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GENETIC VARIABILITY, CHARACTER ASSOCIATION AND PATH STUDIES FOR YIELD AND YIELD RELATED TRAITS IN CHICKPEA (*CICER ARIETINUM* L.)

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ABSTRACT

Present investigation was conducted at Zonal Agricultural Research Station (ZARS), Kalaburagi, University of Agricultural Sciences, Raichur Karnataka India in *rabi season* 2019-20 using 54 diverse chickpea genotypes including 10 checks for different yield and yield attributing traits. The analysis of variance reveals that significant differences among the genotypes for all the traits considered for the study. The magnitude of PCV (phenotypic coefficient of variability) was higher than GCV (genotypic coefficient of variability) for all the characters. Higher heritability coupled with percent genetic advance were exhibited by secondary branches per plant, total number of pods per plant, seed yield per plot specify that these traits are control by additive gene action and selection maybe effective for these traits. The trait 100-seed weight showed significant and strong positive association with seed yield per plot at both phenotypic and genotypic level and total number of secondary branches per plant at genotypic level. Path analysis studies showed that the total number of pods per plant, hundred seed weight and total number of seeds per pod had positive and direct effect on seed yield. Hence, these characters maybe considered for further crop improvement programme.

Keywords: Genetic variability, heritability, genetic advance, correlation coefficient

Introduction

Chickpea (*Cicer arietinum* L.), popularly also called as Gram, Chana, Bengal gram, Garbanzo bean or Egyptian pea, Chickpea is one of the first grain legumes to have been domesticated by humans in the old world (Van der Maesen, 1984). Chickpea (*Cicer arietinum* L.) is the only species out of 44 species documented, have been cultivated worldwide on a large scale. Currently, it stands third ranks in terms of world grain legume crop production (Singh *et al.*, 2014) followed by dry bean (*Phaseolus vulgaris* L.) and field pea (*Pisum sativum* L.). In our country (India), chickpea is cultivated an area of about 9.67 mha (million hectares) with the production of 10.09 Mt (million tonnes) with a productivity of 1043 kg per hectare (Directorate of Economics and Statistics, 2018-19). In Karnataka state, it is sown in a total area of 1265 Kha (thousand hectares) with production of 783 KT (thousand tonnes) with productivity of 619 kg per hectare (DES 2018-19 (Directorate of Economics and Statistics)) and Karnataka is one of the major chickpeas producing state in the country.

Yield trait is a complex character and that is influenced by environment, genotype, and genotype x environment interaction. In any crop breeding programme, for breeders, one of prime concern is to improve the yield. The heritability (h^2) of a trait represents the extent to which, it is transmitted

from one generation to the next generation. Further estimation of the genetic advance (GA) gives expected gain; this is resulting from selection pressure in breeding material. Heritability (h^2) and genetic advance (GA), phenotypic variances (V_p) and genotypic variances (V_g) have been useful for the assessment of magnitude of variance in population. Thus, for utilization of genotypes in breeding programmes and for effective selection, a thorough knowledge of genetic variability, heritability and genetic advance is essential.

Thorough knowledge of on extent of genetic variation, diversity and nature of gene action available in the genotypes helps the breeders for planning good breeding programmes. Thus, variability is pre-requisite for improvement of any crop in plant breeding programmes.

Material and Methods

To study the genetic (diversity) variability, traits correlation and path analysis studies, a field experiment was conducted during *rabi* 2019-20 at Zonal Agricultural Research Station (ZARS), Kalaburagi, Karnataka, India, which is located in North-Eastern Dry Zone (Zone-2) of Karnataka between (N) 17° 36' latitude and (E) 76° 81' longitude. The experimental material comprised of 54 advanced and stabilized chickpea genotypes, generated and

maintained from six diverse parental crosses, along with ten check varieties viz., MABC-WR-SA-1, WR-315, JG-62, MLT-66-266, ICCV-4958, ICCV-10, MLT-411-111, JG-11, A-1, GBM-2. The list of genotypes and checks used in this study are presented in Table 1. These lines were obtained through pedigree method and selection was carried out in sick plot at ZARS, Kalaburagi. Evaluation of different genotypes was done by using Lattice Design (8 x 8). 2 rows each genotype was sown in 4-meter length by adopting spacing of 30 cm and 10 cm between rows and plants respectively, in two replications. The observations were recorded in each genotype on randomly selected five plants in each replication for number of days to taken for 50 % flowering, number of days to taken for maturity, plant height, number of primary branches per plant, number of secondary branches per plant, total number of pods per plant, total number of seeds per pod, hundred seed weight, seedling vigor and seed yield per plot and mean values were used for statistical analysis.

The data taken on mean value for all the characters was used to analyzed for the variance by applying Lattice design as recommended by Cochran and Cox (1957). Both genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated for each character as per the method advise by Burton and Davane (1953). Heritability in broad sense expressed as percentage was calculated as propose by Hansen *et al.* (1956). Genetic advance was worked out by using the formula as suggested by Johnson *et al.* (1955). The ANOVA (analysis of Covariance) was analyzed by using method originated by Singh and Chaudhary (1977) and path coefficient analysis was worked out agreeing with the method given by Wright (1921) and accompanied by Dewey and Lu (1959).

Results and Discussion

The analysis of variance showed significant differences among the genotypes for all quantitative characters, show considerable magnitude of genetic variability available in the material used for the study. The details of analysis of variance are depicted in Table 2. A broad range of variability was observed for all quantitative characters.

The calculated PCV (phenotypic coefficient of variation) in general, were higher than the calculated GCV (genotypic coefficient of variation) for all quantitative traits, which is suggested that the unclear variation is not only due to the genotypes but also due to the influence of the environment. The genetic variability parameters for different traits in chickpea were given in Table 3. The maximum GCV noticed in seed yield per plot followed by total number of pods per plant, total number of secondary branches per plant and seedling vigour. This is an expressive of less amenability of these traits to environmental fluctuations and hence, breeder should give more emphasis on these characters, similar reports were observed by Saki *et al.* (2009), Padmavathi *et al.* (2013), Tiwari *et al.* (2016), Arora and Kumar (2018), Banik *et al.* (2018), Barad *et al.* (2018), Kishor *et al.* (2018), Munde *et al.* (2018), Kumar *et al.* (2019), Mayuriben *et al.* (2019) and Kumar *et al.* (2020).

The higher PCV (phenotypic coefficient of variation) observed in number of secondary branches per plant followed by seed yield per plot and total number of pods per plant. The magnitude of phenotypic coefficient of variation ranged from

4.31 (days to maturity) to 38.39 (number of secondary branches per plant).

The traits show high phenotypic coefficients of variation specify more influence of environmental factors. Therefore, caution has to be taken during the selection program because the environmental variations are uncertain in nature and this going to mislead the results. The heritability observed for most of the characters ranged from 25 (number of primary branches per plant) to 93 (days to maturity).

The heritability values were recorded high for days to maturity, seed yield per plot, seedling vigour, number of pods per plant, plant height and days to 50 % flowering. The expected GA (genetic advance) was high for seed yield per plot succeed by total number of pods per plant, seedling vigour, plant height and total number of secondary branches per plant.

High heritability coupled with high genetic advance as percent of mean together provide a better judgment rather than heritability alone in predicting the effect of selection. High heritability coupled with high genetic advance over mean was recorded for seed yield per plot, seedling vigour, total number of pods per plant and plant height. This advise that these characters can be improved through selection without progeny testing and this may be due to additive gene action. Similar results were found by Padmavathi *et al.* (2013).

The study of interrelationship among various characters is very important aspects in selection programme for the breeder to make an effective selection. Knowledge on nature of gene action and degree of associations among different characters are important. Indirect selection is effective only when desirable characters have low heritability that is measured in one sex only. The efficiency of indirect selection depends on correlated response. Knowledge of correlation is essential when selection is to be made on several characters at a time. If, our objective is to make selection on a single trait, the knowledge of correlation is also essential here to avoid the undesirable correlated changes in other characters.

In general, measure of genotypic correlation was higher than the phenotypic correlation coefficients in most of the characters reveals that a strong inherent association exists for the characters studied and phenotypic selection may be effective. Similar results in accordance with Mushtaq *et al.* (2013).

Higher genotypic correlation observed for particular traits means give a better response for seed yield improvement (Robinson *et al.* 1951).

At phenotypic level, seed yield per plot given significant positive correlation coefficient with 100-seed weight (0.299). While number of days taken for maturity (-0.492), number of days taken for 50 % flowering (-0.440), plant height (-0.329) showed significant negative correlation coefficient at phenotypic level.

At genotypic level, seed yield per plot exhibited highly significant positive correlation coefficient with number of secondary branches per plant (0.495), hundred seed weight (0.435) and significant negative character association with number of days taken for maturity (-0.550), number of days taken for 50 % flowering (-0.511), plant height (-0.489),

number of primary branches per plant (-0.379). The same findings were reported by Mushtaq *et al.* (2013), Padmavathi *et al.* (2013) and Agrawal *et al.* (2018). The correlation coefficient values with respect yield and yield attributing characters were given in Table 4 and Table 5.

Path coefficient analysis were specified in Table 6, for seed yield per plot, total number of pods per plant (0.305), hundred seed weight (0.104) and total number of seeds per pod (0.064) had showed positive direct effect. Whereas, number of days taken for maturity (-0.298), number of days taken for 50 % flowering (-0.227), plant height (-0.120), number of primary branches per plant (-0.061), seedling vigour (-0.058) and number of secondary branches per plant (-0.057) had showed negative direct effect on seed yield. The

similar results are in accordance with the earlier reports of Agrawal *et al.* (2018). The phenotypic path diagram given in Fig.1.

Conclusion

One of the breeding strategies for improvement of yield potential in chickpea genotypes under drought stress condition would aim on selection of plants having higher seed yield per plot, hundred seed weight, number of secondary branches per plant, total number of pods per plant and seedling vigour, these associated characters may be useful for breeder to formulate appropriate breeding plans for selection of the genotype which tolerate high drought stress condition.

Table 1: Following genotypes used in the study

Sl. No.	Genotype	Parentage	Source
1.	KCD-1	RCBM-3 x IPC-2010-134	ZARS, Kalaburagi
2.	KCD-2	RCBM-3 x IPC-2010-134	ZARS, Kalaburagi
3.	KCD-3	RCBM-3 x IPC-2010-134	ZARS, Kalaburagi
4.	KCD-4	RCBM-3 x IPC-2010-134	ZARS, Kalaburagi
5.	KCD-5	RCBM-3 x IPC-2010-134	ZARS, Kalaburagi
6.	KCD-6	RCBM-3 x IPC-2010-134	ZARS, Kalaburagi
7.	KCD-7	RCBM-3 x IPC-2010-134	ZARS, Kalaburagi
8.	KCD-8	RCBM-3 x IPC-2010-134	ZARS, Kalaburagi
9.	KCD-9	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
10.	KCD-10	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
11.	KCD-11	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
12.	KCD-12	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
13.	KCD-13	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
14.	KCD-14	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
15.	KCD-15	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
16.	KCD-16	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
17.	KCD-17	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
18.	KCD-18	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
19.	KCD-19	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
20.	KCD-20	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
21.	KCD-21	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
22.	KCD-22	RCBM-2 x IPC-2010-134	ZARS, Kalaburagi
23.	KCD-23	GBM-2 x IPC-2016-134	ZARS, Kalaburagi
24.	KCD-24	GBM-2 x IPC-2016-134	ZARS, Kalaburagi
25.	KCD-25	GBM-2 x IPC-2016-134	ZARS, Kalaburagi
26.	KCD-26	GBM-2 x IPC-2016-134	ZARS, Kalaburagi
27.	KCD-27	GBM-2 x IPC-2016-134	ZARS, Kalaburagi
28.	KCD-28	GBM-2 x IPC-2016-134	ZARS, Kalaburagi
29.	KCD-29	GBM-2 x IPC-2016-134	ZARS, Kalaburagi
30.	KCD-30	GBM-2 x IPC-2016-134	ZARS, Kalaburagi
31.	KCD-31	RCBM-3 x GNG-2226	ZARS, Kalaburagi
32.	KCD-32	RCBM-3 x GNG-2226	ZARS, Kalaburagi
33.	KCD-33	RCBM-3 x GNG-2226	ZARS, Kalaburagi
34.	KCD-34	RCBM-3 x GNG-2226	ZARS, Kalaburagi
35.	KCD-35	RCBM-3 x GNG-2226	ZARS, Kalaburagi
36.	KCD-36	RCBM-3 x GNG-2226	ZARS, Kalaburagi
37.	KCD-37	RCBM-3 x GNG-2226	ZARS, Kalaburagi
38.	KCD-38	RCBM-3 x GNG-2226	ZARS, Kalaburagi
39.	KCD-39	RCBM-2 x GNG-2226	ZARS, Kalaburagi
40.	KCD-40	RCBM-2 x GNG-2226	ZARS, Kalaburagi
41.	KCD-41	RCBM-2 x GNG-2226	ZARS, Kalaburagi
42.	KCD-42	RCBM-2 x GNG-2226	ZARS, Kalaburagi
43.	KCD-43	RCBM-2 x GNG-2226	ZARS, Kalaburagi
44.	KCD-44	RCBM-2 x GNG-2226	ZARS, Kalaburagi

45.	KCD-45	RCBM-2 x GNG-2226	ZARS, Kalaburagi
46.	KCD-46	RCBM-2 x GNG-2226	ZARS, Kalaburagi
47.	KCD-47	GBM-2 x GNG-2226	ZARS, Kalaburagi
48.	KCD-48	GBM-2 x GNG-2226	ZARS, Kalaburagi
49.	KCD-49	GBM-2 x GNG-2226	ZARS, Kalaburagi
50.	KCD-50	GBM-2 x GNG-2226	ZARS, Kalaburagi
51.	KCD-51	GBM-2 x GNG-2226	ZARS, Kalaburagi
52.	KCD-52	GBM-2 x GNG-2226	ZARS, Kalaburagi
53.	KCD-53	GBM-2 x GNG-2226	ZARS, Kalaburagi
54.	KCD-54	GBM-2 x GNG-2226	ZARS, Kalaburagi
55.	MABC-WR-SA-1 (Wilt check)	A-1 x WR-315	ZARS, Kalaburagi
56.	WR-315 (Wilt check)	Landrace	NA
57.	JG-62 (Wilt check)	Desi chickpea cultivar	JNKVV
58.	MLT-66-266 (Drought check)	A-1 x WR-315	ZARS, Kalaburagi
59.	ICCV-4958 (Drought check)	Drought tolerant cultivar	ICRISAT, Patancheru
60.	ICCV-10 (Drought check)	P-1231 x P-1265	ICRISAT, Patancheru
61.	MLT-411-111 (Yield check)	A-1 x WR-315	ZARS, Kalaburagi
62.	JG-11 (Yield check)	[(Phule G 5 x Narsinghpur bold) x ICCV 37] ICCX-860263-BF-BP-91 BP	Jabalpur, Sehore, ICRISAT, Patancheru
63.	A-1 (Yield check)	Cultivar developed from landrace Annigeri	UAS, Bengaluru
64.	GBM-2 (Yield check)	Pure line selection	ZARS, Kalaburagi

NA = Not Available

Table 2 : ANOVA (Analysis of variance) for different characters under normal sown condition in chickpea

Source of variation	DF	DFE	DM	PH	PBP	SBP	NPP	NSP	HSW	SY	SV
Replications	1	9.03	4.13	0.50	0.42	1.67	4.65	0.034	4.73	2835.98	1660.32
Genotypes	63	18.50**	25.44**	73.85**	0.43*	3.20*	83.16**	0.02*	6.61**	184079.80**	345032.80**
Blocks	14	4.41	0.89	14.11	0.50	1.56	11.18	0.01	2.78	15883.40	7965.42
Error	49	3.41	0.79	14.64	0.19	1.90	13.42	0.01	2.98	17144.42	19484.89
Total	127	11.05	13.06	43.84	0.35	2.50	47.70	0.02	4.77	99703.19	179567.00

* Significant at 0.05 probability level,

** Significant at 0.01 probability level

Where, DFF= Days to 50 % flowering (in days)

DM= Days to Maturity (in days)

SV= Seedling Vigour

PH= Plant Height (cm)

NPP= Total Number of Pods per plant

HSW= 100-Seed Weight (g)

PBP= Number of Primary Branches per plant

NSP= Total Number of Seeds per pod

SY= Seed Yield per plot (kg ha⁻¹)

SBP= Number of Secondary Branches per plant

Table 3 : Genetic variability parameters for different characters under normal sown condition in chickpea

Sl. No.	Character	Mean	Range		Coefficient Variation		h ² bs (%)	GA (5%)	GAM (5%)
			Minimum	Maximum	GCV (%)	PCV (%)			
1	Days to 50% flowering	45.35	36.00	50.50	6.01	7.33	67	4.60	10.14
2	Days to maturity	83.96	78.50	89.00	4.18	4.31	93	7.00	8.33
3	Plant height (cm)	42.19	29.67	53.50	12.91	15.75	67	9.19	21.79
4	No. of primary branches/plant	2.99	2.00	4.33	9.90	19.78	25	0.30	10.22
5	No. of secondary branches/ plant	4.13	1.33	8.00	20.04	38.39	27	0.89	21.55
6	No. pods/plant	27.71	16.83	52.50	21.38	25.00	73	10.43	37.65
7	No. seeds/pod	1.17	1.00	1.55	7.55	12.49	36	0.11	9.40
8	Hundred seed weight	18.94	14.19	23.60	7.15	11.53	38	1.73	9.14
9	Seedling vigour	2002.09	1450.00	2893.75	14.44	15.83	83	543.37	27.14
10	Seed yield/plot (kg/ha)	1519.36	813	2618	26.65	28.00	90	794.39	52.28

NS = Normal sown

LS = Late sown

Where,

h²bs= Heritability in broad sense

GAM= Genetic advance as per cent mean

GCV= Genotypic coefficient of variability

GA= Genetic advance

PCV= Phenotypic coefficient of variability

Table 4 : Correlation coefficient between yield and yield attributing traits under normal sown condition at phenotypic level

Trait	DFF	PH	PBP	SBP	DM	NPP	NSP	HSW	SV
DFF	1	0.499**	0.234	-0.276*	0.531**	0.102	0.029	-0.370**	-0.150
PH		1	0.378**	-0.202	0.608**	0.287*	0.044	-0.192	-0.460**
PBP			1	0.008	0.243	0.318*	-0.069	-0.184	-0.159
SBP				1	-0.294*	0.361**	0.028	0.185	0.043
DM					1	0.020	-0.019	-0.295*	-0.397**
NPP						1	0.218	-0.009	-0.186
NSP							1	0.019	-0.015
100-SW								1	-0.020
SV									1
SY	-0.440**	-0.329**	-0.149	0.245	-0.492**	0.225	0.130	0.299*	0.096

Significant at 0.05= * and Significant at 0.01= **

Where, DFF= Days to 50 % flowering (days)
 PH= Plant Height (cm)
 PBP= Primary Branches/plant
 SBP= Secondary Branches/plant

DM= Days to Maturity (days)
 NPP= Number of Pods/plant
 NSP= Number of Seeds/pod

SV= Seedling Vigour
 HSW= 100-Seed Weight (g)
 SY= Seed Yield/plot (kg ha⁻¹)

Table 5 : Correlation coefficient between yield and yield attributing traits under normal sown condition at genotypic level

Trait	DFF	PH	PBP	SBP	DM	NPP	NSP	HSW	SV
DFF	1	0.795**	0.760**	-0.581**	0.690**	0.192	0.041	-0.629**	-0.242
PH		1	0.847**	-0.749**	0.770**	0.265*	0.108	-0.336**	-0.576**
PBP			1	0.223	0.463**	0.673**	-0.069	-0.359**	-0.093
SBP				1	-0.658**	0.664**	0.302*	0.607**	0.149
DM					1	0.009	0.043	-0.557**	-0.427**
NPP						1	0.411**	-0.065	-0.229
NSP							1	-0.088	-0.107
100-SW								1	-0.051
SV									1
SY	-0.511**	-0.489**	-0.379**	0.495**	-0.550**	0.153	0.223	0.435**	0.114

Significant at 0.05= * and Significant at 0.01= **

Where, DFF= Days to 50 % flowering (days)
 PH= Plant Height (cm)
 PBP= Primary Branches/plant
 SBP= Secondary Branches/plant

DM= Days to Maturity (days)
 NPP= Number of Pods/plant
 NSP= Number of Seeds/pod

SV= Seedling Vigour
 HSW= 100-Seed Weight (g)
 SY= Seed Yield/plot (kg ha⁻¹)

Table 6 : Phenotypic direct and indirect effects of quantitative characters under normal sown condition on seed yield per plot.

Trait	DFF	PH	PBP	SBP	DM	NPP	NSP	HSW	SV
DFF	-0.227	-0.113	-0.053	0.062	-0.120	-0.023	-0.006	0.083	0.034
PH	-0.06	-0.120	-0.045	0.024	-0.073	-0.034	-0.005	0.023	0.055
PBP	-0.014	-0.023	-0.061	-0.0005	-0.014	-0.019	0.004	0.011	0.009
SBP	0.015	0.011	-0.0005	-0.057	0.016	-0.020	-0.001	-0.010	-0.002
DM	-0.158	-0.181	-0.072	0.087	-0.298	-0.006	0.005	0.087	0.118
NPP	0.031	0.087	0.097	0.110	0.006	0.305	0.066	-0.002	-0.057
NSP	0.001	0.002	-0.004	0.001	-0.001	0.014	0.064	0.001	-0.001
100-SW	-0.038	-0.02	-0.019	0.019	-0.030	-0.0009	0.002	0.104	-0.002
SV	0.008	0.026	0.009	-0.002	0.023	0.010	0.0009	0.001	-0.058
SY	-0.440	-0.328	-0.149	0.245	-0.492	0.225	0.130	0.299	0.096

Phenotypic Residual Value = 0.7848

Where, DFF= Days to 50 % flowering (days)
 PH= Plant Height (cm)
 PBP= Primary Branches/plant
 SBP= Secondary Branches/plant

DM= Days to Maturity (days)
 NPP= Number of Pods/plant
 NSP= Number of Seeds/pod

SV= Seedling Vigour
 HSW= 100-Seed Weight (g)
 SY= Seed Yield/plot (kg ha⁻¹)

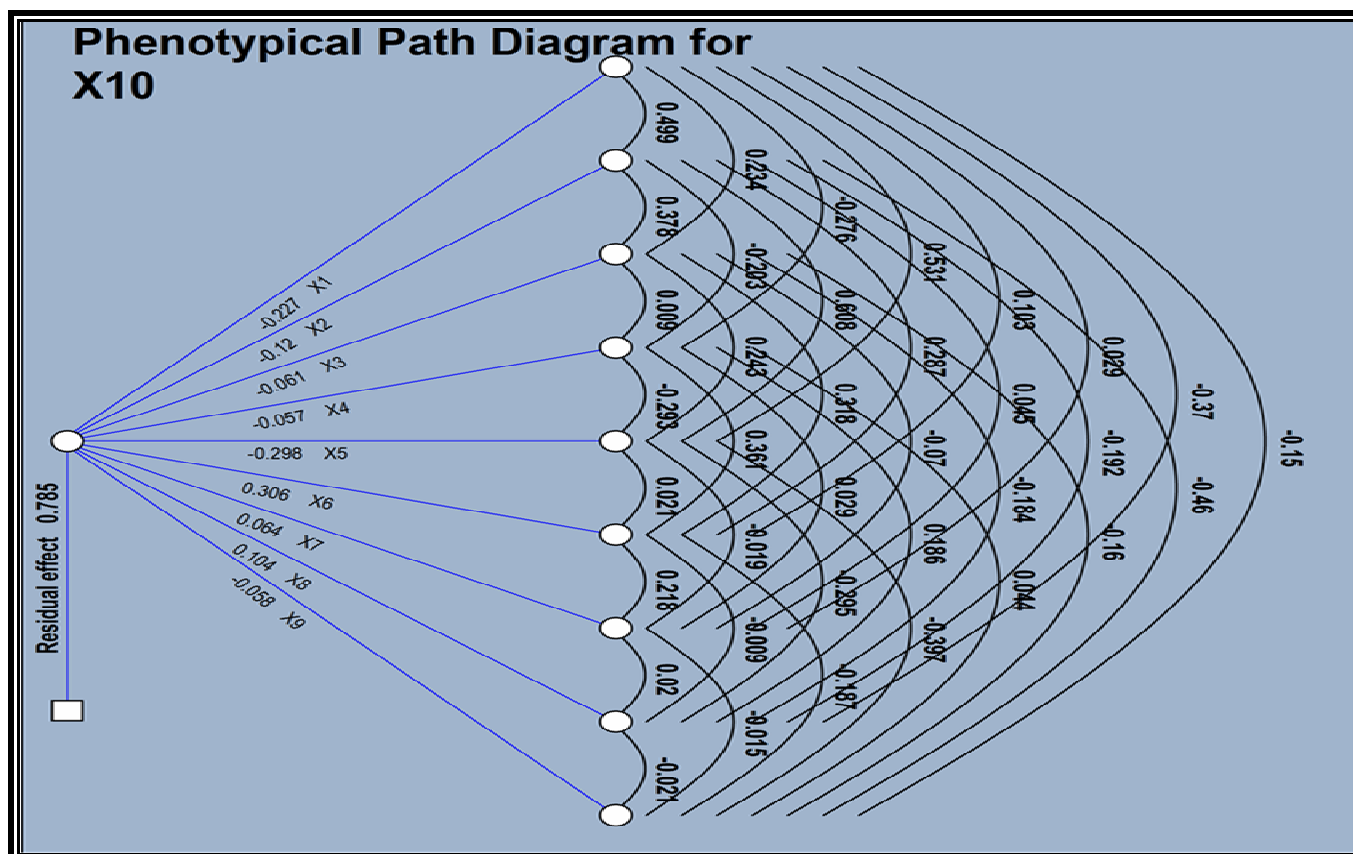


Fig. 1 : Phenotypical path diagram shows Direct and indirect effects of quantitative characters on seed yield at phenotypic level under field condition.

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