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Genetic variability and path analysis for yield and yield contributing traits in chickpea (*Cicer arietinum* L.)

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Abstract

Pulses have been cultivated globally for many centuries and are recognized for their nutritional value, being rich in protein, dietary fiber and essential micronutrients. Pulses including chickpeas play a pivotal role in diets. In the present research work, thirty-one genotypes of Chickpea were evaluated in a Randomized Block Design with two replications in field during *Rabi* 2022-23. The biochemical analysis for zinc and iron content was done in Laboratory. Observations were recorded for days to 50% flowering, days to maturity, plant height, plant spread, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight, seed yield per plant, iron content, zinc content and protein content. As per the path analysis the number of pods per plant exhibited the highest direct positive impact on seed yield per plant followed by days to maturity, plant height, 100 seed weight and plant spread. Based on divergence study and the mean performance of the chickpea genotypes *viz.*, Phule G 1511-29-1 for the number of seeds per pod and seed yield, Phule G 1424-4-2 for secondary branches per plant, seed yield and plant height, Phule G 1415-13-20 for plant spread, days to maturity and seed yield, BDNG-2021-53 for days to maturity and 100 seed weight and Phule Vikram for secondary branches per plant and plant spread were observed promising and should be used in future breeding programme.

Keywords: Chickpea, correlation, path analysis, diversity

Introduction

Pulses have been cultivated globally for many centuries and are recognized for their nutritional value, being rich in protein, they are also source of dietary fibre and essential micronutrients. Chickpea (*Cicer arietinum* L.) is a self-pollinated crop belonging to family Fabaceae of the tribe Cicereae. It is a diploid species with chromosome number $2n=2x=16$. Chickpeas, in particular, dominate the pulse production in India, accounting for approximately 49% of total pulse production. The major chickpea-producing states in India are Maharashtra, Madhya Pradesh, Rajasthan, Uttar Pradesh, Gujarat, Andhra Pradesh, and Karnataka. In Maharashtra chickpea occupied 26.69 lakh ha area during the year 2023-24 with production of 28.60 lakh tons having the average productivity of 1072 kg/ha (Anonymous 2023) ^[1].

In many developing countries across Asia and Africa, protein-energy malnutrition is prevalent among young children and infants, significantly impacting their health due to insufficient dietary protein and energy intake. Chickpea play a pivotal role in Afro-Asian diets and can help to mitigate malnutrition by providing a significant percentage of dietary protein. Micronutrients are indeed crucial for the proper functioning of the immune system and their deficiency can have far-reaching health consequences. Zinc plays a vital role in variety of biological processes. It also helps to regulate the balance between the production of reactive oxygen species (ROS) and their scavenging activities in plants. Iron and zinc deficiencies are pressing global challenges, contributing to poor health, anaemia and increased mortality rates particularly in developing countries. Identifying food sources rich in these micronutrients such as chickpeas can contribute to improving the health. The primary goal is to achieve high yields with percentuality produce. This repercentuaires consideration of both genotypic (genetic) and environmental factors, as they are the key determinants of yield and crop percentuality.

Therefore, understanding the effects of genotypic and phenotypic factors is necessary for making informed selections and optimizing chickpea cultivation practices. The impact of the environment on yield and percentuality is not heritable, so plant breeders must examine the influence of genotypic factors on yield and percentuality.

The genotypic correlation *i.e* inherent and heritable correlation is estimated from values of genotypic variances and covariances. Path analysis is designed to percentuantify the interrelationship of different components and their direct and indirect effects on seed yield.

Material and Methods

The details of materials used and the method adopted in the present study comprised of 31 chickpea genotypes trial was conducted at Pulses Improvement Project, MPKV, Rahuri during the *Rabi* 2022-23.

The 31 genotypes were evaluated in a Randomized Block Design with two replications. The gross plot size was 4.00 x 1.80 m (6 rows). The rows were spaced at 30 cm apart with intra plant spacing of 10 cm. A basal dose of 25: 50: 00 NPK kg/ha was applied at the time of sowing.

Field operations *viz.*, gap filling, thinning and inter culturing were carried out as and when repercentured so that the field was kept free from weeds. Recommended plant protection measures were adopted for control of pests and diseases.

Observations recorded on Days to 50% Flowering, Days to maturity, Plant height (cm), Primary branches per plant (No.), Plant spread (cm), Secondary branches per plant (No.) Pods per plant (No) Seeds per pod (No.) 100 seed weight (g), Seed yield per plant (g) Iron content (mg/100 g), Zinc content (mg/100 g), Protein content (%).

Zinc and Iron content was estimated in the sample by using atomic absorption spectrophotometer (Perkin Elmer) while the protein content was determined by Micro-Kjeldahl method.

Analysis of variance commonly applicable to the Randomized Block Design (Panse and Sukhatme, 1985) ^[11]. The genotypic and phenotypic covariances were calculated by Singh and Chaudhary (1977) ^[13]. Path co-efficient analysis was carried out and the simple correlation coefficients (genotypic) were partitioned into direct and indirect effects by path analysis as suggested by Dewey and Lu (1959) ^[5].

Results and Discussion

The analysis of variance for the thirteen characters is presented in (Table 1). Genotypic differences were found to be significant for all studied traits at both the 5% and 1% levels of significance, except of the number of seeds per pod. The observed variability implies significant potential for selecting promising lines within the existing gene pool, particularly concerning seed yield and traits contributing to yield.

The parameters like mean, range, GCV, PCV, heritability in broad sense and percent genetic advance over mean for thirteen yield attributing traits presented in (Table 2). The assessment of Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) for the studied traits revealed a marginal difference, with PCV slightly surpassing GCV. This suggests that variability in these traits is influenced not only by genetic factors but also by environmental factor. Iron (Fe) content exhibited the highest GCV (20.76%), while the number of seeds per pod showed the lowest GCV (1.99%). Similarly, Iron (Fe) content recorded the maximum PCV (21.07%), while moderate values observed for traits such as plant spread (cm) (12.93%), no of secondary branches/plant (10.22%), number of

Pods/plant (15.54%), 100 seed weight (10.01%) and seed yield/plant (13.57%).

Iron (Fe) content emerged as a trait with significant potential for improvement, as evidenced by its highest GCV and PCV. This finding aligns with Kishor *et al.* (2018) ^[7] and Dar *et al.* (2012) ^[4].

The highest estimates of heritability exhibited in iron content (97.1%), protein content (89.2%) followed by plant spread (cm) (86.00%), number of pods/plant (70.90%), zinc (Zn) content (mg) (67.20%) and no. of secondary branches/plant (67.1%).

Moderate heritability estimates were observed for seed yield/plant (58.7%), plant height (cm) (58.5%), 100 seed weight (g) (53.2%), and number of primary branches (44.4%), Days to maturity (39.6), Days to 50 per cent flowering (31.1). The high heritability for traits such as, iron and zinc content, number of pods per plant, 100 seed weight, plant height as well as seed yield per plant similar finding were also reported by Bhanu *et al.*, (2017) ^[2].

The range of genetic advance spans from 0.009 to 16.668. The highest genetic advance is noted for the number of pods per plant (16.67) followed by plant height (6.21), days to maturity (3.68) and 100-seed weight (3.61). Conversely, the lowest genetic advance values are observed for the number of seeds per pod (0.009) succeeded by the number of primary branches per plant (0.23), zinc content (0.62), and days to 50 percent flowering (1.142). These evidences accord with the work of Gul *et al.* (2013) ^[6].

The classification of the range of genetic advance as a percentage of the mean reveals notable figures for various traits. Specifically, Iron (Fe) Content (mg) exhibited a substantial genetic advance of 42.16%, with Number of pods per plant 26.95%, and plant spread (cm) at 24.71%. Number of seeds per pod demonstrated the lowest genetic advance as a percentage of the mean, recording a modest 0.80%. These findings align with previous studies by Noor *et al.* (2003) ^[10], Singh *et al.* (2014) ^[15] and Shengu *et al.* (2018) ^[12].

A significant positive correlation between seed yield per plant and factors like the number of pods per plant, number of primary branches per plant, and number of secondary branches per plant observed at both genotypic and phenotypic levels (Table 3). These findings supported by Singh (2007) ^[14], Dawane *et al.* (2020) ^[3] also reported positive and significant correlations with traits such as the number of pods per plant, 100 seed weight, number of seeds per pod, and plant height.

Duration for 50 percent flowering shown significant positive associations with days to maturity at genotypic level ($r_g = 0.380$). A significant positive correlation observed at the genotypic level with 100 seed weight ($r_g = 0.291$). The duration until maturity demonstrated significant positive relationship at both the genotypic.as.well.as phenotypic levels with the count of primary branches (genotypic correlation, $r_g = 0.929$; phenotypic correlation, $r_p = 0.272$). Additionally, substantial negative correlation at genotypic level with the 100-seed weight ($r_p = -0.522$). The height of plants exhibited a significant positive correlation ($r_g = 0.308$) with seed yield per plant at the genotypic level. A significant negative correlation ($r_g = -0.466$) was observed between plant height and the number of primary branches per plant at the genotypic level. The expansion of plant spread exhibited significant positive correlation with seed yield per plant (genotypic: $r_g = 0.479$, phenotypic: $r_p = 0.305$), the number of secondary branches per plant (genotypic: $r_g = 0.362$, phenotypic: $r_p = 0.341$), and the number of pods per plant (genotypic: $r_g = 0.449$, phenotypic: $r_p = 0.321$) at both the genotypic.as well as phenotypic levels. Number of primary

branches per plant demonstrated non-significant positive correlations at both the genotypic and phenotypic levels with the number of secondary branches per plant ($r_g=0.165$, $r_p=0.127$). However, a non-significant negative correlation was observed with seed yield per plant ($r_g = -0.084$, $r_p = -0.114$) at both genotypic as well as phenotypic levels. Number of secondary branches per plant shown significant positive correlations at both the genotypic and phenotypic levels with the number of pods per plant ($r_g=0.693$, $r_p=0.501$). The correlation analysis revealed significant positive association between the number of pods per plant and seed yield per plant, both at the genotypic ($r_g = 0.83$) and phenotypic ($r_p = 0.83$) levels. The study revealed a non-significant negative correlation between yield per plant and the assessed traits at both the genotypic ($r_g= -0.057$) and phenotypic ($r_p= -0.010$) levels. This finding aligns with the results reported by Mohan and Thiyagarajan (2019)^[9].

Path analysis is crucial for understanding the influence of individual traits on seed yield, beyond simple correlation studies. The path analysis results presented in (Table 4). In indirect effect Days to 50 per cent flowering showed a direct positive impact (0.020) on seed yield. It showed positive indirect effects through other variables, namely days to maturity (0.123), number of primary branches per plant (0.022), number of secondary branches per plant (0.013), number of pods per plant (0.008), and 100 seed weight (0.064). These indirect effects collectively contributed to a positive correlation (0.223) with seed yield. The duration of maturity demonstrated a direct positive impact on seed yield (0.324). It impacts negatively and indirectly through factors such as the number of primary branches per plant (-0.228), the number of pods per plant (-0.195), and the 100-seed weight (-0.114). These indirect effects contributed to an overall negative correlation (-0.219) with seed yield. The height of the plant exhibited a positive direct impact (0.296) on seed yield, with positive indirect influence through number of primary branches per plant (0.114). It had indirect negative impacts on seed yield per plant through number of secondary branches per plant (-0.016), number of pods per plant (-0.068), The overall genotypic correlation is positive (0.308) with seed yield. Plant spread exhibited a positive. Direct effect (0.088) on seed yield in this study. Indirect effects were observed through the positive contributions of the number of pods per plant (0.436) and 100 seed weight (0.081) to the overall seed yield. Indirect negative of plant spread on seed yield per plant is recorded through number of primary branches per plant (-0.047), number of secondary branches per plant (0.038), The comprehensive genotypic correlation with seed yield demonstrated a positive association, measuring at 0.479. The number of primary branches per plant showed direct negative impact (-0.246) on seed yield. This factor resulted in negative effects through the number of secondary branches per plant (-0.017) and the number of pods per plant (-0.015). Number of primary branches per plant shows indirect positive impacts on seed yield per plant through 100 seed weight (0.015). Number of secondary branches showed direct negative effect on seed yield (-0.104), while showed positive indirect effect through number of pods per plant (0.674) on seed yield. It is having positive and highly significant correlation with seed yield per plant (0.627). The number of pods per plant exhibited a high and positive direct impact on seed yield (0.972). It showed a positive indirect

effect through plant spread (0.040) and indirectly contributed to negative impacts through days to maturity (-0.065), plant height (-0.021), number of secondary branches per plant (-0.072), and 100 seed weight (-0.027). A positive and highly significant correlation (0.830) was observed with seed yield per plant. The 100-seed weight exhibited a positive direct impact on seed yield (0.218). While showed negative indirect effects through days to maturity (-0.169), the number of pods per plant (-0.129), and the number of primary branches per plant (-0.017). A non-significant negative correlation (-0.057) was observed between 100-seed weight and seed yield.

In present research, the trait number of pods per plant exhibited the highest direct positive impact on seed yield per plant (0.972) followed by days to maturity (0.324), plant height (0.296) 100 seed weight (0.218) and plant spread (0.088), while number of primary branches per plant and number of secondary branches per plant showed negative direct effect on seed yield per plant. These direct effects contribute significantly to the positive correlation of these characteristics with seed yield per plant. Previous studies, including Kumar *et al.* (2021)^[8] and Bhanu. *et al.* (2017)^[2] also underscored the importance of factors such as number of seeds per pod and number of secondary branches per plant for their direct positive effects on seed yield per plant.

Days to 50 per cent flowering displayed a negative direct effect on seed yield, consistent with findings by Zena *et al.* (2008)^[17] showing similar negative impact on gram yield.

The residual effect ($R=0.429$) indicates that approximately 57% of the included characteristics explain the variability in the dependent variables. The exclusion of the remaining 43% from the study was deemed appropriate for capturing variability.

The analysis of variance (Table 1) highlighted significant variations among the investigated genotypes. For all examined characteristics. Mean sum of squares due to genotypes underscored this variability. Utilizing D^2 values, the thirty-one genotypes grouped into four clusters, where genotypes within the same cluster exhibited smaller average D^2 values than those in different clusters. The distribution of clusters is given in (Table 5), with clusters I and II being, comprising 11 and 18 genotypes, respectively. Clusters III and IV were solitary genotypes (Table 5). This clustering pattern aligns with findings from Temesgen *et al.* (2015)^[16]. Analysis of average intra and inter-cluster D^2 values among 31 genotypes as presented. In (Table.6), revealed distinct genetic variations within clusters. Cluster II exhibited the minimum intra-cluster value (48.02), indicating lower genetic variability among its genotypes. Cluster I displayed the highest intra-cluster D^2 value (61.15), suggesting presence of diverse genotypes within this cluster. Cluster III and IV were solitary.

Inter-cluster D values ranged between 10.72 and 17.08. Minimal inter-cluster D values were seen in between cluster II and III, signifying a close genetic relationship among the genotypes within these clusters. The maximum inter-cluster value was noted between clusters II and IV (17.08), followed by cluster III and IV (14.35), cluster I and III (12.11), cluster I and II (11.66), and cluster I and IV (11.43). These findings suggesting, the genotypes between mentioned clusters possess significant genetic diversity, potentially leading to a high heterotic response. Similar results previously reported by Temesgen *et al.* (2015)^[16].

Table 1: Analysis of variance for thirteen different characters of thirty-one chickpea genotypes

Sr. No.	Characters	Mean sum of percentuares		
		Replications	Genotypes	Error
	DF	1	30	30
1.	Days to 50 per cent flowering	1.613	4.152*	2.176
2.	Days to maturity	17.885	28.363*	12.268
3.	Plant height (cm)	14.420	42.087**	11.033
4.	Plant spread (cm)	0.956	10.878**	0.819
5.	No. of primary branches per plant	0.078	0.088**	0.034
6.	No. of secondary branches per plant	0.100	5.923**	1.168
7.	Number of pods per plant	8.831	222.734**	37.972
8.	Number of seeds per pod	0.005	0.013	0.012
9.	100 seed weight(g)	0.000	16.632**	5.084
10.	Iron (Fe) content (mg/100 g)	0.058	2.226**	0.032
11.	Zinc (Zn) content (mg/100 g)	0.003	0.336**	0.066
12.	Protein content (%)	2.170**	1.964**	0.111
13.	Seed yield plant (g)	4.232	12.875**	3.350

Table 2: Variability parameters for seed yield and its contributing characters in thirty-one chickpea genotypes

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	ECV (%)	Heritability (bs) (%)	Genetic. Advance	Genetic Advance% of Mean
1.	Days to 50 per cent flowering	45.68	43.50 to 48.50	2.17	3.90	3.23	31.1	1.14	2.50
2.	Days to maturity	94.92	88.60 to 102.35	2.99	4.75	3.69	39.6	3.68	3.88
3.	Plant height (cm)	49.71	40.70 to 57.80	7.93	10.37	6.68	58.5	6.21	12.49
4.	Plant spread (cm)	17.34	14.65 to 25.25	12.93	13.95	5.22	86	4.28	24.71
5.	Number of primary branches per plant	2.5	2.15 to 2.9	6.57	9.86	7.34	44.4	0.23	9.02
6.	Number of secondary branches per plant	15.09	11.55 to 19.20	10.22	12.48	7.16	67.1	2.60	17.24
7.	Number of pods per plant	61.84	36.90 to 83.70	15.54	18.46	9.96	70.9	16.67	26.95
8.	Number of seeds per pod	1.12	1.00 to 1.40	1.99	10.20	10.01	3.8	0.01	0.80
9.	100 seed weight (g)	24.01	19.55 to 30.50	10.01	13.76	9.39	53.2	3.61	15.04
10.	Iron (Fe) content (mg/100 g)	5.04	3.40 to 7.05	20.76	21.07	3.56	97.1	2.13	42.16
11.	Zinc (Zn) content (mg/100 g)	4.71	3.60 to 5.15	7.81	9.52	5.46	67.2	0.62	13.18
12.	Protein content (%)	20.69	19.15 to 22.40	4.65	4.92	1.62	89.2	1.87	9.05
13.	Seed yield per plant (g)	16.09	11.05 to 19.85	13.57	17.71	11.37	58.7	3.45	21.41

Table 3: Genotypic (above diagonal) and phenotype correlation coefficients (below diagonal) among seed yield and eight yield contributing. Characters in thirty-one chickpea genotypes

Sr. No	Name of character	Days to.50 per cent flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No. of primary branches per plant	No. of secondary branches per plant	Number of pods per plant	100 seed weight (g)	Yield per plant (g)	
1.	Days.to.50 per cent flowering	rg	1.000	0.380**	-0.028	-0.196	-0.087	-0.122	0.008	0.291*	0.223
		rp	1.000	0.158	-0.009	-0.139	0.112	0.053	0.073	-0.008	-0.025
2.	Days to maturity	rg	1.000	-0.015	-0.013	0.929**	0.074	-0.201	-0.522**	-0.219	
		rp	1.000	-0.120	-0.051	0.272*	0.076	-0.066	-0.059	-0.067	
3.	Plant height (cm)	rg	1.000	-0.113	-0.466**	0.150	-0.070	-0.017	0.308*		
		rp	1.000	-0.015	-0.115	0.098	-0.098	-0.121	0.163		
4.	Plant spread (cm)	rg	1.000	1.000	0.192	0.362**	0.449**	0.371**	0.479**		
		rp	1.000	1.000	0.133	0.341**	0.321**	0.208	0.305*		
5.	No. of primary branches per plant	rg	1.000	1.000	1.000	0.165	-0.016	0.071	-0.084		
		rp	1.000	1.000	1.000	0.127	-0.000	-0.058	-0.114		
6.	No. of secondary branches per plant	rg	1.000	1.000	1.000	0.693**	0.002	0.627**			
		rp	1.000	1.000	1.000	0.501**	-0.042	0.411**			
7.	Number of pods per plant	rg	1.000	1.000	1.000	1.000	-0.125	0.830**			
		rp	1.000	1.000	1.000	1.000	-0.125	0.830**			
8.	100 seed weight (g)	rg	1.000	1.000	1.000	1.000	1.00	-0.057			
		rp	1.000	1.000	1.000	1.000	1.000	-0.010			

*and ** significant at P= 5 and P = 1 level of significance, respectively

Table 4: Direct (diagonal) and indirect genotypic effects (above and below diagonal) for different. Characters in 31 Chickpea genotypes

Sr. No.	Name of character	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Plant spread (cm)	No. of primary branches per plant	No. of secondary branches per plant	Number of pods per plant	100 seed weight (g)	Genotypic Correlation with Yield per plant (g)
1.	Days to 50 per cent flowering	0.020	0.123	-0.008	-0.017	0.022	0.013	0.008	0.064	0.223
2.	Days to maturity	0.008	0.324	-0.005	-0.001	-0.228	-0.008	-0.195	-0.114	-0.219
3.	Plant height (cm)	-0.001	-0.005	0.296	-0.010	0.114	-0.0157	-0.068	-0.004	0.308*
4.	Plant spread (cm)	-0.004	-0.004	-0.033	0.088	-0.047	-0.038	0.436	0.081	0.479**

5.	No. of primary branches per plant	-0.002	0.301	-0.138	0.017	-0.246	-0.017	-0.015	0.015	-0.084
6.	No. of secondary branches per plant	-0.002	0.024	0.045	0.032	-0.041	-0.104	0.674	0.000	0.627**
7.	Number of pods per plant	0.000	-0.065	-0.021	0.040	0.004	-0.072	0.972	-0.027	0.830**
8.	100 seed weight (g)	0.006	-0.169	-0.01	0.033	-0.017	-0.000	-0.129	0.218	-0.057

Residual effect (R) = 0.429 Note: Bold figures indicates direct effect

Table 5: Distribution of Thirty-one Chickpea Genotypes into Different Clusters

Cluster No.	Number of genotypes includes	Name of Genotypes	Origin
I	11	Phule G 1521-12-3	PIP, MPKV Rahuri
		Phule G 2111-03	PIP, MPKV Rahuri
		Phule G 2111-10	PIP, MPKV Rahuri
		Phule Vikram	PIP, MPKV Rahuri
		Digvijay	PIP, MPKV Rahuri
		Phule G 1517-1-8	PIP, MPKV Rahuri
		AKG-1402	PDKV, Akola
		BDNG-2020-68	ARS, Badnapur
		BDNG-797	ARS, Badnapur
		Phule G 1521-12-2	PIP, MPKV Rahuri
		Phule G-1403-18-14	PIP, MPKV Rahuri
II	18	AKG-1506	PDKV, Akola
		Phule G 1511-29-7	PIP, MPKV Rahuri
		Phule-G-1415-13-28	PIP, MPKV Rahuri
		Phule Vikrant	PIP, MPKV Rahuri
		BDNG-2018-16	ARS, Badnapur
		Phule G 1504-5-7	PIP, MPKV Rahuri
		BDNG-2020-45	ARS, Badnapur
		AKG-1710	PDKV, Akola
		Phule G 1504-8-4	PIP, MPKV Rahuri
		Phule G 1511-29-1	PIP, MPKV Rahuri
		Phule G-1424-4-2	PIP, MPKV Rahuri
		Phule- G1221-2-6	PIP, MPKV Rahuri
		BDNG-2020-22	ARS, Badnapur
		PDKV-Kanak	PDKV, Akola
		TRCH-4	PIP, MPKV Rahuri
		Phule G 1511-17-4	PIP, MPKV Rahuri
		BDNG-2021-5	ARS, Badnapur
Phule G 1415-13-20	PIP, MPKV Rahuri		
III	1	BDNG-2021-53	ARS, Badnapur
IV	1	JAKI-9218	PDKV, Akola

Table 6: Average Intra (Bold) and Inter-Cluster D Values for Four Clusters in 31 Chickpea Genotypes

Cluster	I	II	III	IV
I	7.82 (61.15)	11.66 (135.96)	12.11 (146.65)	11.43 (130.64)
II		6.93 (48.02)	10.72 (114.91)	17.08 (291.72)
III			0.00 (0.00)	14.35 (205.92)
IV				0.00 (0.00)

Conclusion

The present investigation understands the association among the economically important traits and to identify the traits with the highest direct and indirect effects on seed yield. The correlation and path analysis exhibited highest positive direct effects of number of pods per plant, days to maturity, plant height and 100 seed weight on grain yield per plant indicating that the direct selection for these traits would improve the grain yield in chickpea. Chickpea genotypes JAKI-9218 and Phule G-2111-03, Phule G 1511-29-7 are rich source of iron and zinc content respectively which can be used in further biofortification program. Based on divergence classes and the individual performance of chickpea genotypes, Phule G-1511-29-1 for the number of seeds per pod and seed yield, secondary branches per plant, seed yield, and plant height Phule G 1424-4-2, 100-seed weight Phule G 1511-17-4, plant spread, days to maturity and

seed yield Phule 1415-13-20, days to maturity and 100 seed weight BDNG-2021-53, secondary branches per plant and plant spread Phule Vikram should be used in future breeding programme.

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