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Assessment of genetic variability, correlation and path coefficient analysis for yield and its attributing traits in chickpea (*Cicer arietinum* L.)

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Abstract

Chickpea (*Cicer arietinum* L.) is a legume crop belonging to the family Leguminosae (Fabaceae). High yield is the main aim of crop breeders involved in crop improvement programmes. A better insight to the association of yield with its component traits can be helpful in improving the chickpea yield. The present study comprised of 57 genotypes grown in Randomized Block Design with two replications during *Rabi* 2021-22. The genotypes were evaluated to assess the genetic variability, heritability and genetic advance, correlation and direct and indirect effects among yield and yield components. The correlation studies revealed that seed yield per plant was positively and significantly correlated with biological yield, number of secondary branches per plant and number of pods per plant. The path analysis indicated that biological seed yield per plant was observed the maximum positive direct effect on seed yield per plant and thus, may be considered as useful traits for yield improvement of chickpea.

Keywords: Chickpea, genetic variability, heritability, genetic advance, correlation, path coefficient analysis

Introduction

Chickpea (*Cicer arietinum* L.) is a temperate self-pollinated legume crop, originated from southeastern Turkey. It is an annual species with the haploid genome size of 738 Mb and chromosomal number $2n = 2x = 16$ (Varshney *et al.*, 2013) [49]. According to their seed morphology, chickpeas can be broadly separated into two types: *desi*, with small seeds having brown coat colour, and *Kabuli*, with big seeds having cream- or beige-colored coat (Solanki *et al.*, 2019) [37]. The nutritional value of chickpeas is very enriching because of their high content of vitamins (Gupta *et al.*, 2021) [14], minerals *viz.*, calcium, magnesium, phosphorus, and potassium, and important amino acids, including lysine, methionine, threonine, valine, and leucine, along with β -carotene, (Jukanti *et al.*, 2012; Thudi *et al.*, 2014) [18, 44]. Chickpea productivity reduced by an array of abiotic factors *i.e.*, drought, heat, excessive salt, and cold (Asati *et al.*, 2022) [2] and biotic factors including Ascochyta blight, Fusarium wilt, and Helicoverpa (Sahu *et al.*, 2020a; Sahu *et al.*, 2020b) [38-39].

Any crop development programmes effectiveness largely depends on a selection that is further influenced by the presence and frequency of genetic heritability in the population of a particular crop species (Yadav *et al.*, 2005; Tripathi *et al.*, 2015; Mishra *et al.*, 2020; Makwana *et al.*, 2021; Mishra *et al.*, 2021a; Mishra *et al.*, 2021b; Shyam *et al.*, 2021; Tripathi *et al.*, 2022) [56, 46, 26, 24, 28-29, 40, 48]. The environment has a major impact on seed productivity, which is a major polygenic trait (Singh *et al.*, 2014) [41]. The assessment of major characteristics and their interrelatedness is important in developing selection criteria for improving existing genotypes. Path coefficient analysis helps to determine the direct effect of traits and their indirect effects on another trait. The phenotypic co-efficient assesses the influence of the environment on the genotype, whereas the genotypic co-efficient of variation estimates the heritable variability. Hence heritability, selection intensity, and genetic gain are all elements of effective selection (Barfa *et al.*, 2017, Asati and Yadav, 2020; Rajpoot *et al.*, 2020; Verma *et al.*, 2021; Choudhary *et al.*, 2021; Yadav *et al.*, 2021; Yadav *et al.*, 2022a; Yadav *et al.*, 2022b) [8, 2, 33, 50, 12, 53, 54, 55]. A directional model based on seed yield and its components that provides the chance for selection is employed in correlation analysis to evaluate the mutual relationship between two parameters (Khan and Qureshi, 2001) [19]. So, on the basis of above background the present study was conducted with the objective to estimate the total genotypic variability

and determine the heritability of specific agronomic parameters along with correlations, and path analysis among important traits for selection criteria for improving yield in chickpea under normal sown condition.

Materials and Method

The investigation was carried out to know the genetic variability, correlation, and path analysis of 57 chickpea genotypes (Table 1). These genotypes were collected from Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, India, and RAK College of Agriculture, Sehore, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, India. The experiment was carried out at Agriculture Research Farm, Department of Plant Breeding & Genetics, College of Agriculture, Gwalior, India in randomized block design with two replications. The genotypes were planted during 2nd week of November, 2021 and harvested during the third week of March, 2022. Each entry was planted in 4 rows of 3m length, keeping row to row and plant to plant distance of 30 x 15 cm, correspondingly. Data were recorded on eleven different yield attributing characters including days to 50% flowering, days to maturity, plant height, numbers of primary and secondary branches per plant, numbers of pods per plant, numbers of seeds per pod, 100-seed weight, harvest index, biological yield per plant and seed yield per plant. Five plants from each replication were randomly selected from each genotype for recording observations for all the traits.

Genotypic (GCV) and phenotypic coefficient of variation (PCV) was calculated as per formula given by Burton (1952)^[10], heritability in the broad sense (h^2) as suggested by Burton and De (1953)^[11] and genetic advance as per the method described by Johnson *et al.* (1955)^[17]. The correlation coefficients were determined the degree of a character's relationship with yield as well as among the variables that contribute to yield. The correlation between genotype and phenotype was calculated using formula given (Weber and Moorthy 1952)^[51] and modified (Miller *et al.*, 1958)^[25]. The path coefficient analysis in order to figure out the direct and indirect impacts of the various characters on yield was calculated using method adopted (Dewey and Lu. 1959)^[4].

Results and Discussion

Genetic variability studies

The analysis of variance presented significant differences for all the characters studied (Table 2) *viz.*, days to 50% flowering, days to maturity, plant height, numbers of primary branches and secondary branches per plant, numbers of pods per plant, numbers of seeds per pod, 100 -seed weight, harvest index, biological yield per plant and seed yield per plant. This substantial variability provides a good prospect for improving traits of interest in chickpea breeding programmes. In some of the previous studies conducted by Dehal *et al.* (2016)^[5] and Kumar *et al.* (2014)^[20] similar findings have been reported for genetic variability in chickpea.

Genetic parameters of yield and its attributing traits are presented in Table 3; Fig.1. Results revealed that PCV% was higher than GCV% for all the traits under studied. High PCV and GCV were documented for biological yield per plant tracked by numbers of pods per plant and 100-seed weight. Similarly, the moderate estimates of PCV and GCV were recorded for numbers of seeds per pod followed by numbers of primary and secondary branches per plant, harvest index, plant height and seed yield per plant, while the least estimate

of PCV and GCV was recorded for days to 50% flowering and maturity. These results are similar to finding of Yadav *et al.* (2015)^[57], Kumar *et al.* (2018)^[21] and Kumar *et al.* (2020)^[22].

Higher estimates of heritability in broad sense were documented for plant height, numbers of pods per plant, biological yield per plant, day to maturity, 100-seed weight, numbers of primary and secondary branches per plant, harvest index, yield per plant, numbers of seeds per pods and day to 50% flowering. These results were in close conformity with the findings of Malik *et al.* (2010)^[23] for 100- seed weight, harvest index, numbers of secondary branches per plant and yield per plant, Babbar *et al.* (2012)^[6] for days to 50% flowering, days to maturity, plant height, 100- seed weight and yield per plant, Pandey *et al.* (2013)^[32] for days to 50% flowering, numbers of seeds per pod, plant height and numbers of pods per plant, Monpara and Gaikwad (2014)^[29] for seed yield per plant, 100-seed weight, plant height and numbers of primary branches per plant, Sowjanya *et al.* (2017)^[43] for most of the traits and Honnappa *et al.* (2018)^[15] for numbers of seeds per pod, biological yield per plant, 100-seed weight and yield per plant.

The higher genetic advance documented for biological yield per plant tracked by numbers of pods per plant, 100- seed weight, numbers of primary and secondary branches per plant, harvest index, plant height, numbers of seeds per pod and yield per plant. Whilst moderate estimate of genetic advance as percent of means was recorded for days to maturity and low estimate for days to 50% flowering. These results were in close agreement with the findings of Solanki *et al.* (2019)^[37], Tsehaye *et al.* (2020)^[45] and Kumar *et al.* (2020)^[22].

Correlation coefficient analysis

Correlation coefficient is a method for identifying the important characteristics influencing the dependent characteristics, such as seed yield, and they assist in developing the selection criteria for simultaneously improving several characters and economic production. Correlations among different traits are presented in Table 4 and 5.

Highly significant and positive genotypic correlation for seed yield per plant was recorded with biological yield per plant tracked by numbers of secondary branches per plant and numbers of pods per plant, whereas it exhibited significantly and negative with harvest index. These findings showed close similarity with earlier work conducted by Ali *et al.* (2011)^[11] and Mushtaq *et al.* (2013)^[30] for numbers of secondary branches per plant, Shukla and Babbar (2011)^[36] and Tadesse *et al.* (2016)^[47] for numbers of pods per plant, Babbar *et al.* (2012)^[6] and Jain *et al.* (2022)^[16] for biological yield per plant and numbers of pods per plant, while highly significant positive phenotypic correlation for seed yield per plant was invented with biological yield per plant and numbers of secondary branches per plant by Shanmugam and Kalaimagal (2019)^[34] and Kumar *et al.* (2020)^[22].

Path-coefficient analysis

The direct and indirect effects of different independent traits on the dependent character are measured *via* path coefficient analysis. It demonstrates the relationship between these independent characters and seed yield results from their direct influence on yield or from their indirect impact through other component characters. The direct and indirect effects of various yield components towards yield are presented in

Table 6 and Table 7.

Path coefficient analysis at genotypic level revealed that days to 50% flowering had the maximum positive direct effect on seed yield per plant tracked by numbers of secondary branches per plant, plant height, numbers of pods per plant, days to maturity and 100-seed weight. Whilst substantial negative direct effects on seed yield per plant were contributed by harvest index followed by biological yield per plant, numbers of primary branches per plant and numbers of

seeds per pod. These findings revealed direct positive effect on 100- seed weight. These findings are in accordance with earlier work reported by Babbar *et al.* (2012) [6], Shrivastava *et al.* (2012) [35] and Jain *et al.* (2022) [16] for days to 50% flowering, numbers of secondary branches per plant, plant height, numbers of pods per plant and days to maturity. Similar reports also documented for direct negative effect on numbers of primary branches per plant by Dawane *et al.* (2020) [13] and Nath *et al.* (2022) [31].

Table 1: List of chickpea genotypes with their sources used in the investigation

S. No.	Genotype name	Pedigree/ Source of collection	S. No.	Genotype name	Pedigree/ Source of collection
1	ICCV-201102	COA, JNKVV, Jabalpur	30	SAGL-152258	JG 135 x FG 711
2	ICCV-201104	COA, JNKVV, Jabalpur	31	SAGL-152265	PUSA 1088 x VIJAY
3	ICCV-201105	COA, JNKVV, Jabalpur	32	SAGL-152273	KAK 2 x IPC 9494
4	ICCV-201109	COA, JNKVV, Jabalpur	33	SAGL-152278	JSC 37 x JSC 36
5	ICCV-201111	COA, JNKVV, Jabalpur	34	SAGL-152318	JSC 19 x JG 16
6	ICCV-201112	COA, JNKVV, Jabalpur	35	SAGL-152324	IPC 4958 X IPC 9494
7	ICCV-201113	COA, JNKVV, Jabalpur	36	SAGL-152327	KAK 2 x JSC 19
8	ICCV-201115	COA, JNKVV, Jabalpur	37	SAGL-152330	ICC 4958 x PHULE G 5
9	ICCV-201116	COA, JNKVV, Jabalpur	38	SAGL-152339	JG16 x KAK 2
10	ICCV-201118	COA, JNKVV, Jabalpur	39	SAGL-152344	IPC9494 x JG16
11	ICCV-201205	COA, JNKVV, Jabalpur	40	SAGL-152347	KAK 2 x JSC 19
12	ICCV-201206	COA, JNKVV, Jabalpur	41	SAGL-162299	RAK, Sehore, RVSKVV, Gwalior
13	ICCV-201209	COA, JNKVV, Jabalpur	42	SAGL-152349	KAK 2 x PHULE G5
14	ICCV-201210	COA, JNKVV, Jabalpur	43	SAGL-152403	RAK, Sehore RVSKVV, Gwalior
15	ICCV-201211	COA, JNKVV, Jabalpur	44	SAGL-152404	RAK, Sehore RVSKVV, Gwalior
16	ICCV-201212	COA, JNKVV, Jabalpur	45	SAGL-152405	RAK, Sehore RVSKVV, Gwalior
17	ICCV-201214	COA, JNKVV, Jabalpur	46	SAGL-162370	PG 9425-9 x BG 2064
18	ICCV-201217	COA, JNKVV, Jabalpur	47	SAGL-162376	JSC 52 x RSG 888
19	SAGL-152210	IPC 9494 x ICC 506	48	SAGL 22-101	KAK-2 X BG-362
20	SAGL-152216	JG 16 x VIJAY	49	SAGL 22-102	JG-6 X RVSSG-2
21	SAGL-152223	RAK, Sehore, RVSKVV, Gwalior	50	SAGL 22-103	JG-130 X FG-703
22	SAGL-152231	KAK2 x JG130	51	SAGL 22-104	JSC-33 X JG-11
23	SAGL-152234	JSC 19 x ICC 4958	52	SAGL 22-105	JAKI-9218 X BGD-112
24	SAGL-152236	KAK-2 x BG 362	53	SAGL 22-106	RVG-204 X JSC-37
25	SAGL-152237	BG 2064 x KAK -2	54	GCP-101	RAK, Sehore, RVSKVV, Gwalior
26	SAGL-152238	PG -9425-9 x IPC 9494	55	RVSSG-64	RAK, Sehore, RVSKVV, Gwalior
27	SAGL-152250	KAK 2 x BG 2064	56	JG-36	COA, JNKVV, Jabalpur
28	SAGL-152252	ICC 4958 x BG 1108	57	JG-14	COA, JNKVV, Jabalpur
29	SAGL-152254	BG 362 x ICC 506			

Table 2: Analysis of variance for yield and its attributing characters

Source	df	Days to 50% flowering	Days to maturity	Plant height	Numbers of primary branches per plant	Numbers of secondary branches per plant	Numbers of pods per plant	Numbers of seeds per pod	100- seed weight	Harvest Index	Biologic al yield per plant	Seed yield per plant
Replication	1	1.974	0.035	2.938	0.001	1.719	9.437	0.003	5.141	0.000	6.319	0.965
Treatments	56	7.749*	71.954**	113.011**	0.770*	4.779*	92.203**	0.120*	47.182*	117.877**	70.527**	3.998*
Error	56	3.009	2.624	1.758	0.036	0.506	2.397	0.044	2.055	16.264	1.913	0.961

Table 3: Components of genetic variability for grain yield and its attributing traits

S. No.	Characters	Mean	Range		PCV %	GCV %	Heritability (Broad Sense)	Genetic advance as % of mean 5%
			Min.	Max				
1	Days to 50% flowering	54.85	50.50	57.50	3.59%	2.81%	61.17	4.52
2	Days to maturity	111.47	95.60	121.50	5.38%	5.28%	96.35	10.68
3	Plant height (cm)	54.27	36.70	72.65	13.85%	13.74%	98.44	28.09
4	Numbers of primary branches per plant	3.73	2.70	4.70	16.62%	16.23%	95.27	32.62
5	Numbers of Secondary branches per plant	9.60	6.00	12.20	16.11%	15.23%	89.42	29.67
6	Numbers of pods per plant	32.43	17.00	44.90	20.94%	20.67%	97.40	42.01
7	Numbers of seeds per pod	1.31	1.00	1.90	18.67%	14.88%	63.54	24.43
8	100 -seed weight (gm)	23.92	14.31	34.70	20.30%	19.85%	95.64	40.00
9	Harvest index (%)	47.78	22.82	58.33	16.07%	14.92%	86.20	28.53
10	Biological yield per plant(gm)	22.74	13.66	43.21	26.12%	25.76%	97.29	52.34
11	Seed yield per plant(gm)	10.48	7.01	13.32	13.49%	11.76%	75.98	21.12

GCV- Genotypic Coefficient of Variation, - Phenotypic Coefficient of variation

Table 4: Genotypic correlation coefficient for grain yield and its attributing characters

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Numbers of primary branches per plant	Numbers of secondary branches per plant	Numbers of pods per plant	Numbers of seeds per pod	100-seed weight (gm)	Harvest Index (%)	Biological yield per plant(gm)	Yield per plant (gm)
Days to 50% flowering	1	0.0717	-0.3755**	-0.0008	-0.0901	0.0050	-0.1478	0.0145	-0.0238	0.0531	0.0245
Days to maturity		1	0.0885	0.3435**	0.2542*	0.0952	-0.1658	-0.0816	-0.1468	0.1253	-0.0611
Plant height (cm)			1	-0.0620	-0.0847	-0.2823*	-0.0500	0.2690*	-0.2720*	0.2579*	0.0692
Numbers of primary branches per plant				1	0.9604**	0.2712*	-0.0642	-0.0591	-0.2063	0.1684	0.1040
Numbers of Secondary branches per plant					1	0.2502*	0.0204	0.2640*	-0.1986	0.2550*	0.3275**
Numbers of pods per plant						1	0.0308	-0.0159	0.0084	0.3970**	0.2591*
Numbers of seeds per pod							1	0.1040	0.3587**	0.2090	0.2199
100 -seed weight (gm)								1	0.0560	0.0141	0.2311
Harvest Index (%)									1	-0.9075**	-0.3037*
Biological yield per plant(gm)										1	0.6259**

* = 0.05 level of significance; ** = 0.01 level of significance.

Table 5: Phenotypic correlation coefficient for grain yield and its attributing characters

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Numbers of primary branches per plant	Numbers of secondary branches per plant	Numbers of pods per plant	Numbers of seeds per pod	100-seed weight (gm)	Harvest Index (%)	Biological yield per plant(gm)	Yield per plant (gm)
Days to 50% flowering	1	0.0556	-0.2817*	-0.0185	-0.0603	-0.0087	-0.0455	0.0461	-0.0127	0.0341	0.0256
Days to maturity		1	0.0859	0.3339**	0.2493*	0.0849	-0.1169	-0.0796	-0.1280	0.1253	-0.0370
Plant height (cm)			1	-0.0587	-0.0919	-0.2799*	-0.0150	0.294*	0.2500*	0.2524*	0.0605
Numbers of primary branches per plant				1	0.8938**	0.2747*	-0.0641	-0.0550	-0.1815	0.1704	0.1125
Numbers of secondary branches per plant					1	0.2819*	-0.0041	0.2841*	0.2806*	0.2467	0.2737*
Numbers of pods per plant						1	0.0091	-0.0185	0.2723*	0.2814*	0.2246
Numbers of seeds per pod							1	0.0861	-0.1342	0.1699	0.1950
100- seed weight (gm)								1	0.0471	0.0138	0.1963
Harvest Index (%)									1	-0.8460**	-0.1108
Biological yield per plant(gm)										1	0.5727*

* = 0.05 level of significance; ** = 0.01 level of significance

Table 6: Genotypic path coefficient for yield and its attributing traits

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Numbers of primary branches per plant	Numbers of secondary branches per plant	Numbers of pods per plant	Numbers of seeds per pod	100-seed weight (gm)	Harvest Index (%)	Biological yield per plant(gm)	Seed yield per plant (gm)
Days to 50% flowering	0.7880	0.0565	-0.2959	-0.0006	-0.0710	0.0040	-0.1165	0.0114	-0.0188	0.0418	0.0245
Days to maturity	0.0216	0.3018	0.0267	0.1036	0.0767	0.0287	-0.0500	-0.0246	-0.0443	0.0378	-0.0611
Plant height (cm)	-0.1661	0.0391	0.4424	-0.0274	-0.0375	0.0497	-0.0221	-0.0443	-0.1203	0.1141	0.0692
Numbers of primary branches per plant	0.0050	-0.2410	0.4044	-0.5245	-0.2662	-0.5736	0.4187	0.3856	0.3461	-0.0985	0.1040
Numbers of secondary branches per plant	-0.5999	0.6932	-0.5645	0.3970	0.6607	0.6668	0.1357	-0.1571	-0.3229	0.6982	0.3275
Numbers of pods	0.0016	0.0310	0.0366	0.0786	0.0815	0.3259	0.0100	-0.0052	0.0028	0.0358	0.2591

per plant											
Number of seeds per pod	0.0282	0.0316	0.0095	0.0122	-0.0039	-0.0059	-0.1906	-0.0198	0.0406	-0.0398	0.2199
100- seed weight (gm)	0.0032	-0.0183	-0.0224	-0.0132	-0.0053	-0.0036	0.0233	0.2240	0.0125	0.0031	-0.0277
Harvest Index (%)	0.0474	0.2917	0.5403	0.4099	0.3946	-0.0168	0.4228	-0.1112	-0.9868	0.8030	0.7874
Biological yield per plant(gm)	-0.1046	-0.2468	-0.5080	-0.3316	-0.5021	-0.2161	-0.4116	-0.0277	0.7874	-0.9696	-0.9696

R Square = 0.9994, Residual effect = 0.0244

Table 7: Phenotypic path coefficient analysis for grain yield and its attributing traits

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Numbers of primary branches per plant	Numbers of secondary branches per plant	Numbers of pods per plant	Numbers of seeds per pod	100- seed weight (gm)	Harvest Index (%)	Biological yield per plant (gm)	Seed yield per plant (gm)
Days to 50% flowering	0.0046	0.0003	-0.0013	-0.0001	-0.0003	0.0000	-0.0002	0.0002	-0.0001	0.0002	0.0256
Days to maturity	-0.0047	-0.0850	-0.0073	-0.0284	-0.0212	-0.0072	0.0099	0.0068	0.0109	-0.0106	-0.0370
Plant height (cm)	-0.0015	0.0005	0.0052	-0.0003	-0.0005	0.0006	-0.0001	-0.0005	-0.0013	0.0013	0.0605
Numbers of primary branches per plant	0.0020	-0.0359	0.0063	-0.1075	-0.0961	-0.0242	0.0069	0.0059	0.0195	-0.0183	0.1125
Numbers of secondary branches per plant	-0.0142	0.0588	-0.0217	0.2107	0.2358	0.0547	-0.0010	-0.0033	-0.0449	0.0582	0.2737
Numbers of pods per plant	-0.0002	0.0019	0.0025	0.0051	0.0053	0.0229	0.0002	-0.0004	0.0001	0.0025	0.2246
Numbers of seeds per pod	-0.0031	-0.0081	-0.0010	-0.0044	-0.0003	0.0006	0.0691	0.0060	-0.0093	0.0117	0.1950
100- seed weight (gm)	0.0047	-0.0080	-0.0096	-0.0056	-0.0014	-0.0019	0.0087	0.1011	0.0048	0.0014	0.1963
Harvest Index (%)	-0.0158	-0.1597	-0.3119	-0.2265	-0.2379	0.0029	-0.1675	0.0588	0.2479	-0.0557	-0.1108
Biological yield per plant(gm)	0.0540	0.1982	0.3993	0.2695	0.3903	0.1763	0.2689	0.0218	-0.3383	0.5820	0.5727

R Square = 0.8622, Residual effect = 0.3713

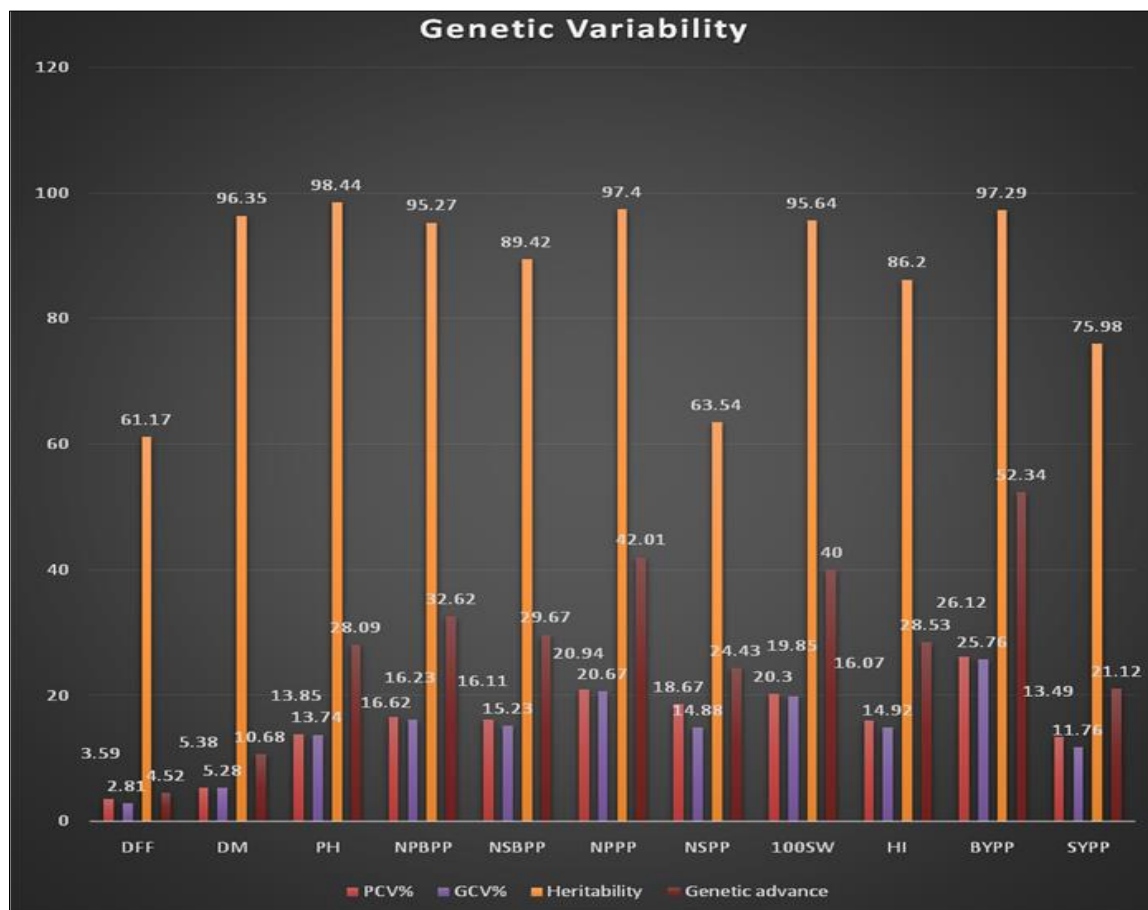


Fig 1: Graphical representation of genetic variability parameters

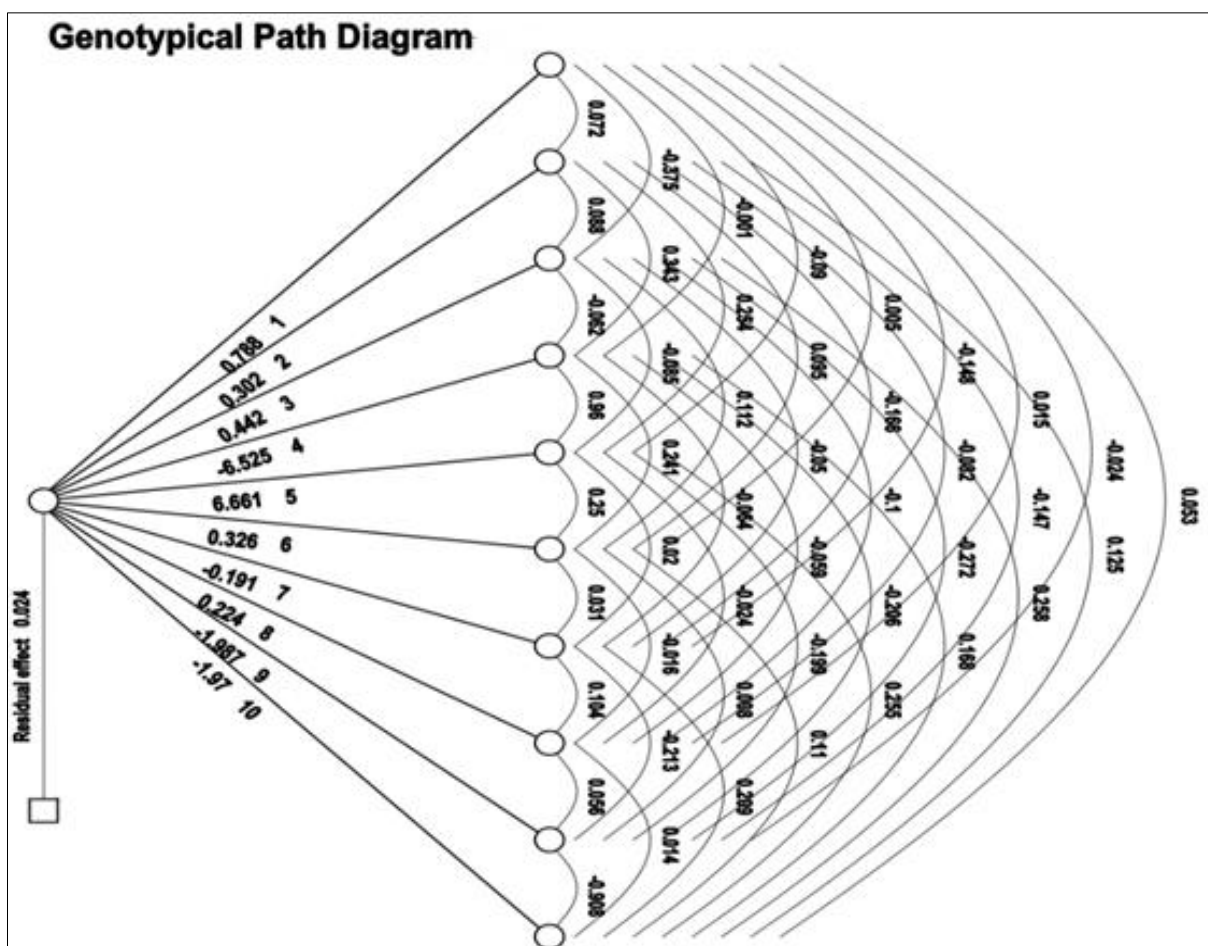


Fig 2: Genotypical path diagram

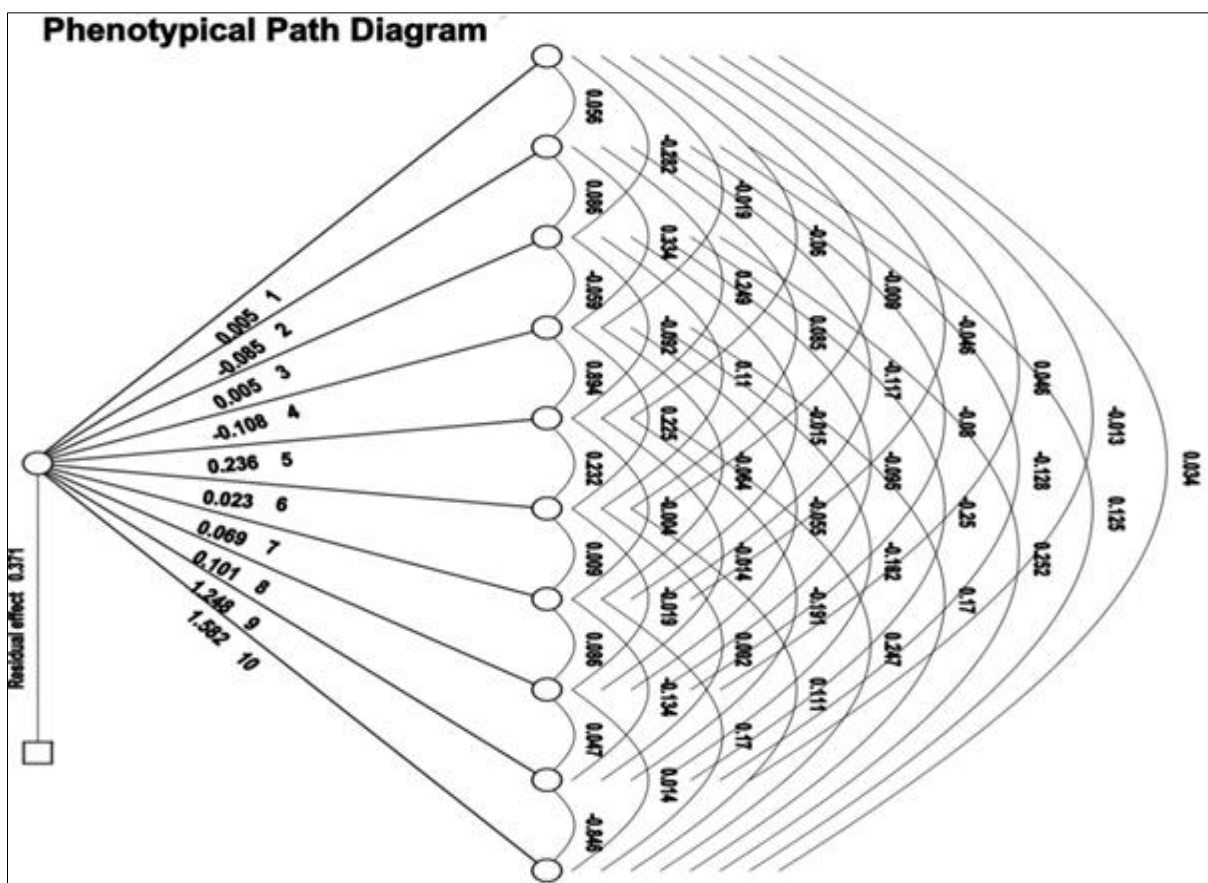


Fig 3: Phenotypical path diagram

Conclusion

Higher genotypic coefficient of variation and heritability coupled with genetic advance as percentage of mean was recorded for biological yield per plant tracked by numbers of pods per plant, 100-seed weight and seed yield per plant indicating the predominance of additive gene action and selection based on these traits may be rewarding. Seed yield per plant shared highly significant and positive association with biological yield, numbers of secondary branches per plant and numbers of pods per plant. Path analysis revealed biological seed yield per plant was positive and direct effect on seed yield per plant. Thus, selection of any trait can increase the other one, consider these traits for constricting plant type for higher yield, hence, for enhancement of yield these traits may be selected directly.

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