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Research Note

Multivariate analysis in chickpea genotypes under timely sown condition

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Abstract
Yield, a multifaceted trait influenced by genetic and environmental factors, requires a comprehensive assessment beyond emphasizing only on yield alone. Thus, understanding the intricate relationship between yield and its associated traits across diverse chickpea genotypes is essential. The current investigation was undertaken at the Breeder seed production unit, JNKVV, Jabalpur, Madhya Pradesh, during the 2021-22 cropping season. Significant variations were found by analysis of variance (ANOVA) among the 40 genotypes under study, indicating substantial variability. Post hoc DMRT analysis further confirmed notable genetic diversity across all traits. Regression and Principal component analysis highlighted the significance of optimizing biological yield per plant, effective pods, total number of pods, and secondary branches to enhance grain yield. Strategic selection prioritizing these traits can facilitate the development of high-yielding chickpea varieties with enhanced agronomic characteristics. This analysis identified five principal components explaining 80.74% of genotypic variability. Ultimately, the genotypes ICCV 211210, RVG-204, and ICCV 211206 emerged as promising based on PC scores.

Keywords: Chickpea, DMRT, Regression, PCA, Yield

Chickpea (*Cicer arietinum* L.) is an earliest self-pollinated diploid legume crop (2n=2X=16), thought to have originated in South-Eastern Turkey and parts of Syria (Singh, 1997). Apart from its center of origin, chickpea has found widespread consumption globally, particularly in Afro-Asian countries (Sofi *et al*., 2020). The domestication of cultivated chickpeas traces back over an extensive period, giving rise to two distinct types, namely 'desi' and 'kabuli' which differ in terms of floral shape, color, and surface, as well as seed size and color. In chronological terms, desi types are regarded as more primitive when compared to kabuli (Warkentin *et al*., 2005). Predominantly, chickpeas are recognized as indeterminate types, where their vegetative stage continues even after flowering. Worldwide, there is an increasing demand for chickpeas due to their cost-effective protein content and substantial nutritional value including phytochemicals, carbohydrates, dietary fibers, micronutrients and all essential amino acids (excluding Sulphur containing). Particularly in South Asia, East Asian nations, and among the predominantly vegetarian population in India, chickpeas play a crucial role as a key source of protein. Consequently, chickpeas are viewed as a favorable alternative to wheat flour and a boon for individuals with diabetes (Nam *et al*., 2023).

The primary objective of breeding chickpea is to enhance genetic potential of cultivars or eliminate the detrimental effects of biotic and abiotic stresses in order to boost the production (Singh, 1997). Given the indeterminate

nature of chickpeas, they tend to exhibit lower seed yield due to an extended vegetative phase when cultivated under favorable conditions such as optimal temperature, soil moisture, and other supporting environmental factors (Ambika *et al*., 2021). In addition, the narrow genetic base within cultivated chickpea has posed a challenge, impeding the advancement of substantial yield improvements in breeding programs (Singh *et al*., 2008). As yield is a complex quantitative trait that can be influenced by diverse genetic factors as well as fluctuations in the environment, so prioritizing only to yield could be misleading. Therefore, it's imperative to investigate the intricate relationship between yield and its associated traits across various chickpea genotypes. This comprehensive study is pivotal for formulating effective selection strategies aimed at breeding superior varieties with improved agronomic traits. Consequently, the current study was targeted to assess the performance of chickpea genotypes for yield and its attributing traits under timely sowing conditions through rigorous statistical analysis, including Analysis of Variance (ANOVA), Regression Analysis, Duncan's Multiple Range Test (DMRT), and Principal Component Analysis (PCA).

The field trial was executed at the experimental farm of the breeder seed production unit in Jabalpur, Madhya Pradesh, during the cropping season of 2021-22. The site is situated at latitude of 23.90ºN and longitude of 79.58ºE, with an elevation of 411.87 meters above mean sea level. The soil composition at the experimental farm is predominantly vertisol, exhibiting a clay loam texture, with a neutral pH ranging from 7.2 to 8.0. The experimental material encompassed 40 chickpea genotypes including the checks *viz.* JG12, JG24, and JG36 were evaluated in RCBD design under timely sowing conditions, incorporating three replications, with each plot having a gross area of 4.80 m². Observations were systematically recorded on fourteen yield and its attributing traits namely days to 50% flowering (DTF), days to physiological maturity (DTM), plant height (PH), height of the first fruiting node (HFFN), stem thickness (ST), number of primary branches per plant (NPBPP), number of secondary branches per plant (NSBPP), total number of pods per plant (TNPPP), number of effective pods per plant (NEPPP), number of seeds per pod (NSPP), hundred seed weight (HSW), biological yield per plant (BY), harvest index (HI), and seed yield per plant (SYPP) under field conditions with the data collected from five competitive random plants per plot in each replication. The performance of genotypes was statistically examined through ANOVA, DMRT for post hoc mean separation at a 5% significance level, Regression Analysis, and PCA using R software version 4.3.2.

ANOVA is a statistical technique employed to study the variation in traits among different groups within a plant breeding population. This aids in the identification of significant differences in means. ANOVA conducted for all

Table 1. Analysis of variance for quantitative traits in chickpea genotypes

S. No.	Characters	Mean Sum of Squares		
		Replication	**Genotype**	**Residuals**
1	DF	2	39	78
2	DFF	1.22	158.06**	7.44
3	DTM	14.03	85.80**	4.96
4	PH	0.41	83.49**	5.43
5	HFFN	0.88	49.77**	6.36
6	ST	0.006	0.449**	0.015
7	NPBPP	0.53*	1.09**	0.15
8	NSBPP	0.74	14.86**	1.74
9	TNPPP	119.9	1536.43**	150.22
10	NEPPP	357.32	1484.97**	145.71
11	NSPP	0.04	0.12**	0.02
12	HSW	2.84	61.74**	0.92
13	BY	27.04	470.58**	19.66
14	HI	1.13	193.29**	37
15	SYPP	5.32	124.72**	6.87

* Significant at 5%   ** Highly significant at 1%

(DFF- Days to 50% flowering, DTM- Days to maturity, PH- Plant height (cm), HFFN- Height of first fruiting node (cm), NPBPP- Number of primary branches per plant, NSBPP- Number of secondary branches per plant, TNPPP- Total number of pods per plant, NEPPP- Number of effective pods per plant, NSPP- Number of seeds per pod, HSW- Hundred seed weight, BY- Biological yield (g), HI- Harvest index, SYPP- Seed yield per plant (g))

yield and its attributing traits which demonstrated a highly significant difference among the forty studied genotypes, indicating ample variability among the investigated genotypes represented in **Table 1**. Comparable results were documented in previous studies conducted by Jivani *et al.* (2014), Astereki *et al.* (2017), Bhanu *et al.* (2017) and Janghel *et al.* (2020).

The post hoc DMRT analysis indicated a significant genetic variability across all quantitative traits within chickpea genotypes represented in **Table 2**. Similar findings were reported by Kobraee *et al.* (2010), Ejara *et al.* (2020) and Vyshnavi *et al.* (2024) showing the ample amount of variability. The population mean for days to 50% flowering was 70.05 days, with the genotype JG 2016-14-16-11 (50.00 days) exhibiting the shortest flowering time and ICCV 211210 (79.67 days) showing the longest. Similarly, days to maturity ranged from 97.67 days (earliest - JG 2016-14-16-11) to 123 days (latest - ICCV 211209). The mean plant height was 63.70 cm, with ICCV191609 reaching the maximum height of 71.48 cm and JG 2016-36 displaying the minimum height at 52.33 cm. Stem thickness varied from 3.58 to 2.16 mm, with ICCV 211208 recorded the highest and JG 2020-634958 the lowest. The range for the number of primary branches per plant was 2.65 to 5.28, with ICCV 211205 having the highest (5.28) followed by ICCV191606 (5.05). For the number of secondary branches per plant, the variation was 7 to 15.39, with JG 24 showing the highest and JG 2020-23 the lowest. The total number of pods per plant ranged from 30.69 to 114.85, with ICCV191609 recording the lowest (30.69) and JG 2018-549 exhibiting the highest (114.85), followed by RVG-204 (112.01). For the number of effective pods per plant, the range was 24.37 to 106.64, with RVG-204 registering the highest (106.64) and JG 2018-51 the lowest (24.37). The highest and lowest value for number of seeds per pod recorded in JG 2020-634958 (1.85) and ICCV 211209 (1.13), with population mean of 1.37. The variation for hundred seed weight ranged between 16.64g to 36.35g. The genotype JG 2020-15118 (36.35 g) showed the highest hundred seed weight followed by ICCV 181108-2 (34.36 g). The variation for biological yield ranged between 21.11 to 67.36 g and ICCV 211206 (67.36 g) showed the highest biological yield followed by ICCV 211210 (65.15 g). Highest and lowest value of harvest index recorded in PG 205 (68.44) and JG 12 (34.56) respectively with population mean of 52.5. The variation for seed yield per plant ranged between 12.11 to 33.97 g. The highest value was observed in ICCV 211206 (33.97 g) followed by JG 24 (33.32 g).

Among the forty genotypes assessed, a noteworthy majority, exceeding fifty percent, demonstrated superior performance over the population mean for traits such as stem thickness (23), number of primary branches per plant (25), and number of secondary branches per plant (25). In contrast, traits such as harvest index (19), number of seeds per pod (19), hundred seed weight (18), biological yield (19), and seed yield per plant (18) exhibited less than 50% of the genotypes displaying superior performance relative to the population mean. However, for remaining traits such as days to maturity, plant height, number of primary branches per plant, number of effective pods per plant, and total number of pods per plant, precisely 20 genotypes demonstrated performance levels superior to the population mean for their respective traits.

Among the 40 genotypes evaluated, the genotype ICCV 211206 (33.97 g) emerged as the top performer with the highest seed yield per plant surpassing all three checks *viz*., JG 12 (22.39 g), JG 24 (33.32 g) and JG 36 (27.74 g) followed closely by ICCV 211210 (32.97 g) which was on par with JG 24. Additionally, both ICCV 211210 and ICCV 211206 outperformed the checks in total number of pods per plant, number of effective pods per plant, biological yield per plant and hundred seed weight. However, both ICCV 211210 and ICCV 211206 have lower harvest indices than the checks (JG 24 and JG 36) and the population mean, indicating, production of a lot of biomasses part of which may not be contributing to the economic yield. In contrast, RVG-204 is comparable to the checks in both yield and harvest index. Additionally, RVG-204 showed better results than checks for the trait total number of pods per plant, number effective of pods per plant. One more genotype, JG 2020-15118 achieved comparable yield and harvest index as that of checks while exhibiting the highest hundred seed weight (36.35g). In conclusion, ICCV 211210, ICCV 211206, RVG-204 and JG 2020-15118 emerge as promising chickpea genotypes exhibiting superior yield and attributing traits compared to assigned check varieties. Additionally, their prolonged time to reach 50% flowering and maturity indicates a positive relationship between delayed phenological stages and increased yield. The results were analogous with the previous findings by Malik *et al.* (2014), Dhuria and Babbar (2015), Tadesse *et al.* (2016), Agrawal *et al.* (2018) for days to flowering maturity.

Regression analysis facilitates the elucidation of interrelationships among diverse variables within chickpea populations, enabling the construction of predictive models for estimating chickpea yields. It facilitates the identification of crucial factors governing chickpea growth, yield, and quality, enabling researchers to strategically allocate resources and efforts towards optimizing these determinants, thereby fostering improved chickpea production. The graphical representation of the regression analysis indicates strong coefficients of determination for various chickpea yield attributing traits illustrated in **Fig. 1**. Among these, biological yield per plant exhibits the highest coefficient (0.756), followed by total number of pods per plant (0.702), number of effective pods per plant (0.685), and number of secondary branches per plant (0.555). This emphasizes their significant impact on grain yield. Positive linear correlations are evident between grain yield and these traits, emphasizing the pivotal role

Table 2. Comparison of means for yield and its attributing traits of 40 chickpea genotypes

Genotype	DFF	DTM	PH	HFFN	ST
JG 2016-14-16-11	50.00[n]	97.67[o]	56.11[lmn]	25.11[cdefgh]	2.60[mn]
ICCV 181108-2	72.00[defghi]	105.00[klmn]	71.41[a]	25.85[bcdef]	3.10[fghij]
JG 2020-1614	69.67[ghijk]	106.67[ghijklm]	59.55[hijkl]	21.37[fghij]	3.15[efghi]
JG 2016-36	75.33[abcdef]	106.00[hijklmn]	52.33[n]	23.78[defgh]	2.65[mn]
JG 2020-12-16-13	68.00[hijkl]	109.00[fghijk]	65.78[cdef]	27.52[abcd]	3.35[abcde]
ICCV 191618	69.67[ghijk]	112.00[def]	71.45[a]	29.56[abc]	2.77[klm]
ICCV 191608	70.67[efghij]	105.67[ijklmn]	71.22[a]	25.30[cdefg]	3.57[ab]
ICCV 181667	63.00[l]	101.67[n]	62.51[fghij]	26.26[bcdef]	3.13[efghi]
JG 2020-75	72.00[defghi]	110.00[fghi]	56.52[klmn]	23.96[defgh]	3.13[efghi]
JG 2020-23	67.00[ijkl]	105.67[ijklmn]	64.00[defgh]	22.96[defgh]	2.89[jkl]
ICCV181109	72.00[defghi]	109.67[fghij]	63.33[efghi]	26.43[abcdef]	3.07[ghij]
ICCV191609	70.00[fghij]	109.00[fghijk]	71.48[a]	30.36[ab]	3.29[cdefg]
JG 2018-51	71.33[defghi]	105.33[jklmn]	60.78[ghijk]	26.57[abcde]	2.48[no]
ICC181612	50.33[n]	102.67[mn]	69.56[abc]	31.11[a]	3.23[defgh]
JG 2021-96029	73.00[cdefgh]	106.00[hijklmn]	59.11[ijkl]	26.04[bcdef]	2.71[klmn]
JG 2020-15118	72.67[defgh]	108.00[fghijkl]	61.67[fghij]	24.81[cdefgh]	2.93[ijk]
ICCV191606	76.00[abcde]	110.00[fghi]	64.22[defg]	26.00[bcdef]	3.34[abcde]
ICCV191616	70.00[fghij]	109.67[fghij]	67.77[abcde]	26.59[abcde]	3.00[hij]
JG 2020-634958	63.33[l]	109.67[fghij]	62.89[fghij]	23.89[defgh]	2.16[p]
JG 2017-49	67.00[ijkl]	110.33[efgh]	64.33[defg]	23.00[defgh]	3.42[abcd]
JG 2020-1614	76.00[abcde]	110.67[defg]	65.89[bcdef]	25.07[cdefgh]	2.72[klm]
JG 2016-1411	71.00[defghi]	102.67[mn]	62.22[fghij]	24.63[cdefgh]	3.14[efghi]
JG 2018-54	79.00[ab]	104.00[lmn]	53.00[n]	23.33[defgh]	2.48[no]
ICC181106	74.33[bcdefg]	105.33[jklmn]	65.89[bcdef]	26.78[abcde]	2.68[lmn]
PG 205	76.33[abcd]	106.33[ghijklm]	66.22[bcdef]	24.15[defgh]	2.69[lmn]
ICCV181602	73.33[cdefgh]	105.67[ijklmn]	62.56[fghij]	24.52[defgh]	3.29[cdefg]
RVG-204	72.67[defgh]	114.67[cd]	62.45[fghij]	22.22[efghi]	3.48[abc]
ICCV 211207	78.00[abc]	120.00[ab]	69.85[abc]	24.00[defgh]	3.55[ab]
ICCV 211202	65.67[jkl]	110.67[defg]	60.71[ghijk]	16.29[kl]	3.33[bcdef]
ICCV 211204	71.33[defghi]	111.67[def]	70.34[ab]	20.13[hijk]	3.55[ab]
ICCV 211201	51.33[n]	106.00[hijklmn]	62.93[fghij]	14.39[l]	3.52[abc]
ICCV 211208	72.67[defgh]	112.33[def]	69.56[abc]	21.37[fghij]	3.58[a]
ICCV 211203	64.67[kl]	109.33[fghijk]	66.01[bcdef]	20.36[ghijk]	3.21[defgh]
ICCV 211210	79.67[a]	119.00[b]	63.41[defghi]	17.31[jkl]	3.55[ab]
ICCV 211209	78.00[abc]	123.00[a]	54.45[mn]	16.71[jkl]	2.57[mno]
ICCV 211206	72.33[defghi]	116.33[bc]	66.00[bcdef]	15.67[kl]	3.20[defgh]
ICCV 211205	78.00[abc]	119.67[ab]	58.45[jklm]	18.02[ijkl]	3.01[hij]
JG 12 (ch)	74.00[bcdefg]	114.33[cde]	69.07[abc]	15.89[kl]	2.65[mn]
JG 24 (ch)	72.67[defgh]	109.33[fghijk]	67.89[abcd]	26.78[abcde]	3.57[ab]
JG 36 (ch)	58.00[m]	103.67[lmn]	55.34[lmn]	23.14[defgh]	2.37[o]
Mean±SE$_m$	70.05±1.14	109.10±0.84	63.70±0.83	23.43±0.64	3.05±0.06
CD	4.43	3.62	3.79	4.10	0.20

Table 2. (Continued)

Genotype	NPBPP	NSBPP	TNPPP	NEPPP	NSPP
JG 2016-14-16-11	3.36^{hijkl}	7.33^{j}	58.13^{ijklmnopq}	49.37^{hijklmn}	1.66^{abcd}
ICCV 181108-2	4.33^{bcdef}	11.00^{defgh}	54.43^{ijklmnopqr}	49.78^{hijklmn}	1.24^{ijklm}
JG 2020-1614	3.14^{kl}	13.22^{abcde}	81.52^{cdefgh}	74.27^{cdefg}	1.30^{fghijklm}
JG 2016-36	4.30^{bcdef}	10.11^{fghi}	50.71^{klmnopqrs}	44.94^{ijklmnop}	1.69^{abc}
JG 2020-12-16-13	4.12^{defgh}	9.00^{hij}	49.46^{lmnopqrs}	43.73^{jklmnop}	1.24^{ijklm}
ICCV 191618	3.30^{ijkl}	13.67^{abc}	66.04^{ghijklmn}	58.86^{fghijkl}	1.35^{efghijklm}
ICCV 191608	4.52^{bcde}	11.85^{cdef}	72.91^{efghijk}	66.09^{defghij}	1.16^{klm}
ICCV 181667	2.65^{l}	8.22^{ij}	43.68^{nopqrs}	35.32^{mnop}	1.57^{abcdefg}
JG 2020-75	3.76^{efghijk}	12.33^{bcdef}	65.37^{hijklmno}	57.79^{ghijklm}	1.54^{bcdefgh}
JG 2020-23	3.35^{hijkl}	7.00^{j}	42.66^{opqrs}	38.11^{lmnop}	1.50^{bcdefghij}
ICCV181109	4.95^{abc}	12.33^{bcdef}	47.35^{mnopqrs}	35.76^{mnop}	1.38^{defghijklm}
ICCV191609	4.42^{bcdef}	9.33^{ghij}	30.69^{s}	26.34^{op}	1.38^{defghijklm}
JG 2018-51	3.78^{efghijk}	8.82^{hij}	31.52^{rs}	24.37^{p}	1.62^{abcde}
ICC181612	3.73^{fghijk}	8.22^{ij}	35.94^{qrs}	29.97^{nop}	1.51^{bcdefghi}
JG 2021-96029	4.00^{defghij}	11.67^{cdefg}	52.08^{jklmnopqrs}	48.45^{hijklmno}	1.29^{ghijklm}
JG 2020-15118	4.42^{bcdef}	12.18^{bcdef}	95.33^{abcde}	84.11^{bcde}	1.18^{klm}
ICCV191606	5.05^{ab}	9.33^{ghij}	90.15^{bcdef}	82.26^{bcde}	1.22^{ijklm}
ICCV191616	4.59^{bcd}	10.78^{efgh}	43.72^{nopqrs}	39.10^{lmnop}	1.23^{ijklm}
JG 2020-634958	4.25^{cdefg}	8.11^{ij}	74.82^{efghij}	58.62^{fghijkl}	1.85^{a}
JG 2017-49	3.42^{hijk}	13.62^{abcd}	40.83^{pqrs}	37.67^{lmnop}	1.24^{ijklm}
JG 2020-1614	4.22^{cdefg}	12.33^{bcdef}	76.35^{defghi}	67.40^{defghi}	1.53^{bcdefgh}
JG 2016-1411	4.38^{bcdef}	13.33^{abcde}	45.77^{mnopqrs}	43.44^{jklmnop}	1.45^{cdefghijk}
JG 2018-54	3.65^{fghijk}	13.00^{abcde}	114.85^{a}	106.11^{a}	1.27^{hijklm}
ICC181106	4.42^{bcdef}	12.56^{bcdef}	63.47^{hijklmnop}	58.86^{fghijkl}	1.23^{ijklm}
PG 205	3.22^{kl}	14.22^{abc}	73.47^{efghijk}	68.68^{defgh}	1.37^{defghijklm}
ICCV181602	4.37^{bcdef}	13.24^{abcde}	95.07^{abcde}	86.23^{abcd}	1.17^{klm}
RVG-204	3.51^{ghijk}	13.67^{abc}	112.01^{ab}	106.64^{a}	1.15^{lm}
ICCV 211207	3.10^{kl}	14.15^{abc}	73.89^{efghijk}	67.51^{defghi}	1.21^{jklm}
ICCV 211202	3.17^{kl}	10.32^{fghi}	84.61^{cdefgh}	79.45^{bcdefg}	1.14^{lm}
ICCV 211204	3.27^{jkl}	12.71^{bcdef}	45.95^{mnopqrs}	42.14^{klmnop}	1.68^{abc}
ICCV 211201	3.35^{hijkl}	12.51^{bcdef}	74.03^{efghijk}	70.08^{defgh}	1.16^{klm}
ICCV 211208	3.35^{hijkl}	14.33^{abc}	63.11^{hijklmnop}	59.19^{fghijkl}	1.23^{ijklm}
ICCV 211203	4.06^{defghi}	13.85^{abc}	68.29^{fghijklm}	63.51^{efghijk}	1.16^{klm}
ICCV 211210	4.10^{defgh}	12.69^{bcdef}	97.96^{abcd}	94.07^{abc}	1.17^{klm}
ICCV 211209	4.26^{cdefg}	12.45^{bcdef}	99.96^{abc}	94.18^{abc}	1.13^{m}
ICCV 211206	3.53^{ghijk}	14.23^{abc}	88.92^{cdefg}	80.95^{bcdef}	1.44^{cdefghijkl}
ICCV 211205	5.28^{a}	13.53^{abcd}	71.45^{fghijk}	65.05^{defghij}	1.23^{ijklm}
JG 12 (ch)	3.52^{ghijk}	14.52^{ab}	66.94^{ghijklmn}	63.31^{efghijk}	1.63^{abcde}
JG 24 (ch)	4.34^{bcdef}	15.39^{a}	95.26^{abcde}	86.25^{abcd}	1.77^{ab}
JG 36 (ch)	3.44^{hijk}	13.22^{abcde}	102.45^{abc}	98.38^{ab}	1.58^{abcdef}
Mean±SE$_m$	3.89±0.09	11.85±0.35	67.50±3.57	62.41±3.51	1.37±0.03
CD	0.63	2.14	19.23	18.81	0.24

Table 2. (Continued)

| Genotype	HSW	BY	HI	SYPP
JG 2016-14-16-11	18.98^q	36.89^{nopq}	40.66^{kl}	15.01^{opq}
ICCV 181108-2	34.36^b	46.99^{ghijkl}	44.46^{hijkl}	20.89^{ijklmn}
JG 2020-1614	26.62^{hi}	52.33^{defg}	53.80^{defghij}	28.06^{cdef}
JG 2016-36	30.23^e	45.88^{ghijklm}	42.68^{jkl}	19.57^{jklmno}
JG 2020-12-16-13	25.90^{hijkl}	27.66^{rs}	49.68^{fghijk}	13.58^{pq}
ICCV 191618	33.14^{bc}	60.10^{abcd}	46.51^{ghijk}	28.03^{cdef}
ICCV 191608	30.45^e	48.33^{fghijk}	45.99^{ghijkl}	21.94^{ghijkl}
ICCV 181667	21.74^{op}	24.45^{rs}	50.90^{efghijk}	12.11^q
JG 2020-75	19.26^q	27.42^{rs}	68.12^{ab}	18.52^{lmnop}
JG 2020-23	26.42^{hij}	26.87^{rs}	59.86^{abcdef}	16.09^{nopq}
ICCV181109	26.53^{hi}	28.33^{rs}	66.94^{abc}	18.94^{klmno}
ICCV191609	24.91^{ijklm}	28.55^{rs}	49.19^{fghijk}	14.00^{pq}
JG 2018-51	18.86^q	29.43^{qrs}	42.43^{jkl}	12.54^q
ICC181612	22.46^{nop}	31.54^{opqr}	43.05^{ijkl}	13.51^{pq}
JG 2021-96029	24.64^{jklm}	21.11^s	65.00^{abcd}	13.72^{pq}
JG 2020-15118	36.35^a	57.09^{bcde}	56.44^{bcdefgh}	32.23^{abcd}
ICCV191606	31.21^{de}	44.87^{ghijklmn}	58.88^{abcdef}	25.84^{efghi}
ICCV191616	25.05^{ijklm}	39.65^{lmno}	40.46^{kl}	15.98^{nopq}
JG 2020-634958	26.07^{hijk}	43.89^{ghijklmn}	48.21^{fghijk}	21.20^{hijklm}
JG 2017-49	27.57^{gh}	30.99^{pqr}	51.89^{efghijk}	16.03^{nopq}
JG 2020-1614	24.55^{klm}	57.10^{bcde}	51.82^{efghijk}	29.66^{abcde}
JG 2016-1411	25.48^{ijkl}	36.89^{nopq}	46.17^{ghijkl}	16.90^{mnopq}
JG 2018-54	16.64^r	43.33^{hijklmn}	62.57^{abcde}	26.78^{efg}
ICC181106	31.26^{de}	41.11^{jklmn}	57.17^{abcdefg}	23.67^{fghijk}
PG 205	22.58^{nop}	38.22^{mnop}	68.44^a	26.17^{efgh}
ICCV181602	26.66^{hi}	56.11^{cdef}	53.07^{defghij}	29.78^{abcde}
RVG-204	30.37^e	63.07^{abc}	52.00^{efghijk}	32.78^{abc}
ICCV 211207	25.20^{ijkl}	51.78^{efgh}	55.08^{cdefghi}	28.45^{bcdef}
ICCV 211202	24.14^{lmn}	42.10^{jklmn}	57.69^{abcdefg}	24.22^{fghij}
ICCV 211204	24.82^{ijklm}	42.66^{ijklmn}	52.65^{efghijk}	22.41^{ghijkl}
ICCV 211201	21.60^{op}	40.29^{klmn}	56.48^{bcdefgh}	22.77^{ghijkl}
ICCV 211208	30.06^{ef}	37.26^{mnopq}	58.25^{abcdefg}	21.21^{hijklm}
ICCV 211203	24.11^{lmn}	39.00^{lmnop}	57.69^{abcdefg}	22.46^{ghijkl}
ICCV 211210	31.08^{de}	65.15^{ab}	50.62^{efghijk}	32.97^{ab}
ICCV 211209	23.30^{mno}	49.45^{efghij}	43.79^{ijkl}	21.70^{ghijklm}
ICCV 211206	32.55^{cd}	67.36^a	50.56^{efghijk}	33.97^a
ICCV 211205	28.55^{fg}	50.78^{efghi}	51.71^{efghijk}	26.12^{efgh}
JG 12 (ch)	24.91^{ijklm}	64.84^{ab}	34.56^l	22.39^{ghijkl}
JG 24 (ch)	31.02^{de}	62.19^{abc}	53.55^{defghij}	33.32^{ab}
JG 36 (ch)	20.87^p	44.44^{ghijklm}	62.59^{abcde}	27.74^{def}
Mean±SE$_m$	26.26±0.71	43.63±1.98	52.54±1.26	22.58±1.01
CD	1.56	7.20	9.88	4.26
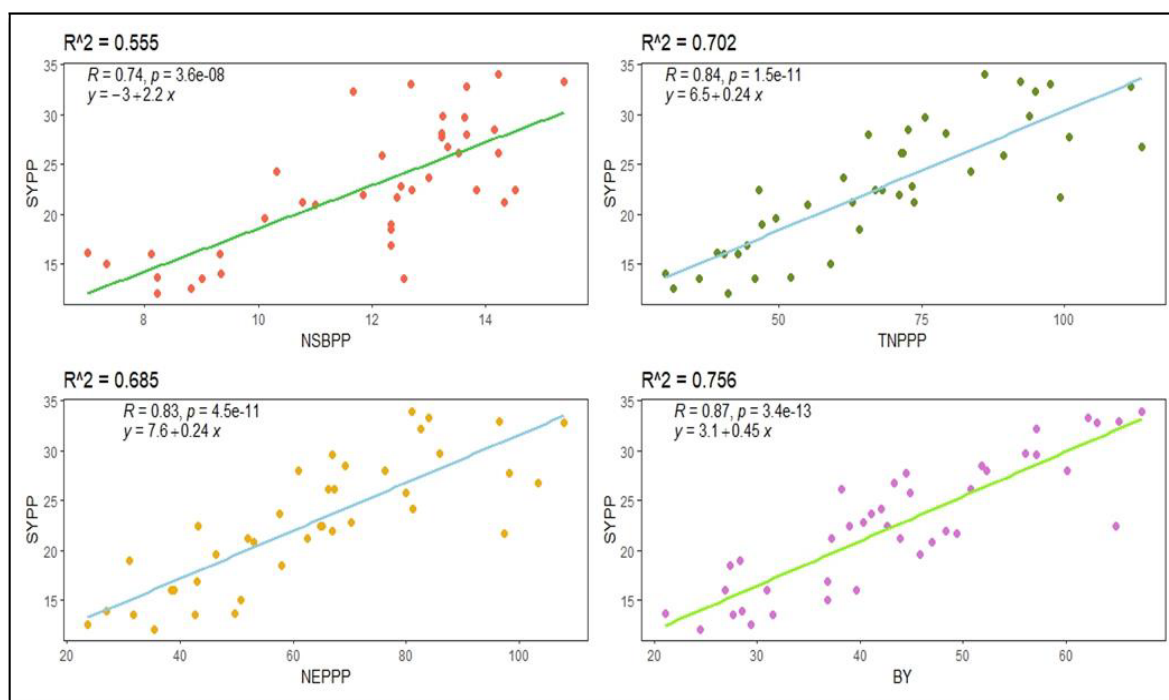
Fig. 1. Linear regression analysis of yield and its attributing traits in chickpea genotypes

of optimizing these factors to enhance grain yield. The results were consistent with prior studies conducted by Hasanuzzaman *et al.* (2007) for pods per plant, Atta *et al.* (2008) for total number of pods per plant and number of secondary branches, Kayan and Adak (2012) for biological yield per plant, pods per plant, and seed yield per plant and Petrova (2021) for number of pods per plant and number of branches per plant exhibiting higher coefficients with seed yield.

PCA functions as a fundamental non-parametric technique for obtaining relevant information from complex datasets. It is a well-established method for dimension reduction, where a large set of variables can be transformed into a smaller set while retaining the majority of pertinent information (Massay, 1965; Jolliffe, 2002). PCA was employed to explore the interrelationship between yield and its component traits in chickpea. The distribution of variability is depicted by the scree plots, which were constructed using principal components and their corresponding Eigenvalues, were presented in **Table 3** and illustrated in **Fig. 2**. Total fourteen principal components were identified and among them only five principal components with Eigenvalues greater than 1 were chosen for interpretation. The foremost principal component (PC 1) captured the largest proportion of variability (36.48 %) within the traits contributing to yield. Subsequent principal components exhibited progressively diminishing levels of variability such as PC 2 (15.91 %), PC 3 (10.39 %), PC 4 (10.04 %), and PC 5 (7.92 %) respectively. These components collectively accounted

for 80.74% of the variability within the 40 elite chickpea breeding lines.

The rotated component matrix (depicted in **Fig. 3**) has provided insights into how each Principal Component is associated with various yield-related traits. PC1 accounted for the highest proportion of variability, primarily exhibiting associations with traits related to yield such as number of secondary branches per plant, total number of pods per plant, number of effective pods per plant, biological yield and seed yield per plant (**Table 4**). On the other hand, PC2 was predominantly characterized by plant height, stem thickness, and hundred-seed weight. Similarly, PC3 is mainly influenced by traits such as the number of primary branches per plant, number of seeds per pod, and biological yield per plant. Likewise, PC4 and PC5 were primarily driven by traits like plant height and days to maturity, respectively. The genotype ICCV 211210 exhibited the highest PC score, succeeded by RVG-204 and ICCV 211206, implying their superior performance across traits including the number of secondary branches per plant, total number of pods per plant, number of effective pods per plant, biological yield, and seed yield per plant. The results were in align with the findings of Rafiq *et al.* (2020) for seed yield and pods per plant, Kumar *et al.* (2001) for grain yield per plant and biological yield, Jain *et al.* (2023) for number of pods per plant, Qulmamatova *et al.* (2023) for number of pods per plant and seed yield, Talekar *et al.* (2023) for branches per plant, pods per plant, and seed yield per plant. Similarly, current findings are also consistent with those of

Table 3. Total variability explained by principal components among the chickpea genotypes

Trait	Principal component (PC)	Eigenvalue	Variability (%)	Cumulative (%)
Days to 50% flowering	PC1	5.11	36.48	36.48
Days to maturity	PC2	2.23	15.91	52.39
Plant height (cm)	PC3	1.45	10.39	62.78
Height of first fruiting node (cm)	PC4	1.41	10.04	72.82
Stem thickness (mm)	PC5	1.11	7.92	80.74
Number of primary branches per plant	PC6	0.85	6.09	86.84
Number of secondary branches per plant	PC7	0.53	3.75	90.59
Total number of pods per plant	PC8	0.47	3.35	93.94
Number of effective pods per plant	PC9	0.34	2.43	96.37
Number of seeds per pod	PC10	0.25	1.79	98.16
Hundred seed weight (g)	PC11	0.15	1.11	99.26
Biological yield per plant (g)	PC12	0.09	0.63	99.89
Harvest index (%)	PC13	0.01	0.06	99.95
Seed yield per plant (g)	PC14	0.01	0.05	100.00

Table 4. Elucidation of significant trait association using rotated component matrix for traits in each principal component

	PC1	PC2	PC3	PC4	PC5
Traits	Number of secondary branches per plant	Plant height	Number of primary branches per plant	Plant height	Days to maturity
	Total number of pods per plant	Stem thickness	Number of seeds per pod		
	Number of effective pods per Plant	Hundred seed weight	Biological yield per plant		
	Biological yield per plant				
	Seed yield per plant				
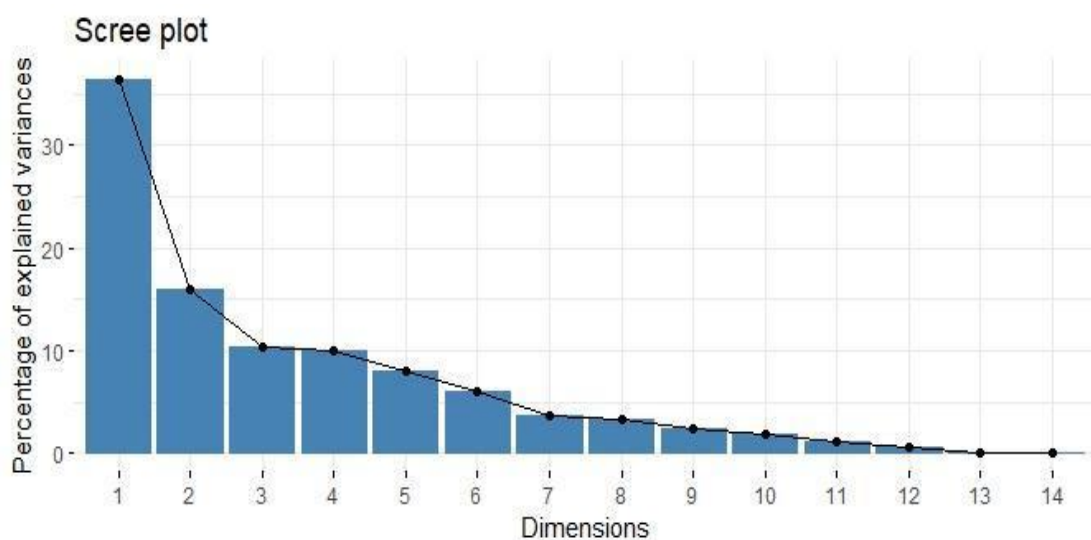
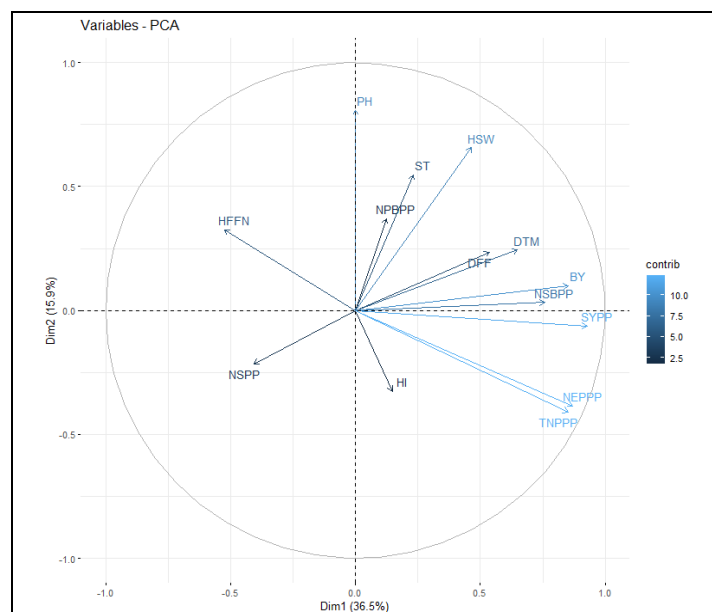**Fig. 2. Scree plots constructed based on fourteen principal components and their eigenvalues**

Fig. 3. Principal component analysis of variables

Samyuktha *et al.* (2017) and Vikram *et al.* (2023), where PC1 explained more variation for seed yield, number of secondary branches per plant, total number of pods per plant, effective pods per and plant biological yield per plant.

The results indicated significant variability among the chickpea genotypes for all the quantitative traits. Post hoc DMRT analysis further confirmed significant differences among the genotypes across all traits. Regression analysis and principal component analysis highlighted the importance of specific yield attributing traits, like number of secondary branches per plant, total number of pods per plant, number of effective pods per plant, and biological yield per plant, in explaining a significant portion of variability contributing to overall yield. Hence, prioritizing these key traits for strategic selection can facilitate the development of superior chickpea varieties with enhanced agronomic characteristics. The genotypes ICCV 211210, RVG-204 and ICCV 211206 were identified as promising and could be exploited in future breeding programs.

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