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Genetic Variability and Correlation for Quantitative Traits of Chickpea Genotypes (*Cicer arietinum* L.)

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ABSTRACT

The present study was conducted using 124 genotypes of chickpea (*Cicer arietinum* L.) during *rabi*, October, 2019 to March, 2020 at Regional Research Station, Faculty of Agriculture, Wadura, Sopore, SKUAST-K to assess the variability, correlation among yield and yield contributing traits. The trial was performed by using an Augmented block design. The study included estimates of variability such as genetic variability, phenotypic variability, genotypic coefficient of variability, phenotypic coefficient of variability and inter-relationship among yield and yield contributing traits. The ANOVA estimations showed that there was a significant variation across genotypes for all ten traits investigated in the experiment. The significant magnitude of phenotypic and genotypic coefficient of variation indicated considerable level of variability. Traits such as Plant height, seed yield plant^{-1}, pods plant^{-1}, and days to 50% flowering, all exhibited higher levels of variability whereas Traits like pods plant^{-1}, seeds pod^{-1} and seed yield plant^{-1} recorded high genotypic and phenotypic coefficient of variation. The Phenotypic Coefficient of Variation was consistently higher than the Genotypic Coefficient of Variation for all traits. Seed yield plant^{-1} showed highly significant and correlated positively with pod width, pods plant^{-1}, plant height and days to pod formation. Therefore, these traits could serve as effective selection criteria for genotype improvement in chickpeas because they exhibited high variability. This study would help to identify superior genotypes, leading to the development of high-yielding elite chickpea varieties with desirable characteristics.

KEYWORDS: Chickpea, correlation, GCV, PCV, seed yield, variability

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Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a native of southern Europe and also an important food crop in Asia, Africa and Central America. It is an economically major legume crop of the arid and semi-arid tropics of the world. Its genome size is approximately 740 Mbp (Arumuganathan and Earle, 1991). It is a valuable source of high quality protein for human and animal consumption as well as offers economic benefits to farmers because of the high market value for its grains (Yegrem, 2021). It is also known as Bengal gram or, Garbanzo bean, after dried beans, second-most prominent cool-season edible legume worldwide. (Mallikarjuna et al., 2017; Varshney et al., 2013). Often referred to as "Poor Man's Meat" and "Rich Man's Vegetable" due to their high protein content that accounts for almost 40% of its weight (Merga and Haji, 2019) and abundance of essential amino acids, especially lysine. The protein content of chickpeas is relatively lower than that of other pulses, but they have higher biological value and protein digestibility (Gu et al., 2023). It is rich in fiber, minerals (phosphorus, calcium, magnesium, iron and zinc) and β-carotene (Jukanti et al., 2012). Chickpea not only meets its own nitrogen requirement but also leaves residual nitrogen for succeeding crop and maintaining soil fertility (Dutta et al., 2022), improves physical and chemical properties of the soil, and decreases pests, diseases and weeds of rainy season (*kharif*) crops (Dotaniya et al., 2022). Furthermore, they provide cattle with nutrient-rich pasture. Chickpea varieties are categorized as 'desi' and 'kabuli' based on seed shape and color (Knights and Hobson, 2016), Desi (originated from India) cultivars have small, wrinkled and dark coloured seeds and Kabuli (originated from Mediterranean and the Middle East) cultivars have large, smooth coated and white to cream coloured (Purushothaman et al., 2014). Desi types are primarily grown in Australia, Central America, East Africa, and India, while kabuli types are more common in the Mediterranean, Middle East, North Africa, and North America (Knights and Hobson, 2016; Grasso et al., 2022).

Southern and South-Eastern Asian nations yield over 8% of the world's chickpea production. The top five global producers of chickpeas are India, Australia, Turkey, Myanmar, and Ethiopia (Jha et al., 2014; Gaur et al., 2012). India is the single largest producer of chickpea in the world, sharing for 73% (11.08 mt) of the total production under chickpea (Anonymous, 2022). It is grown in fifty-four countries, with more than 90% of that land being cultivated in developing nations (Gaur et al., 2012). In total, global chickpea cultivation spans 14.56 mha, producing approximately 15 mt annually (Anonymous, 2021). Major producers of chickpeas include India, Australia, Pakistan, Central America, and East Africa (Knights and Hobson, 2016). The key chickpea producing states in India are Madhya Pradesh, Rajasthan, Maharashtra, Andhra Pradesh, Uttar Pradesh, Karnataka and Gujarat which collectively account for 80% of the total cultivate area. Among these states, Madhya Pradesh recorded highest production with 3299.1 thousand tonnes followed by Rajasthan and Maharashtra. The highest productivity was observed in Andhra Pradesh (1448 kg ha^{-1}) followed by Bihar (984 kg ha^{-1}) and Gujarat (977 kg ha^{-1}). Global climate change and the growing human population pose significant challenges to food and nutritional security. Despite advancements in agricultural productivity, more than 820 million people globally still experience food insecurity, and at least 2 billion suffer from nutritional insecurity (Jha et al., 2024).

Seed yield is a complex trait influenced by multiple yield components. Identification of key traits and their interrelationship is essential when selection criteria for creating elite genotypes. If there is a quantitative interaction among the traits, direct selection for seed yield may not be very effective. Therefore, selecting traits that contribute to yield can result in significant yield improvement. Hence, the present study was conducted to assess the variability, inter-relationship among yield and yield contributing traits.

2. MATERIALS AND METHODS

An experiment was performed during *rabi*, October, 2019 to March, 2020 at Regional Research Station, Faculty of Agriculture, Wadura, Sopore, SKUAST-K to quantify the genetic variability, correlation among yield and yield contributing traits. The experimental site was located at 34.35 latitude and 74.40 longitude and about 1589 m above mean sea level. It comprised of 124 genotypes along with 4 checks ILC 482, ILC263, ILC533 and Shalimar chickpea-1 (Table 1). The trial was carried out by using an Augmented block design, whereas checks were repeated and randomized within each block. All the genotypes, except for Shalimar chickpea-1 were obtained from International Centre for Agriculture Research in the Dry Areas (ICARDA), Syria. Shalimar chickpea-1 was a locally adopted variety of Jammu and Kashmir. Each genotype was sown in a plot of 2 m length, with a row spacing of 30 cm and 10 cm spacing between plants within rows. The data on ten morpho-physiological characters were recorded viz. plant height, days to 50% flowering, days to pod formation, days to maturity, number of pods plant^{-1}, number of seeds pod^{-1}, pod length (mm), pod width (mm), 100-seed weight (g) and seed yield plant^{-1} (g). The procedure recommended by Johnson et al. (1955), was employed to compute the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV).

Table 1: List of chickpea genotypes used in the experiment

Sl. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype
1.	FLIP12-21C	32.	FLIP12-71C	63.	FLIP12-297C	94.	FLIP12-43C
2.	FLIP12-26C	33.	FLIP12-39C	64.	FLIP12-123C	95.	FLIP12-38C
3.	FLIP12-339C	34.	FLIP12-285C	65.	FLIP12-329C	96.	FLIP12-301C
4.	FLIP12-115C	35.	FLIP12-58C	66.	FLIP12-220C	97.	FLIP12-318C
5.	FLIP12-49C	36.	FLIP12-250C	67.	FLIP12-338C	98.	FLIP12-175C
6.	FLIP12-12C	37.	FLIP12-59C	68.	FLIP12-65C	99.	FLIP12-313C
7.	FLIP12-157C	38.	FLIP12-62C	69.	FLIP12-336C	100.	FLIP12-303C
8.	FLIP12-27C	39.	FLIP12-41C	70.	FLIP12-229C	101.	FLIP12-213C
9.	FLIP12-95C	40.	FLIP12-218C	71.	FLIP12-267C	102.	FLIP12-284C
10.	FLIP12-74C	41.	FLIP12-225C	72.	FLIP12-237C	103.	FLIP12-249C
11.	FLIP12-120C	42.	FLIP12-116C	73.	FLIP12-292C	104.	FLIP12-293C
12.	FLIP12-81C	43.	FLIP12-270C	74.	FLIP12-111C	105.	FLIP12-211C
13.	FLIP12-106C	44.	FLIP12-230C	75.	FLIP12-141C	106.	FLIP12-235C
14.	FLIP12-254C	45.	FLIP12-226C	76.	FLIP12-228C	107.	FLIP12-212C
15.	FLIP12-70C	46.	FLIP12-291C	77.	FLIP12-234C	108.	FLIP12-232C
16.	FLIP12-156C	47.	FLIP12-149C	78.	FLIP12-340C	109.	FLIP12-233C
17.	FLIP12-272C	48.	FLIP12-227C	79.	FLIP12-82C	110.	FLIP12-126C
18.	FLIP12-56C	49.	FLIP12-134C	80.	FLIP12-283C	111.	FLIP12-306C
19.	FLIP12-251C	50.	FLIP12-266C	81.	FLIP12-236C	112.	FLIP12-222C
20.	FLIP12-200C	51.	FLIP12-239C	82.	FLIP12-194C	113.	FLIP12-314C
21.	FLIP12-117C	52.	FLIP12-84C	83.	FLIP12-302C	114.	FLIP12-286C
22.	FLIP12-326C	53.	FLIP12-199C	84.	FLIP12-214C	115.	FLIP12-54C
23.	FLIP12-29C	54.	FLIP12-238C	85.	FLIP12-295C	116.	FLIP12-224C
24.	FLIP12-22C	55.	FLIP12-243C	86.	FLIP12-312C	117.	FLIP12-92C
25.	FLIP12-76C	56.	FLIP12-307C	87.	FLIP12-221C	118.	FLIP12-45C
26.	FLIP12-130C	57.	FLIP12-244C	88.	FLIP12-242C	119.	FLIP12-223C
27.	FLIP12-158C	58.	FLIP12-216C	89.	FLIP12-46C	120.	FLIP12-345C
28.	FLIP12-103C	59.	FLIP12-337C	90.	FLIP12-231C	121.	ILC482
29.	FLIP12-181C	60.	FLIP12-247C	91.	FLIP12-323C	122.	ILC263
30.	FLIP12-321C	61.	FLIP12-274C	92.	FLIP12-98C	123.	ILC533
31.	FLIP12-273C	62.	FLIP12-143C	93.	FLIP12-294C	124.	shalimar chickpea-1

3. RESULTS AND DISCUSSION

The ANOVA results (Table 2) showed significant variation among genotypes for each trait studied viz. plant height (125.7^{**}), days to 50% flowering (19.75^{**}), days to pod formation (21.6^{**}), days to maturity (14.54^{**}), number of pods plant^{-1} (2129^{**}), number of seeds pod^{-1}(0.032^{**}), pod length (8.17^{**}), pod width (2.58^{**}), 100-seed weight (7.59^{**}) and seed yield plant^{-1} (93.8^{**}). This indicated that the evaluated material had sufficient variability, which could be utilized in future crop improvement programmes. The variability parameters for all the traits under study were summarized in (Table 3). The results showed significant differences among all 10 traits assessed.

3.1. Estimates of phenotypic, genotypic and environmental variance

The phenotypic and genotypic variance were highest for pods plant^{-1} (2004.21 and 1997.7) followed by plant height (117.26 and 112.78) and seed yield plant^{-1} (80.31 and 79.38, respectively). The environmental variance ranged from 0.008 (seeds pod^{-1}) to 4.47 (plant height). These parameters were essential biometrical tools used to measure genetic variability. Trait like number of pods plant^{-1} exhibited

Table 2: Details of the ANOVA showing results of mean squares for 10 agronomic traits recorded on 120 chickpea genotypes

Source of variation	Df	PH	DF	DP	DM	PPP	SPP	PL	PW	100SW	SYPP
Blocks (ignoring treatments)	5	86.5**	9.72**	14.08**	30.44**	19094**	0.023**	7.32**	6.28**	73.70**	788.3**
Blocks (eliminating treatments)	5	3.9	4.37*	4.1*	0.67	1	0.004**	0.07	0.01	0.04	0.3
Treatments (ignoring blocks)	123	125.7**	19.75**	21.6**	14.54**	2129**	0.032**	8.17**	2.58**	7.59**	93.8**
Treatments (eliminating blocks)	123	122.3**	19.53**	21.18**	13.33**	1353**	0.032**	7.87**	2.33**	4.60**	61.8**
Varieties	119	117.3**	15.86**	15.8**	14.63**	6461**	0.033**	8.02**	2.26**	7.47**	80.3**
Checks	3	442.3**	162.28**	93.37**	11.61**	6461**	0.008**	7.30**	14.94**	11.68**	433.8**
Checks v/s varieties	1	175.6**	55**	495**	12.53*	2004**	0.027**	28.23**	4.29**	10.66**	682.1**
Blocks (eliminating checks and varieties)	120	114.3**	15.96**	19.38**	13.37**	1226**	0.032**	7.89**	2.01**	4.43**	52.5**
Error	15	4.5	1.41	1.01	1.71	7	0.0008	0.05	0.06	0.096	0.9

** and * indicate significance at p=0.01 and p=0.05 levels of significance, respectively

the highest degree of variability which was similar to the outcomes of Pravalika et al. (2024). Bhanu et al. (2017), Nizama et al. (2013), and Jeena et al. (2005) also reported that high amount of genetic variability was expressed by pods plant^{-1}.

3.2. *Phenotypic and genotypic coefficient of variation*

The highest value of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) (82.71 and 82.58, respectively) were recorded for number of pods plant^{-1} followed by seed yield plant^{-1} (60.54 and 60.19). In contrast, lowest value of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) (2.07 and 1.94, respectively) were recorded for number of days to maturity. Environmental factors played a considerable role of in expression of all the characters as indicated by higher values of PCV compared to corresponding GCV.

GCV was used to assess variability across different genotypes for various traits, reflecting the inherent potential of the genotype. Both PCV and GCV were necessary to understand the influence of the environment (E) on quantitative traits. The difference between the coefficients of variation (GCV and PCV) offered valuable insights into the contributions of genotype (G) and environment (E) in determining the trait. The characters such as plant height, seeds pod^{-1}, pod length, pod width and 100 seed weight recorded moderate values for both PCV and GCV. These results suggest that there was considerable amount of variability for majority of the traits studied. These results were similar to outcomes of Karthikeyan et al. (2022) and Borate et al. (2010), noted that pods plant^{-1} showed the high values of phenotypic and genotypic coefficients of variation.

3.3. *Correlation studies*

Correlated characters were important for three main reasons: first, with regard to the genetic basis of correlation which might arise through linkage or pleiotropic action of genes; second, because understanding the interrelationship between characters was crucial for predicting how changes in one character could lead to changes in others; and third, because this knowledge was essential in context of natural selection (Falconer, 1960). The value of the correlation coefficient could not be constant across worldwide. It varies greatly depending on the factors such as type of material being studied, the observational method used, the agricultural practices employed, and the environmental

Table 3: Variability parameters for different traits in chickpea

Trait	PV	GV	EV	GCV (%)	PCV (%)
PH (cm)	117.26	112.78	4.47	14.43	14.71
DF	15.86	14.44	1.41	2.65	2.77
DP	15.79	14.79	1.00	2.48	2.56
DM	14.62	12.91	1.71	1.94	2.07
PPP	2004.21	1997.70	6.52	82.58	82.71
SPP	0.03	0.03	0.008	15.13	15.32
PL (mm)	8.01	7.97	0.051	12.79	12.84
PW (mm)	2.25	2.19	0.06	14.81	15.02
100SW (g)	7.47	7.37	0.09	10.60	10.67
SYPP (g)	80.31	79.38	0.93	60.19	60.54

Table 4: Estimation of genotypic (above diagonal) correlation coefficients in chickpea

Traits	DF	DP	PH	DM	PL	PPP	PW	SPP	100SW	SYPP
DF	1.000	0.887**	-0.145	0.820**	0.162	0.116	-0.031	0.158	0.033	-0.010
DP		1.000	-0.127	0.793**	0.160	0.093	0.004	0.136	0.016	0.048*
PH			1.000	-0.068	0.226*	0.265*	0.046	0.056	-0.050	0.086*
DM				1.000	0.161	0.057	-0.206	0.189	0.244*	-0.172
PL					1.000	0.741**	0.009	-0.040	0.029	0.046*
PPP						1.000	0.119	-0.017	-0.091	0.161**
PW							1.000	-0.277*	-0.945**	0.956**
SPP								1.000	0.282*	-0.074
100SW									1.000	-0.883**
SYPP										1.000

** and * indicate significance at p=0.01 and p=0.05 levels of significance, respectively

circumstances under which the crop was grown.

Extremely significant positive correlation coefficient values revealed a particular stronger association between seed yield plant^{-1} and pod width. Additionally seed yield plant^{-1} was significantly associated positively with pods plant^{-1}, plant height, days to pod formation and pod length. This showed that increasing both qualities simultaneously through selection would increase yield improvement. Likewise, a strong association was observed between days to 50% flowering and days to maturity. These features were shown to be positively correlated with seed yield plant^{-1}, which might aid in the development of early maturing varieties. These results were in agreement with the results of Kebede et al. (2023), Bhanu et al. (2017), reported that number of pods plant^{-1} exhibited a maximum positive direct effect on grain yield. Chopdar et al. (2016) found that seed yield plant^{-1} showed significant and positive correlation with harvest index, number of seeds pod^{-1}, primary branches plant^{-1}, number of pods plant^{-1}, biomass plant^{-1}, and 100-seed weight.

4. CONCLUSION

The 124 genotypes showed considerable genetic variability for all the traits indicating a strong potential for genetic improvement. The significant positive association was found between seed yield plant^{-1} with pod width, pods plant^{-1} revealed that simultaneous improvement of these traits through selection. Based on variability and correlation studies traits such as pods plant^{-1}, seed yield plant^{-1} and pod width could be considered key factors for the chickpea breeding programmes. Therefore, direct selection of these traits would enhance the genetic gain.

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