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Selection Strategy for Yield Improvement of Chickpea Genotypes (*Cicer arietinum* L.)

Kushalam Bharath^{a*} and G. Roopa Lavanya^a

^a Department of Genetics and Plant Breeding, SHUATS, Prayagraj-211007, India.

Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

An investigation was undertaken to assess the genetic variability parameters, correlation and path analysis in 25 chickpea genotypes for 12 quantitative traits during the *Rabi* season of 2022-23 in a Randomized Block Design with three replications. Analysis of variance indicated high significant differences among the genotypes for all the traits. Considerable variability existed in the genotypes for all the characters studied. The study found that CG23, CG159, and CG199 were the most superior genotypes for grain yield per plant among 25 chickpea genotypes. High PCV, GCV, heritability and genetic advance as percent of mean were recorded for test weight and biological yield. Grain yield per plant showed positive significant association with number of pods, days to maturity, days to 50% pod initiation and number of primary branches. High and positive direct effect of grain yield per plant at both phenotypic and genotypic levels were depicted by harvest index. These characters may be taken into consideration for selection of quantitative characters for crop improvement.

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^{*}Corresponding author: Email: bharathk1470@gmail.com;

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1. INTRODUCTION

Pulses have been included into self-sustaining agricultural systems over time, enriching the soil through symbolic atmospheric nitrogen fixation. Pulses have a well-known role in Indian agriculture, food, and nutrition because they fit well in crop rotation patterns and provide a significant amount of protein to the nation's mostly vegetarian population. They are also high in several key amino acids.

Chickpea (*Cicer arietinum* L.) is an annual grain legume that is self-pollinated and diploid (2n=16), classified in the subfamily Papilionoideae and family Leguminosae. *Chana* (chickpeas) is referred to be the "King of Pulses" in India. It came from southeast Turkey.

Selection criteria like as heritability and genetic progress are significant. Heritability estimates combined with genetic progress are usually more useful than heritability estimates alone in estimating the gain under selection. As a result, understanding genetic progress in conjunction with heritability is quite beneficial. A high heritability character does not always imply a great genetic progress. To arrive at a more trustworthy result, high heritability should be accompanied with substantial genetic progress. The expected genetic progress expressed as a percentage of the mean illustrates the manner of gene activity in the manifestation of a characteristic, which aids in the selection of a suitable breeding approach [1].

It's critical to determine the component qualities that might help boost yield. Selection would be more successful for a characteristic with a high genetic progress and a strong link to grain output. The correlation coefficient among characters and their path direction is used to determine the degree of link between yield and its components". Hence, there is present investigation's aim to identify the high yielding chickpea genotypes of 12 quantitative traits and study the interrelationships among grain yield and its component characters.

2. MATERIALS AND METHODS

The present investigation was carried out at the Field Experimentation Center of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj

(Allahabad), U.P. during the Rabi season of 2022-23. The university is situated on the left side of Allahabad Rewa National Highway, about far away 5 km from Prayagraj city. The experimental material consists of 25 chickpea genotypes viz. CG118, CG163, CG174, CG251, CG172, CG19, CG208, CG61, CG159, CG236, CG160, CG147, CG30, CG23, CG25, CG36, CG180, CG73, CG20, CG171, CG93, CG199, CG24, CG121, and CG14. These twenty five genotypes were considered as treatments which were applied into a field laid out in a Randomized Block Design with three replications. All types of necessary facilities for cultivation of the crop including field preparation inputs, irrigation facilities were provided from the department. On basis of five competitive plants selected at random from each replication, specific data were collected for following twelve (12) quantitative traits:1) Days to 50% flowering. 2) Days to 50% pod setting, 3) Days to maturity, 4) plant height, 5) Number of branches per plant, 6) Number of pods per plant, 7) Number of grains per pod, 8) Number of grains per plant, 9) Biological yield per plant, 10) Harvest index, 11) Seed index, 12) Grain yield per plant.

All the recorded data for the characters under consideration were analysed for variance using the Panse and Sukhatme [2] formula [3]. Additionally, the genetic parameters genotypic coeffivcient of variance (GCV), phenotypic coefficient of variance (PCV), heritability in the broad sense, genetic advance as percent of mean, and correlation analysis were carried out using the appropriate statistical by procedure. These additional components of variance included phenotypic, genotypic, and environmental variance.

The software called "R- Language" was used to perform the analysis mentioned above.

The experimental material is subjected to Analysis of variance [3]. Coefficient of variation [4], Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), Heritability broad sense [4], Genetic advance [5], Correlation coefficient analysis [6], Path coefficient analysis [7].

3. RESULTS AND DISCUSSION

The genotype-related mean squares were very significant for each character, indicating a

considerable level of genetic variability in the material. Due to the range of materials employed and the environmental influences on phenotypes, variability may be present in significant amounts (Table-1).

In Table 2 and Fig. 2 which revealed a wide range of variation for all traits studies the mean values, the coefficient of variation (C.V.), standard error of the mean (SEm+), the critical difference (C.D.) at 5% and 1% range of 20 genotypes for 12 quantitative characters are presented" [8].

"On the basis of mean performance, the highest grain yield per plant was observed for chickpea genotypes CG23 (30.5), CG199 (29.9), CG159 (29.9) were found to be superior in Grain Yield per plant. From the present investigation, the PCV was higher than the corresponding GCV for every trait, indicating that the environment had an impact. The lowest GCV (percent) value was 1.05 (Days to maturity, Days to 50% pod initiation) and highest value was 20.86 (grain yield per plant). A similar pattern was followed by PCV (percent), which ranged from lowest value of 1.75 (Days to maturity) to highest value of 21.75 (Grain Yield per plant) [8].

3.1 Heritability

present investigation, From the highest heritability (above 60%, it is high for all the parameters) was observed for Grain Yield per Plant (92.016%), Number of Secondary Branches (87.468%), Number of Primary Branches (83.467%), Seed Index (80.58%), Number of Pods per Plant (71.097%), Biological Yield per Plant (69.406%), Number of Grains per (64.203%), Moderate heritability was Pod observed for Plant Height (39.287%) followed by, Days to Maturity (35.644%), Low heritability was observed for Harvest Index (28.407%), Days to 50% Flowering (29.894%) and Days to 50% Pod Initiation (24.805%).

A higher heritability value suggests that the role of genotypic components may be greater. The estimates demonstrated that heritable factors dominated the variation in these traits, while environments and genetics equally influenced the expression of traits with moderately high heritability, indicating that environment influenced the trait expression more so than genetics.



Fig. 1. Phenotypic path diagram

			Mean Sum of Squa	ares	
51 .NO.	Trait	Replication	Treatment	Error	
	Degrees of freedom	2	24	48	
1	Plant height	30.795	45.072**	15.324	
2	Days to 50% flowering	2.44	11.414*	5.426	
3	Days to 50% pod initiation	9.693	7.68*	3.86	
4	Days to maturity	5.813	8.153**	3.063	
5	Number of Primary branches	0.033	0.278**	0.017	
6	Number of secondary branches	0.084	1.583**	0.072	
7	Number of pods/plants	157.655	455.858**	54.4	
8	Number of seeds/pods	39.102	478.109**	74.931	
9	Biological yield/plant	1.965	58.594**	7.506	
10	Harvest Index	3.699	61.268*	27.972	
11	Seed Index	0.552	30.044**	2.234	
12	Seed yield per plant	2.888	58.612**	1.648	

Table 1. Analysis of Variance for 12 quantitative traits among 25 chickpea genotypes

**significance at 1% level of significance

Table 2. Genetic parameters for 12 quantitative traits of chickpea genotypes

SI. No.	Characters	GCV	PCV	h²(Broad Sense)	GA	GAM
1	Plant height (cm)	6.16	9.82	39.29	4.07	7.95
2	Days to 50% flowering	2.12	4.09	26.89	1.51	2.27
3	Days to 50% pod initiation	1.44	2.89	24.81	1.16	1.48
4	Days to maturity	1.05	1.75	35.64	1.60	1.29
5	Number of Primary branches	14.37	15.73	83.47	0.55	27.05
6	Number of secondary branches	15.83	16.93	87.47	1.37	30.50
7	Number of pods/plants	13.04	15.47	71.10	20.09	22.66
8	Number of grains/pods	10.84	13.53	64.20	19.14	17.89
9	Biological yield/plant (g)	12.96	15.56	69.41	7.08	22.25
10	Harvest Index (%)	5.04	9.46	28.41	3.66	5.54
11	Seed Index	15.35	17.09	80.58	5.63	28.38
12	Grain yield per plant	20.86	21.75	92.02	8.61	41.23

GCV: Genotypic Coefficient of Variation, PCV: Phenotypic Coefficient of Variation, h²: Heritability, GAM: Genetic Advance at Percent of mean

Phenotypic Correlation (Above diagonal) and Genotypic Correlation (Below diagonal)												
TRAITS	PH	DF50	DP50	DM	NPB	NSB	NPP	NSP	BY	HI	SI	SYPP
PH	1	0.0016	-0.0646	0.14	0.0729	-0.066	-0.099	-0.0209	-0.1242	0.0011	-0.0864	-0.0216
DF50	-0.1476	1	-0.0005	-0.0479	-0.0741	-0.294*	-0.1078	0.0685	0.1387	-0.13	-0.1024	-0.1232
DP50	-0.706**	0.084	1	0.2153	0.0755	-0.0055	0.1348	-0.0537	-0.0088	0.0489	0.0406	0.0813
DM	0.270*	-0.344*	0.542**	1	0.0498	-0.0565	0.1025	0.099	0.341*	0.261*	0.1963	0.289*
NPB	0.1137	-0.1561	-0.0545	0.0991	1	0.450**	0.553**	0.499**	-0.0351	0.1869	0.0596	0.321*
NSB	-0.0999	-0.548**	0.0345	-0.0087	0.503**	1	0.300*	0.1121	-0.1458	0.1171	-0.0845	-0.0603
NPP	-0.269*	-0.343*	0.2097	0.231*	0.691**	0.322*	1	0.712**	0.1648	0.418**	0.129	0.492**
NSP	-0.1521	0.026	-0.034	0.309*	0.609**	0.1084	0.846**	1	0.1949	0.366*	0.111	0.407**
BY	-0.1947	-0.0221	0.1507	0.278*	0.073	-0.2093	0.2057	0.298*	1	0.494**	0.649**	0.689**
HI	-0.1115	-0.444**	0.585**	0.716**	0.495**	0.0987	0.512**	0.683**	0.915**	1	0.443**	0.627**
SI	-0.1102	-0.1206	0.223	0.326*	0.1314	-0.1223	0.1694	0.1318	0.861**	0.779**	1	0.760**
SYPP	-0.0766	-0.291*	0.1823	0.516**	0.347*	-0.0974	0.462**	0.394**	0.842**	0.865**	0.866**	1

Table 3. Correlation coefficient analysis for grain Yield component characters

DF50: Days to 50% flowering, DP50: Days to 50% pod setting, DM: Days to maturity, PH: Plant height (cm), NPB: Number of primary branches, NSB: Number of secondary branches, NSPP: Number of grains per plant, NPPP: Number of pods per plant, NSP: Number of Grains per Pod BY: Biological yield per plant, SW: 100 seed weight (g), HI: Harvest Index (%), SY: Grain yield per plant

TRAITS		PH	DF50	DP50	DM	NPB	NSB	NPP	NSP	BY	HI	SI	SYPP
PH	Р	0.0492	0.0001	-0.0032	0.0069	0.0036	-0.0032	-0.0049	-0.001	-0.0061	0.0001	-0.0042	-0.0216
	G	0.0643	-0.0095	-0.0454	0.0174	0.0073	-0.0064	-0.0173	-0.0098	-0.0125	-0.0072	-0.0071	-0.0766
DF50	Р	-0.0002	-0.1122	0.0001	0.0054	0.0083	0.033	0.0121	-0.0077	-0.0156	0.0146	0.0115	-0.1232
	G	0.0717	-0.4856	-0.0408	0.1669	0.0758	0.2663	0.1664	-0.0126	0.0107	0.2155	0.0586	-0.291*
DP50	Ρ	-0.0003	0	0.005	0.0011	0.0004	0	0.0007	-0.0003	0	0.0002	0.0002	0.0813
	G	-0.1567	0.0186	0.222	0.1202	-0.0121	0.0076	0.0466	-0.0076	0.0334	0.1298	0.0495	0.1823
DM	Ρ	0.0004	-0.0001	0.0007	0.003	0.0002	-0.0002	0.0003	0.0003	0.001	0.0008	0.0006	0.289*
	G	-0.0528	0.0672	-0.1059	-0.1956	-0.0194	0.0017	-0.0451	-0.0603	-0.0544	-0.1399	-0.0637	0.516**
NPB	Ρ	0.0158	-0.0161	0.0164	0.0108	0.2171	0.0976	0.1201	0.1083	-0.0076	0.0406	0.0129	0.321*
	G	0.0354	-0.0486	-0.017	0.0308	0.3111	0.1564	0.2151	0.1893	0.0227	0.1539	0.0409	0.347*
NSB	Ρ	0.0136	0.0607	0.0011	0.0117	-0.0928	-0.2065	-0.0619	-0.0232	0.0301	-0.0242	0.0174	-0.0603
	G	0.0418	0.2294	-0.0144	0.0036	-0.2104	-0.4185	-0.1348	-0.0454	0.0876	-0.0413	0.0512	-0.0974
NPP	Р	-0.0274	-0.0298	0.0373	0.0284	0.1531	0.083	0.2767	0.1969	0.0456	0.1157	0.0357	0.492**
	G	0.0629	0.0802	-0.0491	-0.054	-0.1619	-0.0754	-0.2341	-0.198	-0.0482	-0.12	-0.0397	0.462**
NSP	Ρ	0.0006	-0.0018	0.0014	-0.0027	-0.0134	-0.003	-0.0191	-0.0268	-0.0052	-0.0098	-0.003	0.407**
	G	-0.0462	0.0079	-0.0103	0.0936	0.1847	0.0329	0.2567	0.3035	0.0904	0.2073	0.04	0.394**
BY	Р	-0.0361	0.0403	-0.0026	0.0992	-0.0102	-0.0424	0.0479	0.0567	0.2908	0.1435	0.1887	0.689**
	G	-0.0208	-0.0024	0.0161	0.0298	0.0078	-0.0224	0.022	0.0319	0.1071	0.098	0.0922	0.842**
HI	Р	0.0002	-0.0199	0.0075	0.04	0.0287	0.018	0.0641	0.0562	0.0757	0.1533	0.068	0.627**
	G	-0.0226	-0.09	0.1185	0.1451	0.1003	0.02	0.1039	0.1385	0.1855	0.2027	0.158	0.865**
SI	Р	-0.0373	-0.0442	0.0175	0.0848	0.0258	-0.0365	0.0557	0.048	0.2804	0.1916	0.4321	0.760**
	G	-0.0536	-0.0587	0.1085	0.1586	0.0639	-0.0595	0.0825	0.0642	0.4191	0.3792	0.4866	0.866**

Table 4. Path coefficient analysis for grain yield component characters

DF50: Days to 50% flowering, DP50: Days to 50% pod setting, DM: Days to maturity, PH: Plant height (cm), NPB: Number of primary branches, NSB: Number of secondary branches, NSPP: Number of grains per plant, NPPP: Number of pods per plant, NSP: Number of Grains per Pod BY: Biological yield per plant, SW: 100 seed weight (g), HI: Harvest Index (%), SY: Grain yield per plant



Fig. 2. Genotypic path diagram

3.2 Genetic Advance

In the present study a perusal of genetic advance showed that it was high for Number of Pods per Plant (20.093) followed by Number of Grains per Pod (19.135), Grain Yield per Plant (8.611), Biological Yield per Plant (7.082) and Seed Index (5.63) respectively and lowest for Number of Primary Branches (0.554), Days to 50% Pod Initiation (1.158), Number of Secondary Branches (1.367), & Days to 50% Flowering (1.509) respectively.

3.3 Genetic Advance as Percent Mean

High genetic gain was recorded for Days to 50% Pod Initiation (41.228) followed by, Biological Yield per Plant (30.5), Days to 50% Flowering (28.375) and Number of Pods per Plant (27.048). Moderate estimates were recorded for Number of Grains per Pod (22.655), Days to Maturity (22.248), Plant Height (17.891), Grain Yield per Plant (7.948), Harvest Index (5.537) and Number of Secondary Branches (2.265). Low estimation of GCV was recorded for Seed Index (1.286) and Number of Primary Branches (1.478).

3.4 Phenotypic Correlation Coefficient

In the present investigation from Table 3. Grain yield per plant showed positive significant

association with Days to Maturity (0.289*), primary Number of **Branches** $(0.321^*).$ Number of Pods per Plant (0.492**), Number of grains per Pod (0.407**), Biological Yield per Plant (0.689**), Harvest Index (0.627**) Seed Index (0.760**). Positive nonand significant association showed with Days to 50% Pod Initiation (0.0813). Negative non-significant association showed with Plant height (-0216) and Days to 50% Flowering (-0.1232).

3.5 Genotypic Correlation Coefficient

The correlation among the yield and yield attributing characters revealed that Grain vield per plant was positively and significantly associated with Days to Maturity (0.516**), Number of primary Branches (0.347*), Number of Pods per Plant (0.462**), Number of grains per Pod (0.394**), Biological Yield per Plant (0.842**), Harvest Index (0.865**) and Seed Index (0.866**). Positive non-significant association showed with Days to 50% Pod Initiation (0.1823) only. Negative significant association showed only by Days to 50% Flowering (-0.291*). Negative non-significant association showed with Plant Height (-0.0766) and Number of secondary Branches (-0.0974). These findings of correlation coefficient were supported by Sharma et al., [9]; Kumar et al.,

[10], Chaudhury *et al.*, [11]; Islam *et al.*, [12]; Singh [13].

3.6 Phenotypic Path Coefficient Analysis

Phenotypic path coefficients are calculated using the phenotypic correlation coefficient. It divides the phenotypic correlation coefficients into direct and indirect impact measurements [7]. A detailed analysis of diagonal values showed positive direct effect of Plant Height (0.0492), Days to 50% Pod Initiation (0.0050), Days to Maturity (0.0030), Number of primary Branches (0.2171), Number of Pods per Plant (0.2767), Biological Yield per Plant (0.2908) Harvest Index (0.1533) and Seed Index (0.4321). Negative direct effects were exhibited by Days to 50% flowering (-0.1122), Number of secondary Branches (-0.2065) and Number of grains per Pod (-0.0268).

3.7 Genotypic Path Coefficient Analysis

"A perusal of the results on path coefficient for yield and yield components genotypic to be of similar direction and magnitude in general. Further the genotypic path co-efficient were observed to be of higher magnitude, compared to path coefficient indicating phenotypic the masking effect of environment. A detailed analysis of diagonal values showed positive direct effect of Plant Height (0.0643), Days to 50% Pod Initiation (0.2220), Number of primary Branches (0.3111), Number of grains per Pod (0.3035), Biological Yield per Plant (0.1071), Harvest Index (0.2027) and Seed Index (0.4866). Negative direct effects were exhibited by Days to 50% flowering (- 0.4856), Days to Maturity (-0.1956), Number of secondary Branches (-0.4185), Number of Pods per Plant (-0.2341). Similar findings of path coefficient analysis were given" by Kumar [14]; Patel and Mehta [15][16-18].

4. CONCLUSION

Based on the current study, it was determined that out of 25 genotypes of chickpeas, CG23 had the highest grain yield per plant, followed by CG159 and CG199. For Grain Yield and biological yield, high PCV, GCV, heritability, and genetic advancement as a percentage of mean were noted. The number of pods, days to maturity, days to 50% pod initiation, and number of major branches all positively and significantly correlated with the amount of grain produced per plant. The Harvest index showed a strong and favourable direct effect of grain yield per plant at both the genotypic and phenotypic levels. When choosing quantitative characters for crop development, these characteristics could be taken into account.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.,) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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