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Research Article

Exploration of potential donors for machine-amenable traits in desi chickpea (*Cicer arietinum* L.): towards enhancing agricultural automation and efficiency

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Abstract

The importance of machine-harvestable traits in chickpeas lies in their capacity to enhance and streamline the harvesting process. By employing machine harvesters, farmers can enjoy numerous advantages over manual harvesting, as it becomes a more efficient and economically viable option. With the aim of achieving this objective, a total of 36 desi chickpea genotypes were selected for a comprehensive study on genetic variability, correlation, and path coefficient analysis. The analysis of variance conducted on 12 distinct characters revealed significant variation, indicating the presence of diversity among these traits. Several traits exhibited significant variability with high PCV and GCV. The height of the first pod, plant height, and hundred seed weight displayed substantial heritability and genetic advance. Remarkably, hundred seed weight was the sole trait with high values of PCV, GCV, heritability, and genetic advance mean (GAM). Taller plants with higher first pod height (HOFP and PH) are associated with increased performance in traits like Plot Yield (PLYG), Harvest Index (HI), Hundred Seed Weight (HSW), Biological Yield (BY), and Number of Secondary Branches (NSB). Genotypic path analysis revealed that both the hundred seed weight and number of secondary branches demonstrated positive direct effects on the height of the first pod. Principal component analysis divided the traits into 12 PCs, where the first four PCs showed eigen values greater than 1 and are responsible for a cumulative variation of 82.9%. Notably, 17 genotypes exhibited a height of the first pod exceeding 30 cm, indicating their suitability for machine harvesting. The genotypes GL 15003, IPCB 2015-132, RVSSG-96, and IPC 2017-253 showed promise for developing machine-harvestable cultivars, based on their height of the first pod and yield attributes.

Keywords: chickpea, machine harvest, height of first pod, correlation, path analysis, variability

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a winter annual crop from the Leguminosae family, known for its high rate of self-pollination. It possesses a diploid chromosome count of 2x=2n=16 and a genome size of around 738 Mb (Varshney *et al*., 2013). It is an annual herb which does not grow more than 1.0 m in height and has an indeterminate growth habit. With ever-increasing production costs and labour displacement from agriculture to non-agricultural sectors, mechanization of maximum practices is essential. According to World Bank data, the agricultural industry employed around 62.56 percent of the workers in 1991, but has since declined to 41.49 percent in 2020. Women account for 53.6 percent of the entire workforce in the current labour force. (Anonymous, 2020). Traditionally, the plants are harvested by manually plucking them out of the ground and then mechanically threshing them. However, this approach has its own limitations, such as a lack of labourers during the harvesting season owing to high demand and the nitrogen-fixing nodules are lost while plucking out the plant, resulting in a loss of N-fixing bacteria in the soil (Golpira *et al.*,2013).

A comparative study in Maharashtra and Madhya Pradesh found that machine-harvested chickpea fields yielded Rs 989, while manually harvested ones yielded Rs. 1168 (Shilpa et al., 2017). Government initiatives like Submission on Agricultural Mechanization (SMAM) and custom hiring centers ensure access to machinery and skilled operators (Mehta et al., 2019). This underscores the growing need for machine-harvestable chickpea cultivars. In 2016, ANGRAU and ICRISAT collaborated to create the first such variety, NBeG 47 (Source: ICRISAT). To minimize harvest losses during machine harvesting, it's essential for machine-harvestable chickpea varieties to have increased height and upright growth, approximately 30-40% taller than current semi-erect types. Additionally, maintaining an optimal first pod height of 30 cm above the ground level is crucial (Sahu et al., 2019). Understanding the link between yield and its components is vital for enhancing crop productivity through strategic breeding. Success hinges on comprehending the relationship's direction, strength, and the relative importance of each contributing element (Adesoji et al., 2015). Investigating mechanical harvesting factors like plant height and first pod height's influence on grain yield provides valuable insights for potential use in cultivating new varieties.

MATERIALS AND METHODS

The study was conducted during the 2020-21 Rabi season at the Research and Instructional Farm, Genetics and Plant Breeding Department, College of Agriculture, Indira Gandhi Agricultural University, Raipur, Chhattisgarh. Chhattisgarh is located between latitudes 17°14'N and 24°45'N and longitudes 79°16' E and 84°15' E, at an elevation of around 289.60 meters above sea level. The highest monthly temperature in March 2021 was 39.6°C, and the lowest in December 2020 was 12.00°C. The cumulative rainfall during the crop production season was 16.00 mm. The study involved evaluating 36 chickpea genotypes (**Table 1**) using a randomized complete block design (RCBD) with three replications. Row and plant spacing were set at 22.5 cm and 10.0 cm, respectively, following standard agronomic practices. Thirteen traits were measured, including days to 50% flowering (DTF), days to maturity (DTM), height of the first pod (HOFP), plant height (PH), number of primary branches (NPB), number of secondary branches (NSB), number of seeds per pod (NSP), number of pods per plant (NPP), 100 seed weight (HSW), biological yield per plant (BY), harvest-index (%) (HI), and plot yield (PLYG) in grams. Mean values were used to calculate variability parameters like range, standard deviation, and coefficient of variation. ANOVA was conducted using OPSTAT software (Sheoran et al., 1998). Coefficient of variation for traits was calculated per Burton and De Vane's formula (1953) and categorized as higher (> 20%), moderate (10% - 20%), or low (<10%). Broad sense heritability was assessed as low, moderate, or high following Hanson et al.'s formula (1956) and Johnson et al.'s criteria (1955). Expected genetic advance (GA) was determined as per Johnson et al.'s approach (1955). Correlation analysis was performed using Miller et al.'s methodology (1958). Path analysis, introduced by Wright (1921) and applied by Dewey and Lu (1959), assessed direct and indirect effects of independent variables on a dependent variable. Interpretation followed Lenka and Mishra's scale (1973). Principal Component Analysis (PCA), a dimension reduction method by Massey (1965) and Jolliffie (1986), was used to condense variables while retaining information. PCA aided in reducing data dimensionality and gaining insights.

RESULTS AND DISCUSSION

The analysis of variance on twelve characters revealed significant mean sum of squares values for all the characters under consideration except for number of seeds per pod. This variability may be exploited and

Table 1. List of chickpea genotypes used in the study

S.No.	Genotypes	S.No.	Genotypes	S.No.	Genotypes
1	RSGD-7714	13	PhuleG191618	25	RKGM20-2
2	PBC582	14	RLBGMHG-3	26	GL117020
3	NBeG1267	15	ICCV191612	27	IPCB 2015-132
4	GL15003	16	RSGD-834	28	H 07-120
5	BG3062	17	JG 16	29	PhuleVikram
6	GJG1913	18	PG251	30	JG2020-57
7	BG4028	19	H 13-03	31	PBC574
8	IG2020-15	20	IPC2017-141	32	RVSSG-96
9	PG252	21	ICCV191608	33	BG4027
10	RKGM20-1	22	PhuleG191616	34	IPC2017-253
11	IG2020-16	23	PhuleG0405	35	RLBGMH-4
12	RVSSG-97	24	JG 24	36	GJG1916

used to enhance the genotypes. When individual genetic characteristics in a population have a predisposition to differ from one another, genetic variability is said to exist. This is the cornerstone for every breeding attempt. The minimum, maximum and mean values for the traits studied are elucidated in **Table 2.**

PCV and GCV are widely used methods to assess the extent of heritable and non-heritable variation in the studied material. The magnitudes of PCV were observed to be higher than those of GCV, indicating the significant influence of the environment in modifying the genotypic effects, consequently affecting the phenotypic outcomes. The detailed results can be found in **Table 3**. Traits such as the number of secondary branches, number of pods per plant, biological yield, hundred seed weight, and plot yield exhibited high PCV and GCV values, suggesting the presence of substantial variation suitable for selection. Overall, the results indicate that the estimations of phenotypic coefficient of variation surpass those of genotypic coefficient of variation which Ramanappa *et al*. (2013) also found in their findings in chickpea. This implies that the variance is caused not just by genes but also by the environment's effect on character expression. Similar findings were reported by Aswathi *et al*. (2019), Babbar *et al.* (2015), Basha *et al*. (2018), Parhe *et al*. (2014), Ramanappa *et al*. (2013) and Vishnu *et al*. (2018) for respective characters in chickpea.

Heritability measures the extent to which variation in a particular phenotypic characteristic within a population can be attributed to genetic diversity among individuals, as opposed to environmental factors. It allows us to determine the proportion of a trait's variation that is genetically influenced. Broad sense heritability is calculated by comparing the total genetic variance to the phenotypic variance.

Additionally, Genetic Advance as a percentage of Mean (GAM) quantifies the increase in the average genotypic value of selected plants over the parental population. By considering both heritability estimates and GAM, we can gain a more comprehensive understanding of the nature of gene action and the transmission of the studied trait to future generations. This approach provides greater insights compared to relying solely on either heritability estimates or GAM interpretations alone. A high heritability value in conjunction with a high GAM percent indicates additive gene activity, whereas a high heritability value in conjunction with a low GAM percent indicates non-additive gene action. High heritability were found for days to maturity, height of first pod, plant height, number of secondary branches, number of pods per plant, biological yield, hundred seed weight and plot yield. High GAM estimates were recorded for biological yield, number of pods per plant, hundred seed weight, number of secondary branches, plot yield, height of first pod, plant height, number of primary branches and harvest index. High heritability and genetic advance values indicate that the traits are ruled by additive genes, and the additive gene effects are most likely the cause of the high heritability. Selection for these characters in successive improvement efforts could be effective. The presence of non-additive gene activity on the characteristics is indicated by high heritability combined with low genetic advance values. The environmental factors, rather than the genotype,

Table 2. Genetic parameters of thirty-six genotypes for twelve yield and yield attributing and machine harvestable traits

Parameters	MSS	Mean	Min.	Max.	PCV (%)	GCV (%)	(h^2_{bs}) (%)	GAM (%)
DTF	135.13**	62.50	48.00	73.33	9.31	7.20	59.78	11.46
DTM	61.28**	104.52	94.67	111.33	4.36	4.31	97.34	8.75
HOFP	87.93**	29.41	20.93	39.00	20.31	17.35	73.08	30.59
PH	221.99**	55.80	41.47	69.13	16.12	15.05	87.12	28.94
NPB	0.41 **	2.00	1.00	3.00	19.33	15.72	66.14	26.33
NSB	20.21**	9.00	4.00	15.00	29.90	27.59	84.99	51.75
NSP	0.1	1.00	1.00	2.00	18.31	12.85	49.22	18.57
NPP	544.22**	39.00	21.00	72.00	35.89	33.78	88.55	65.48
BY	139.38**	17.67	8.27	34.93	40.25	37.71	87.79	72.79
HI	172.68**	48.16	25.88	59.54	17.56	14.76	70.69	25.57
HSW	125.17**	23.34	10.67	35.33	28.49	27.25	87.76	52.20
PLYG	61679.19**	539.29	59.33	876.00	28.89	25.31	76.70	45.66

PCV = Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation; (h^2_{bs})(%) = Heritability in broad sense; GAM = Genetic advance as per cent of mean; DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1st pod (cm); PH = Plant height (cm); NPB = Number of primary branches; NSB = Number of secondary branches; NPP=Numberof pods/ plant; NSP = Number of seeds/ pod; BY = Biological yield (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG = Plot yield (g).

were responsible for the high heritability. Findings by Ramanappa *et al*. (2013), Vishnu *et al*. (2018), Puri *et al*. (2013), Malik *et al*. (2014), Hagos *et al*. (2018) and Biru *et al*. (2017) corroborate similar results in chickpea.

Correlation analysis is used to determine the degree of association between two variables, such as a complicated character and an associated attribute, as well as the direction of change. It suggests an approach for choosing and developing certain linked traits in order to improve a complex attribute such as seed yield. Correlation studies assist in understanding yield components and the influence of other variables on the same (Robinson *et al*., 1951 and Johnson *et al*., 1955). The traits, days to flowering, days to maturity and number of secondary branches, represented negative whereas, harvest index and hundred seed weight positive relationship with plot yield. Similarly, height of first pod, plant height, biological yield and harvest index showed positive association with hundred seed weight and traits namely, plant height and hundred seed weight exhibited positive relation with height of first pod and number of pods per plant showed negative association (**Fig. 1**). For different traits tested, Sharma *et al*. (2019), Jha and Shil, (2015), Biabani *et al.* (2011), Ali and Naveed (2012), Kerketta *et al.* (2018), Yucel and Anlarsal (2010), and Babbar *et al.* (2015) revealed comparable findings. Path analysis provides information on how a component trait influences the dependent trait, both directly and indirectly. This indicates whether the relation with the dependent trait is due to a direct influence of the component trait or an indirect effect *via* other component characteristics. The residual effect sheds light on other key features that were not investigated in this study and their effects on the dependent variable. Biological yield followed by harvest index and hundred seed weight exhibited moderate direct effect on plot yield phenotypically and the traits also possessed significant association with the plot yield (**Table 3**). When height of first pod was taken into consideration, plant height showed high direct effect on the trait followed by moderate effects by biological yield and hundred seed weight showed moderate direct effect on height of first pod (**Table 4**).

The eigenvalues represent the amount of variance explained by each principal component. Higher eigenvalues indicate that the corresponding principal component captures more variability in the data. Based on the eigenvalues, the first four principal components (PC1, PC2, PC3, PC4) have eigenvalues >1 (**Table 5**) (**Fig. 2**). These first four components explain a significant amount of the total variance in the data. The first principal component (PC1) explains the highest variance with a proportion of 31.6%, indicating it captures the most substantial variation, followed by PC2 (22.7%), PC3 (20.3%), and PC4 (8.4%). These four PCs cumulatively explain 82.9% of the total variance present. The first principal component (PC1) exhibits high positive loadings for variables such as Biological Yield, Plant Yield, and No. of pods per plant

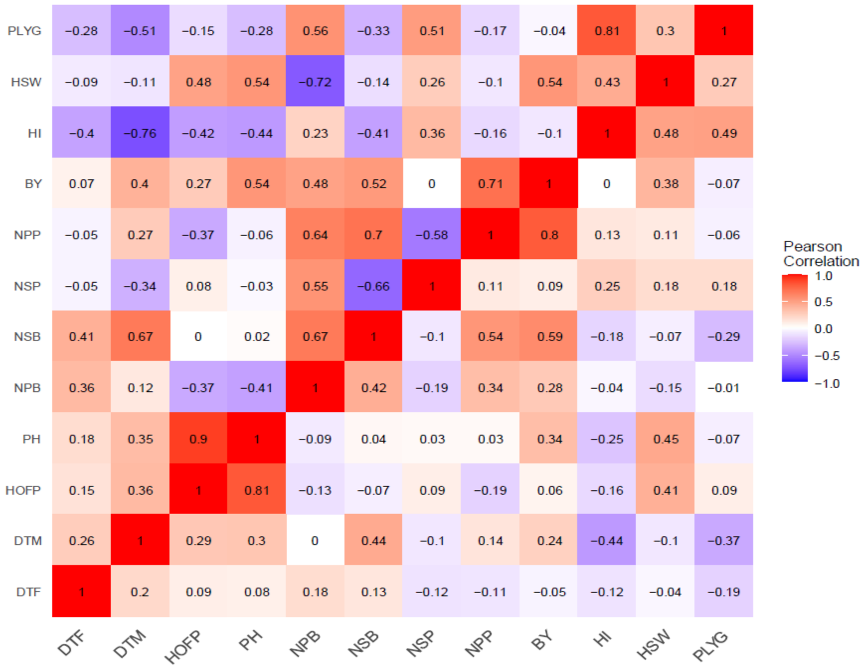

Fig. 1. Correlation heat map of plot yield, hundred seed weight and height of first pod and other yield and yield attributing traits

Upper diagonal = genotypic correlation and lower diagonal = phenotypic correlation

Table 3. Genotypic direct and indirect effects of yield, yield attributing and machine harvestable traits on plot yield (g) as dependent trait

Traits	DTF	DTM	HOFP	PH	NPB	NSB	NSP	NPP	BY	HI	HSW	Genotypic correlationwith PLYG
DTF	**-0.22**	-0.10	-0.01	0.12	-0.05	0.40	0.01	0.06	0.13	-0.67	0.13	-0.283**
DTM	-0.06	**-0.40**	-0.02	0.23	-0.02	0.65	0.07	-0.35	0.70	-1.26	0.16	-0.511**
HOFP	-0.03	-0.14	**-0.06**	0.60	0.06	0.00	-0.02	0.47	0.47	-0.69	-0.71	-0.154
PH	-0.04	-0.14	-0.06	**0.67**	0.06	0.02	0.01	0.08	0.94	-0.72	-0.78	-0.277**
NPB	-0.08	-0.05	0.02	-0.28	**-0.15**	1.61	-0.11	-2.07	0.83	0.39	1.05	0.555**
NSB	-0.09	-0.27	0.00	0.01	-0.24	**0.96**	0.13	-0.89	0.90	-0.68	0.21	-0.331**
NSP	0.01	0.14	-0.01	-0.02	-0.08	-0.63	**-0.20**	0.73	0.01	0.60	-0.38	0.512**
NPP	0.01	-0.11	0.02	-0.04	-0.24	0.68	0.12	**-1.26**	1.22	-0.27	0.14	-0.17
BY	-0.02	-0.16	-0.02	0.36	-0.07	0.51	0.00	-0.89	**1.72**	-0.16	-0.79	-0.04
HI	0.09	0.30	0.03	-0.29	-0.03	-0.40	-0.07	0.20	-0.16	**1.65**	-0.62	0.808**
HSW	0.02	0.04	-0.03	0.36	0.11	-0.14	-0.05	0.12	0.93	0.71	**-1.46**	0.303**

Residual: 0.072

Bold figures are direct effects and un-bold figures are indirect effects

DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1st pod (cm); PH = Plant height (cm); NPB = Number of primary branches; NSB = Number of secondary branches; NPP=Number of pods/ plant; NSP = Number of seeds/ pod; BY = Biological yield (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG = Plot yield (g).

Table 4. Genotypic direct and indirect effects on yield, yield attributing and machine harvestable traits on 1st pod height (cm) as dependant trait

Traits	DTF	DTM	PH	NPB	NSB	NSP	NPP	BY	HI	HSW	PLYG	Genotypic correlationwith HOFP
DTF	**-0.72**	-0.20	0.11	0.09	0.57	-0.04	-0.03	-0.15	0.73	-0.22	0.07	0.154
DTM	-0.19	**-0.77**	0.22	0.03	0.93	-0.27	0.16	-0.82	1.38	-0.27	0.12	0.358**
HOFP	-0.13	-0.27	**0.64**	-0.10	0.03	-0.02	-0.04	-1.11	0.79	1.28	0.06	0.896**
PH	-0.26	-0.09	-0.26	**0.25**	2.31	0.43	0.97	-0.98	-0.43	-1.72	-0.13	-0.374**
NPB	-0.30	-0.52	0.01	0.42	**1.38**	-0.51	0.42	-1.07	0.74	-0.35	0.08	0.004
NSB	0.04	0.26	-0.02	0.14	-0.91	**0.78**	-0.34	-0.01	-0.66	0.63	-0.12	0.077
NSP	0.03	-0.21	-0.04	0.42	0.97	-0.45	**0.59**	-1.44	0.29	-0.23	0.04	-0.374**
NPP	-0.05	-0.31	0.35	0.12	0.73	0.00	0.42	**-2.04**	0.17	1.29	0.01	0.270**
BY	0.29	0.58	-0.28	0.06	-0.57	0.28	-0.10	0.19	**-1.81**	1.02	-0.19	-0.418**
HI	0.07	0.09	0.34	-0.18	-0.20	0.21	-0.06	-1.10	-0.77	**2.39**	-0.07	0.484**
HSW	0.20	0.39	-0.18	0.14	-0.46	0.40	-0.10	0.07	-1.46	0.73	**-0.23**	-0.154

Residual: 0.263

Bold figures are direct effects and un-bold figures are indirect effects

DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1st pod (cm); PH = Plant height (cm); NPB = Number of primary branches; NSB = Number of secondary branches; NPP=Number of pods/ plant; NSP = Number of seeds/ pod; BY = Biological yield (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG = Plot yield (g).

Table 5. Eigen values for PCs for yield, yield attributing and machine harvestable traits of chickpea

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
Eigen Values	3.795	2.719	2.434	1.004	0.758	0.637	0.224	0.147	0.138	0.076	0.056	0.012
Proportion	0.316	0.227	0.203	0.084	0.063	0.053	0.019	0.012	0.012	0.006	0.005	0.001
Cumulative	0.316	0.543	0.746	0.829	0.893	0.946	0.964	0.977	0.988	0.994	0.999	1.000

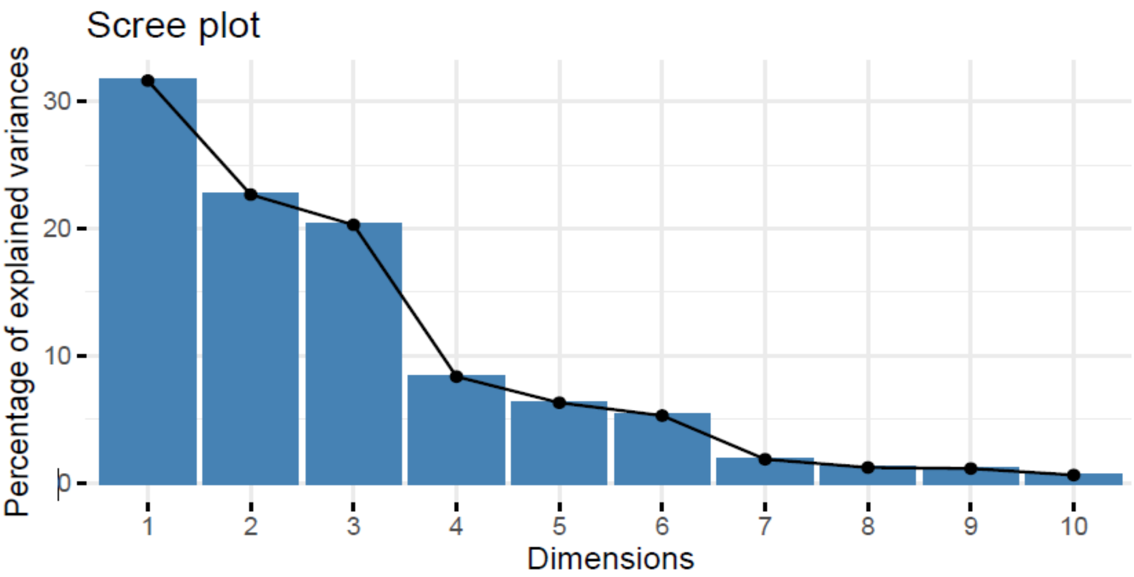

Fig. 2. Screeplot showing significant PCs

(**Table 6**). This indicates that PC1 represents a composite measure of overall plant productivity and yield-related characteristics. It likely captures the main variations in yield-related traits among the plant samples. The second principal component (PC2) has high positive loadings for Harvest Index and 100 seed weight, while showing negative loadings for No. of secondary branches. This suggests that PC2 represents a combination of traits related to seed production and seed weight, possibly indicating that plants with higher seed weights and better harvest index tend to have fewer secondary branches. The third principal component (PC3) shows significant positive loadings for 1st pod height and Plant height. This implies that PC3 represents traits related to plant height. Plants with higher 1st pod height are likely to be taller, and this component helps distinguish between plants with varying heights. The fourth principal component (PC4) exhibits a high negative loading for Days to maturity. This suggests that PC4 captures traits associated with early maturity. Plants with a shorter time to reach maturity are likely to have more negative values along PC4. In the biplot's vector representation, each trait is depicted as a vector extending from the origin of the biplot. This visual representation facilitates the interpretation of relationships between the traits (Kang and Yan, 2002). When the biplot effectively explains a significant portion of the overall variation, the correlation coefficient between any two traits can be approximated using the cosine of the angle

Table 6. Component matrix

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
DTF	0.20	-0.43	0.08	-0.42	0.06	-0.34	0.10	0.66	0.03	-0.12	0.10	-0.03
DTM	0.30	-0.32	0.26	-0.20	0.27	-0.13	-0.59	-0.45	0.22	0.12	0.00	0.04
HOFP	0.12	0.11	0.56	0.04	-0.32	-0.16	-0.10	0.01	-0.43	-0.31	-0.48	0.08
PH	0.23	0.18	0.50	0.18	-0.17	0.16	-0.05	0.20	-0.11	0.41	0.59	-0.05
NPB	0.23	-0.11	-0.30	0.17	-0.79	-0.21	-0.19	-0.02	0.34	-0.02	0.04	0.02
NSB	0.41	-0.23	-0.14	-0.01	-0.02	-0.26	0.55	-0.46	-0.38	0.13	0.13	-0.01
NSP	0.39	0.05	-0.32	0.04	0.10	0.36	-0.31	0.07	-0.35	-0.54	0.29	0.03
NPP	-0.05	0.23	0.02	-0.83	-0.32	0.30	0.07	-0.20	-0.01	0.01	0.07	-0.05
BY	0.46	0.20	-0.04	-0.03	0.11	0.22	0.17	0.16	0.24	0.20	-0.30	0.66
HI	0.42	0.30	-0.16	-0.02	0.11	0.00	-0.07	0.15	0.02	0.25	-0.37	-0.68
HSW	-0.12	0.41	-0.30	-0.16	0.06	-0.54	-0.34	0.08	-0.36	0.27	0.11	0.27
PLYG	0.14	0.50	0.18	-0.01	0.16	-0.38	0.21	-0.14	0.43	-0.46	0.25	-0.06

DTF = Days to 50% flowering; DTM = Days to maturity; HOFP = Height of 1st pod (cm); PH = Plant height (cm); NPB = Number of primary branches; NSB = Number of secondary branches; NPP=Number of pods/ plant; NSP = Number of seeds/ pod; BY = Biological yield (g); HI = Harvest index (%); HSW = Hundred seed weight (g); PLYG = Plot yield (g).

Table 7. Top fifteen genotypes with height of 1st pod more than 30 cm and high yield

S. NO.	Genotype	HOFP	S. NO.	Genotype	PLYG
34	IPC 2017-253	39.00	6	GJG 1913	876.00
24	**JG 24**	**38.40**	17	JG 16	750.33
15	ICCV 191612	38.13	**31**	**PBC 574**	**719.33**
13	Phule G 191618	37.47	2	PBC 582	718.00
36	**GJG 1916**	**36.40**	**36**	**GJG 1916**	**705.33**
21	ICCV 191608	34.93	**24**	**JG 24**	**650.67**
35	**RLBGMH-4**	**34.87**	1	RSGD-7714	646.33
8	**IG 2020-15**	**34.60**	25	RKGM 20-2	646.33
20	IPC 2017-141	33.73	**35**	**RLBGMH-4**	**633.00**
27	IPCB 2015-132	33.47	16	RSGD-834	628.67
12	RVSSG-97	32.93	**8**	**IG 2020-15**	**605.00**
26	GL 117020	32.93	30	JG 2020-57	605.00
28	H 07-120	32.00	**22**	**Phule G 191616**	**587.67**
31	**PBC 574**	**31.93**	10	RKGM 20-1	581.33
22	**Phule G 191616**	**31.87**	19	H 13-03	562.00

Fig. 3. PC_1 vs PC_2 biplot for 36 chickpea genotypes

between their respective vectors (Yan and Rajcan, 2002). If the angle between the vectors is less than 90°, the two traits are positively correlated; if the angle is greater than 90°, they are negatively correlated, and if the angle is exactly 90°, the two traits are independent of each other. Based on the biplot (**Fig. 3**) we can interpret that plant yield is positively correlated with plant height, biological yield, height of first pod, 100 seed weight, harvest index, number of seeds per pod and number of pods per plant. The scattering of the genotypes on the matrix across the quadrants shows the diversity present amongst the genotypes.

From the results, it can be concluded that the trait, height of first pod/node is of utmost importance as it tells the usage of combine harvester for harvesting of chickpea crop. In the present study, there were six promising genotypes *viz*. JG 24, IG 2020-15, RLBGMH-4, PBC 574, GJG 1916 and Phule G 191616 which yielded high along with a hike in height of first pod.

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