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GENETIC VARIABILITY AND CHARACTER ASSOCIATION STUDIES IN CHICKPEA (*CICER ARIETINUM* L.) FOR SEED YIELD UNDER IRRIGATED CONDITION.

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Abstract

Chickpea (*Cicer arietinum* L.) is a legume crop from the family Leguminosae (Fabaceae). Enhancing yield stands as the primary goal for crop breeders engaged in improvement programs. Understanding the relationship between yield and its component traits can aid in boosting chickpea yield. This study involved 25 genotypes cultivated in a Randomized Block Design with three replications during the Rabi season of 2023-24. The genotypes underwent evaluation to determine genetic variability, heritability, genetic advance, correlations, and direct and indirect effects among yield and its components. Correlation analyses revealed significant positive correlations between seed yield per plant and biological yield, number of secondary branches per plant, and number of pods per plant. Path analysis indicated that biological seed yield per plant had the highest positive direct effect on seed yield per plant, suggesting its importance as a trait for improving chickpea yield.

Keywords: Chickpea, Cicer arietinum L., germplasm, seed yield, component traits

Introduction

Chickpea (*Cicer arietinum* L.) is a type of legume crop that primarily grows in temperate regions and is native to Southeastern Turkey. It's an annual plant with a genome size of 738 Mb and a chromosomal count of $2n = 2x = 16$ (Varshney et al., 2013) [48]. Chickpeas can be broadly categorized into two types based on their seed morphology: desi, characterized by small seeds with a brown coat, and Kabuli, which have larger seeds with a cream or beige- colored coat (Solanki et al., 2019) [37]. These legumes are highly nutritious, boasting significant levels of vitamins (Gupta et al., 2021) [21], essential minerals like calcium, magnesium, phosphorus, and potassium, and vital amino acids such as lysine, methionine, threonine, valine, and leucine, as well as ß-carotene (Jukanti et al., 2012; Thudi*et al*., 2014) [18, 43]. However, the productivity of chickpeas can be adversely affected by various environmental factors like drought, heat, excessive salt, and cold, as well as biotic factors including Ascochyta blight, Fusarium wilt, and Helicoverpa infestations (Asati*et al.,* 2022; Sahu *et al.,* 2020a; Sahu *et al*., 2020b) [2, 38, 39].

The effectiveness of crop development programs greatly relies on careful selection, which in turn is influenced by the presence and frequency of genetic traits within the population of a specific crop species. Environmental conditions play a significant role in seed productivity, which is a complex trait influenced by multiple genes. Understanding the major characteristics and their interrelationships is crucial for establishing selection criteria to enhance existing genotypes. Path

coefficient analysis helps in assessing the direct and indirect effects of traits on each other. Phenotypic coefficients evaluate the impact of the environment on the genotype, while genotypic coefficients of variation estimate heritable variability. Therefore, factors such as heritability, selection intensity, and genetic gain are essential for effective selection. A directional model based on seed yield and its components is used in correlation analysis to examine the relationship between different parameters. With this context in mind, the current study aimed to estimate the total genotypic variability. The objective of this study is to assess the heritability of specific agronomic parameters and to analyze correlations and path analysis among important traits for selecting criteria aimed atenhancing yield in chickpeas under normal sown conditions. The investigation aimed to assess the genetic variability, correlations, and path analysis of 25 chickpea genotypes (Table 1). These genotypes were sourced from IIPR, Kanpur and Faculty of Agricultural Sciences and Allied Industries, Rama University Mandhana, Kanpur. The experiment was conducted at the Agriculture Research Farm, Department of Agriculture, Rama University, Kanpu, Uttar Pradesh, using a randomized block design with two replications. Each genotype was planted in four rows, each 3 meters in length, with a row-to-row and plant-to-plant distance of 30 x 15 cm, respectively. Data were collected on twelve yield attributing traits, including days to 50% flowering, days to maturity, plant height, numbers of primary and secondary branches per plant, pod-bearing length, numbers of pods per plant, numbers of seeds per pod, harvest index, biological yield per plant, and seed yield per plant and seed yield/ha. Five plants from each replication were randomly chosen for recording observations for all traits.

Table 1: Detailsofpedigreeof25chickpeagenotypesstudied

Sr. No.	GenotypeName	Sr. No.	GenotypeName
1	JG-14	14	Aparna
2	JG-17	15	Vishwas
3	JG-24	16	K-850
4	GG-2	17	IPC 18-131
5	BDG-72	18	KabuliGold
6	GCP-105	19	IPC-15-108
7	GNG-663	20	IPC-12-131
8	ICC-15614	21	IPC-18-52
9	ICC-1205	22	Radha
10	IPC-18-121	23	Kalimoti
11	JG-74	24	Allahabaddesichana
12	Sadabahar	25	DCP-92
13	Vaibhav	-	-

The genotypic (GCV) and phenotypic coefficient of variation (PCV) were calculated according to the formula provided by Burton (1952) [10], while heritability in the broad sense (h^2) was determined as suggested by Burton and De (1953) [11], and genetic advance was computed using the method described by Johnson et al. (1955) [17]. Correlation coefficients were calculated to assess the degree of relationship between each character and yield, as well as among the variables contributing to yield. The correlation between genotype and phenotype was calculated using the

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formula provided by Weber and Moorthy (1952) [50] and modified by Miller et al. (1958) [25]. Path coefficient analysis, which helps determine the direct and indirect impacts of various characters on yield, was conducted using the method adopted by Dewey and Lu (1959) [4].

Results and Discussion
Genetic variability studies

The analysis of variance revealed significant differences for all the traits examined, 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 (Table 2). This considerable variability offers promising opportunities for enhancing desired traits in chickpea breeding programsPrevious studies by Dehal et al. (2016) [5] and Kumar *et al*. (2014) [20] have reported similar findings regarding genetic variability in chickpeas.

Genetic parameters related to yield and its contributing traits are presented in Table 3. The results showed that the percentage of phenotypic coefficient of variation (PCV%) was higher than the genotypic coefficient of variation (GCV%) for all the traits studied. High PCV and GCV were observed for biological yield per plant, followed by numbers of pods per plant and 100-seed weight. Similarly, moderate estimates of PCV and GCV were recorded for numbers of seeds per pod, as well as numbers of primary and secondary branches per plant, harvest index, plant height, and seed yield per plant. In contrast, the lowest estimates of PCV and GCV were noted for days to 50% flowering and maturity. These findings are consistent with those of Yadav et al. (2015), Kumar *et al.* (2018) [21], and Kumar et al. (2020) [22]. Higher estimates of heritability in the broad sense were observed for traits such as plant height, numbers of pods per plant, biological yield per plant, days to maturity, 100-seed weight, numbers of primary and secondary branches per plant, harvest index, yield per plant, numbers of seeds per pod, and days to 50% flowering. These results are in line with previous studies by Malik *et al.* (2010) [23], Babbar et al. (2012) [6], Pandey *et al.* (2013) [32], Monpara andGaikwad (2014) [29], Sowjanya et al. (2017) [42], andHonnappa*et al.* (2018) [15].

Furthermore, higher genetic advance was documented for biological yield per plant, followed 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. Moderate estimates of genetic advance as a percentage of means were recorded for days to maturity, while a lower estimate was observed for days to 50% flowering. These findings align with those of Solanki *et al*. (2019) [37], Tsehaye *et al*. (2020) [44], andKumar *et al*. (2020) [22].

Correlation coefficient analysis

Correlation coefficients serve as a method to identify the key traits that influence dependent characteristics, such as seed yield. They aid in developing selection criteria aimed at simultaneously improving multiple traits and overall economic production. The correlations among various traits are presented in Tables 4 and 5.A highly significant and positive genotypic correlation was observed between seed yield per plant and biological yield per plant, as well as with the numbers of secondary branches per plant and pods per plant. Conversely, a significant negative correlation was noted between seed yield per plant and harvest index. These findings

closely resemble earlier studies conducted by Ali *et al.* (2011) [1] and Mushtaq *et al.* (2013) [30] for the numbers of secondary branches per plant, and by Shukla and Babbar (2011) [36] and Tadesse *et al.* (2016) [46] for the numbers of pods per plant. Similarly, significant positive phenotypic correlations were found between seed yield per plant and biological yield per plant, as well as with the numbers of secondary branches per plant. These results align with the research conducted by Shanmugam and Kalaimagal (2019) [34] and Kumar *et al*. (2020) [22].

Table2: Meanperformanceofdifferentchickpeagenotypeongrainyieldanditsattributingcharacters

Genotype	DTF	DM	PHT	PB	BY	SYP	HSW	SY	TP	PBL	S/P	HI
JG-14	76.000	111.000	46.333	6.333	33.733	9.467	12.967	16.110	46.933	15.000	1.267	28.333
JG-17	78.333	117.333	34.333	6.333	44.600	15.333	19.133	21.807	51.600	27.000	1.167	34.867
JG-24	73.667	114.000	44.667	6.333	31.933	10.033	19.400	19.307	49.433	19.333	1.133	32.033
GG-2	79.333	115.000	52.667	6.667	28.833	11.167	17.533	13.610	43.300	16.667	1.133	38.367
BDG-72	75.667	115.000	42.667	4.333	25.100	12.567	17.667	17.503	47.300	27.333	1.133	48.233
GCP-105	80.667	116.333	35.333	5.667	46.200	11.533	17.567	16.387	46.267	16.333	1.333	24.900
GNG-663	76.667	114.667	47.333	5.667	36.933	13.667	16.600	15.970	41.033	20.000	1.167	37.400
ICC-15614	64.333	113.000	63.000	6.333	32.700	15.233	17.333	17.360	46.467	18.000	1.233	30.667
ICC-1205	56.333	109.333	35.667	6.000	42.400	13.700	23.333	15.417	48.033	22.000	1.200	32.400
IPC-18-121	67.000	112.000	45.000	6.667	48.400	9.833	24.533	17.640	48.000	21.000	1.500	20.667
JG-74	61.333	108.667	47.333	5.667	51.400	10.867	20.200	21.530	51.767	21.333	1.200	21.000
Sadabahar	62.667	107.333	42.333	6.667	45.533	10.600	24.733	17.700	47.900	15.000	1.333	23.233
Vaibhav	65.667	112.000	57.333	6.667	51.033	11.800	17.600	20.830	51.367	19.333	1.200	23.567
Aparna	64.333	112.667	37.667	6.667	38.900	11.267	19.000	15.137	45.333	13.333	1.400	28.933
Vishwas	65.333	112.333	49.000	4.000	58.500	16.167	20.500	23.750	53.133	18.333	1.400	27.633
K-850	73.667	111.667	48.000	5.333	42.933	9.833	16.200	13.960	45.233	22.667	1.533	22.767
IPC 18-131	71.66	110.667	45.333	6.333	37.200	10.333	12.867	16.113	47.000	18.000	1.233	28.367

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KabuliGold	67.333	109.333	38.000	4.667	35.233	7.233	15.067	14.373	42.200	17.333	1.200	20.667
IPC-15-108	63.333	110.000	39.000	5.000	40.033	15.800	24.433	15.070	44.233	15.333	1.367	39.167
IPC-12-131	71.000	115.333	42.333	4.333	36.500	13.300	15.167	12.363	40.967	20.667	1.267	36.367
IPC-18-52	64.667	111.333	40.333	5.333	40.167	13.333	15.600	15.833	45.467	19.000	1.300	33.600
Radha	61.000	112.333	48.333	5.000	50.233	9.767	25.333	19.517	49.567	24.000	1.200	19.533
Kalimoti	69.000	111.333	47.333	7.000	53.533	15.167	14.200	23.890	54.567	22.333	1.467	28.067
Allahabaddesichana	65.333	111.333	56.333	7.667	50.200	10.067	14.633	19.443	50.367	20.333	1.400	20.067
DCP92-3 (ch)	62.667	111.333	33.000	4.333	32.800	16.567	15.500	13.890	43.233	21.000	1.067	50.167
Min.	56.333	107.333	33.000	4.000	25.100	7.233	12.867	12.363	40.967	13.333	1.067	19.533
Max.	80.667	117.333	63.000	7.667	58.500	16.567	25.333	23.890	54.567	27.333	1.533	50.167
Mean	67.687	112.000	44.055	5.570	40.035	13.209	18.209	19.814	47.936	19.886	1.267	31.775
C.D.	7.600	5.651	7.601	2.167	7.681	4.774	3.502	5.275	7.561	4.166	0.294	11.095
SE(m)	2.665	1.941	2.665	0.753	2.693	1.674	1.228	1.849	2.651	1.460	0.103	3.890
SE(d)	3.768	2.746	3.769	1.065	3.808	2.367	1.737	2.615	3.749	2.065	0.146	5.501
C.V.	6.720	2.997	10.316	22.487	11.266	23.791	11.632	18.430	9.722	12.889	14.015	22.427

DFF: Days to 50% flowering; DM: Days to maturity; PHT: Plant Height (cm); PB: Primary Branches; BY: Biological Yield (g); SYP (Seed yield/Plant); TP: Total pods/Plant; SP (Seeds/Pods); HI: Harvest Index (%)

Table3: Genotypiccorrelationcoefficientforgrainyieldanditsattributing characters

	DTF	DM	PHT	PB	BY	SYP	HSW	TSY	TP	PB	SP	HI
DTF	1.000	-1.156	-0.458	0.501	1.093	0.176	0.018	0.056	0.373	0.517	-0.060	1.069
DM		1.000	0.278*	0.582	0.468	0.224	0.179	0.334	-0.348	0.184	-0.247*	-0.070
PHT			1.000	-0.586	0.329	0.075	0.153	0.862	0.143	-0.212	-0.401	-0.166
PB				1.000	-0.510	0.188	0.320	1.041	0.659	-0.128	0.665	-0.432
BY					1.000	-0.223	-0.438	0.110	0.846	0.420	-0.400	-0.140
SYP						1.000	0.613	0.987	-0.366	0.459	0.102	-0.527
HSW							1.000	-0.757	0.998	-0.018	-0.006	-0.191
TSY								1.000	-0.610	0.331	0.739	-0.291

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TP									1.000	-0.445	-0.167	0.121
PB										1.000	0.654	-0.044
SP											1.000	0.280
HI												1.000

Table4: Genotypiccorrelationcoefficientforgrainyieldanditsattributing characters

	DTF	DM	PHT	PB	BY	SYP	HSW	TSY	TP	PB	SP	HI
DTF	1.000	-0.206	-0.078	0.193	0.899	0.207	0.087	0.083	0.151	0.29	0.001	0.569
DM		1.000	0.089	0.099	0.159	0.200	0.145	0.296	-0.161	0.106	0.004	0.033
PHT			1.000	-0.290	0.101	-0.002	0.066	0.500	-0.043	-0.052	-0.189	0.103
PB				1.000	-0.241	0.056	0.087	0.441	0.076	-0.162	0.040	-0.289
BY					1.000	-0.096	0.043	0.061	0.170	0.136	-0.087	-0.133
SYP						1.000	0.636	0.340	-0.009	0.125	-0.137	-0.351
HSW							1.000	-0.522	0.019	-0.077	-0.176	-0.146
TSY								1.000	-0.288	0.002	0.078	-0.148
TP									1.000	-0.199	-0.237	0.023
PB										1.000	0.233	-0.159
SP											1.000	0.159
HI												1.000

Table5: EstimatesofPCV,GCV,heritability,andgeneticadvancein25germplasmofchickpea

Character	Min.	Max.	Mean	h^2(%)	GCV (%)	PCV (%)	GA %means	%Contribution
DTF	56.33	80.67	67.69	62.898	8.749	11.03	14.29	14.68
DM	107.33	117.33	112.00	16.415	1.328	3.28	1.10	13.22
PHT	33.00	63.00	44.06	69.483	15.565	18.67	26.72	13.44
PB	4.00	7.67	5.57	14.948	10.047	25.99	8.00	8.85
BY	25.10	58.50	40.04	73.690	19.338	22.53	34.19	9.85
SYP	7.23	16.57	13.21	29.463	15.376	28.33	17.19	11.05
HSW	12.87	25.33	18.21	73.507	19.375	22.60	34.22	7.55
TSY	12.36	23.89	19.81	37.854	15.330	24.92	19.429	12.15
TP	40.97	54.57	47.94	23.371	5.369	11.11	5.347	13.48
PB	13.33	27.33	19.89	61.522	16.297	20.78	26.33	10.21
SP	1.07	1.53	1.27	13.649	5.572	15.08	4.24	10.93
HI	19.53	50.17	31.78	54.733	24.661	33.33	37.58	11.03

At the genotypic level, coefficient analysis revealed that days to 50% flowering exhibited the highest positive direct effect on seed yield per plant, followed by the numbers of secondary branches per plant, plant height, numbers of pods per plant, days to maturity, and 100-seed weight.

Conversely, significant negative direct effects on seed yield per plant were observed for harvest index, biological yield per plant, numbers of primary branches per plant, and numbers of seeds per pod. These findings also indicated a direct positive effect on 100-seed weight. Previous studies by Babbar et al. (2012) [6], Shrivastava et al. (2012) [35], and Jain et al. (2022) [16] have reported similar findings regarding the positive direct effect of days to 50% flowering, numbers of secondary branches per plant, plant height, numbers of pods per plant.

Conclusion

In conclusion, higher genotypic coefficient of variation and heritability, along with genetic advance as a percentage of mean, were observed for biological yield per plant, numbers of pods per plant, 100-seed weight, and seed yield per plant. This indicates the prevalence of additive gene action, suggesting that selection based on these traits could be beneficial. Seed yield per plant showed a highly significant and positive association with biological yield, numbers of secondary branches per plant, and numbers of pods per plant. Path analysis revealed that biological yield per plant had a positive and direct effect on seed yield per plant. Therefore, selecting any of these traits may lead to an increase in the others, suggesting that these traits should be considered when developing plant types aimed at achieving higher yields. Thus, for yield enhancement, these traits may be directly selected.

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