	TW	SYPP
DFF	**0.0274**	-0.0139	-0.0036	-0.0199	-0.1758	0.0009	-0.0005	-0.0076	0.0058	-0.187
DM	0.0189	**-0.0202**	-0.0018	-0.0151	-0.1046	0.0014	-0.0007	-0.0059	0.0089	-0.119
PH	-0.0060	0.0022	**0.0167**	0.0246	0.3268	0.0016	0.0001	0.0052	0.0007	0.372**
PBPP	-0.0051	0.0029	0.0038	**0.1070**	0.4267	-0.0015	-0.0002	0.0056	-0.0114	0.528**
PPP	-0.0053	0.0023	0.0060	0.0501	**0.9117**	-0.0008	-0.0002	0.0131	0.0025	0.980**
PeL	-0.0031	0.0037	-0.0035	0.0211	0.0887	**-0.0078**	0.0003	0.0040	0.0057	0.109
PL	-0.0051	0.0049	0.0007	-0.0086	-0.0712	-0.0009	**0.0025**	-0.0005	0.0005	-0.774
SPP	-0.0087	0.0050	0.0037	0.0251	0.4994	-0.0013	-0.0001	**0.0239**	0.0026	0.550**
TW	-0.0037	0.0042	-0.0003	0.0284	-0.0532	0.0010	0.0000	-0.0014	**-0.0428**	-0.060

** Significant at 1% level of significance

DFF= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height, PBPP= Number of primary branches per plant, PPP= Number of pods per plant, PeL= Petiole length, PL= Pod length, SPP= Number of seeds per pod, SYPP= Seed yield per plant, TW= Test weight

Table.6 Genotypic path coefficient analysis (direct and indirect) for seed yield per plant and its component traits in horse gram

Characters	DFF	DM	PH	PBPP	PPP	PeL	PL	SPP	TW	SYPP
DFF	**0.0919**	-0.0098	0.0021	-0.1086	-0.1404	0.0021	-0.0152	-0.0670	0.0336	-0.211
DM	0.0681	**-0.0132**	0.0012	-0.0845	-0.0822	0.0109	-0.0286	-0.0527	0.0457	-0.13
PH	-0.0175	0.0015	**-0.0110**	0.1086	0.2615	0.0171	0.0010	0.0477	0.0024	0.41**
PBPP	-0.0245	0.0027	-0.0029	**0.4078**	0.4447	-0.0056	-0.0211	0.0577	-0.0838	0.77**
PPP	-0.0194	0.0016	-0.0043	0.2724	**0.6659**	-0.0070	-0.0077	0.1058	0.0108	1.018
PeL	-0.0048	0.0036	0.0047	0.0566	0.1160	**-0.0401**	0.0081	0.0411	0.0428	0.228
PL	-0.068	0.0037	0.0001	-0.1030	-0.0617	-0.0039	**0.0835**	0.0052	0.0045	-0.088
SPP	-0.0389	0.0044	-0.0033	0.1484	0.4448	-0.0104	0.0027	**0.1585**	0.0120	0.718**
TW	-0.0156	0.0030	0.0001	0.1723	-0.0363	0.0086	-0.0019	-0.0096	**-0.1984**	-0.061

** Significant at 1% level of significance

DFF= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height, PBPP= Number of primary branches per plant, PPP= Number of pods per plant, PeL= Petiole length, PL= Pod length, SPP= Number of seeds per pod, SYPP= Seed yield per plant, TW= Test weight.

Indirect effects at phenotypic and genotypic level

Days to 50% flowering

This character exhibited positive indirect effect on seed yield per plant through test weight (0.0058) and petiole length (0.0009) at phenotypic level whereas at genotypic level plant height (0.0021), petiole length (0.0021) and test weight (0.0336) showed positive indirect effect, while rest traits showed negative indirect effect at both phenotypic and genotypic level.

Days to maturity

At phenotypic level days to maturity exhibited positive indirect effect through days to 50% flowering (0.0189), petiole length (0.0014) and test weight (0.0089) while at genotypic level days to 50% flowering (0.0681), plant height (0.0012), petiole length (0.0109) and test weight (0.0457) had positive indirect effect while rest traits showed negative indirect effect on seed yield per plant at both phenotypic and genotypic level.

Plant height (cm)

It had shown in direct negative influence on seed yield through days to 50% flowering (-0.0060, -0.0175) while through rest of the characters indirect positive effect was shown at both phenotypic and genotypic level.

Number of primary branches per plant

It had shown indirect negative effect on seed yield through days to 50% flowering (-0.0051, - 0.024),petiole length (-0.0015, -0.0056),pod length (-0.0002, -0.0211) and test weight (-0.0114, -0.0838) whereas characters days to maturity (0.0029, 0.0027), plant height (0.0038, -0.0029), pods per plant (0.4267, 0.4447) and seeds per pod (0.0056, 0.577) have positive indirect impact at both phenotypic and genotypic level.

Number of pods per plant

Number of pods per plant made negative indirect impact on seed yield per plant through days to 50% flowering (-0.0053), petiole length (-0.0008) and pod length (-0.0002) while days to maturity (0.0023), plant height (0.0069), primary branches per plant (0.0501), seeds per pod (0.0131) and test weight (0.0025) made positive indirect impact at phenotypic level whereas at genotypic level it showed negative indirect impact on seed yield through days to 50% flowering (-0.0194),plant height (-0.0043), petiole length (-0.0070) and pod length (-0.0077) while positive indirect impact was shown through days to maturity (0.0016),primary branches per plant (0.2724),seeds per pod (0.1058) and test weight (0.0108) respectively.

Petiole length (cm)

It had shown negative indirect effect towards seed yield through days to 50% flowering (-0.0031) and plant height (-0.0035) whereas through rest characters, it had positive indirect effect at phenotypic level. However, at genotypic level it had negative indirect impact on seed yield through single character, days to 50% flowering (-0.0048) only whereas through rest of the characters, it had positive indirect impact.

Pod length (cm)

Pod length had negative indirect impact on seed yield through days to 50% (-0.0051), primary branches per plant (-0.0086), pods per plant (-0.0712), petiole length (-0.0009) and seeds per pod (-0.0005) while days to maturity (0.0049), plant height (0.0007) and test weight (0.0005) had positive indirect impact at phenotypic level. At genotypic level it had negative indirect impact on seed yield through days to 50% flowering (-0.0168), primary branches per plant (-0.1030),pods per plant (-0.0617) and petiole length (-0.0039) while positive indirect impact through days to maturity(0.0037), plant height (0.0001), seeds per pod (0.0052) and test weight (0.0045) respectively.

Number of seeds per pod

It had negative indirect impact on seed yield per plant through days to 50% flowering (-0.0087),petiole length (-0.0013) and pod length (-0.0001) while rest of the characters had positive indirect impact at phenotypic level; whereas it had showed negative indirect impact through days to 50% flowering (-0.0389), plant height (-0.0033) and petiole length (-0.0104) while through days to maturity (0.0044), primary branches per plant (0.1484), pods per plant (0.4448), pod length (0.0027) and test weight (0.0120) had positive indirect impact on seed yield.

Test weight (g)

It had positive indirect impact on seed yield per plant through days to maturity (0.0042), primary branches per plant (0.0284) and petiole length (0.0010) at phenotypic level and through days to maturity (0.0030), plant height (0.0001), primary branches per plant (0.1723) and petiole length (0.0086)at genotypic level; whereas remaining characters were negative at both phenotypic and genotypic level.

Residual effect

In plant breeding, it is very difficult to have complete knowledge of all component traits of yield. The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. The residual effect is estimated with the help of direct effects and simple correlation coefficients. In the present study the residual effect in germplasm lines of horsegram for direct and indirect effects were (0.179) at phenotypic level and (0.123) at genotypic level. The residual effect is low indicates that besides the characters studied, there are only some other attributes which contributes for yield.

In the present investigation, the genotypic correlation coefficients were in general, observed to be higher than that of phenotypic correlation coefficient indicating the strong inherent association for the various traits studied signifying the opportunity of effective phenotypic selection. Seed yield per plant exhibited significant positive association with plant height, primary branches per plant and seeds per pod at genotypic and phenotypic levels. Thus, it can be inferred that selection based on any one of these traits either alone or in combination, would result in identifying high yielding genotypes.

This study on path coefficient designated that pods per plant, primary branches per plant, days to 50% flowering and seeds per pod were the most central funders to seed yield per plant which could be taken into attention in future hybridization programs. Indirect contribution of plant height, primary branches per plant and seeds per pod through pods per plant of high magnitude was also observed. The results on path analysis indicated that, the number of pods per plant is most pronounced character contributing directly to seed yield and most of the other component characters associated to seed yield are contributing indirectly through this character.

Therefore, from this correlation and path coefficients studies it can be inferred that selection for high yield in horsegram could be enhanced by inclusion of pods per plant as a selection criteria along with the primary branches per plant and seeds per pod.

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