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RESEARCH ARTICLE

Identification and morphological characterization of promising kabuli chickpea genotypes for short-season environment in central India

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Abstract. Chickpea (*Cicer arietinum* L.) is an important food legume crop grown in arid and semi-arid regions of the world. In India, kabuli chickpea is grown in central India in ~0.5 million ha, predominantly under short winter (< 110 days). Efforts are underway to select promising genotypes at the Food Legume Research Platform (FLRP), Amlaha, located in intensive kabuli chickpea growing area of India. Sixty-four kabuli chickpea lines were evaluated for agronomic traits during 2017–2018 and 2018–2019 crop seasons at FLRP following simple 8 × 8 lattice design with two replications. The analysis of variance over two years revealed significant variation exists for days to flowering, plant height, maturity period, biomass, seed size and seed yield. It was observed that with similar maturity time (106 days), FLIP09-432C produced 2273 kg/ha, which out-yielded the popular variety in central India, JGK-3 by 15%. The breeding lines, FLIP09-436C, FLIP09-171C, FLIP09-373C and FLIP09-247C were also found promising for earliness (104–110 days), and high yielding with the good yield ability (1003–2273 kg/ha). These promising genotypes for a short duration with good yield have been selected and can be used for various chickpea breeding programmes to develop high yielding varieties in central India.

Keywords. kabuli chickpea; phenotyping; early maturing; yield; genetic variability.

Introduction

Chickpea (*Cicer arietinum* L.; family: Fabaceae) is a self-pollinated and diploid (2*n*=16), cool-season pulse crop with a genome size ~738 Mb and an estimated 28,269 genes (Varshney *et al.* 2013). Chickpea is grown in more than 50 countries which represents all the continents (Upadhyay *et al.* 2011; Gaur *et al.* 2012). India and Ethiopia are the secondary centres of diversity of cultivated chickpea (Harlan 1992). It is the most important food legume crop, grown in tropical, sub-tropical and temperate regions (Mohammed *et al.* 2017). Globally chickpea growing area is recorded as 14.56 million ha with an annual production of 14.78 million tons (FAOSTAT 2017). The narrow genetic base among cultivated chickpea accessions due to repeatedly using of some varieties is limiting the genetic improvement of chickpea through the breeding efforts (Bharadwaj *et al.* 2011a). Sixty-four lines were selected based on agronomic traits from different chick pea nurseries received from ICARDA and evaluated for two years 2017–18 and 2018–19 at the Food Legume Research platform-ICARDA, Amlaha, India. Increase in grain yield potential is the major goal of almost all breeding programmes and most of the success in breeding of high yielding crops has been achieved through selections and further used in hybridization programmes to increase the yield (Qureshi *et al.* 2004). Adaptation of the crop to the existing environments and development of lines for new environments where chickpea would be grown in future can also be accomplished through hybridization between selected germplasm lines (Roberts *et al.* 1980). The objective of the present study was to evaluate new chickpea lines for genetic variability, for qualitative and quantitative traits and to find new lines as a donor for the hybridization programmes.

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Materials and methods

Sixty-four lines were selected based on agronomic traits from different chickpea nurseries received from ICARDA and evaluated for two years 2016–2017 and 2017–2018 at the Food Legume Research Platform-ICARDA, Amlaha, India (table 1). Each genotype was grown in four rows of 4 m length with 45 cm spacing between rows in simple lattice design (8 × 8). The established agronomic practices were followed during the crop season for proper crop growth. The crop was maintained free from weeds, diseases, and pests by applying appropriate plant protection measures. To estimate the amount of genetic variability among the genotypes, observations were made on five randomly selected plants of each genotype in each replication.

All the data were taken for quantitative characters such as days to flowering (DTF), days to maturity (DTM), plant height (PH), biomass (g), 100 seed weight, yield (g) and for the harvest index. The time (days) taken by a genotype from sowing to the stage was recorded as days to flowering and days to maturity. Days to flowering were recorded at the stage when 50% of the plants had flowered. Days to maturity was recorded when 90% of the plot was ready to harvest. Plant height was recorded from the soil surface until the top of the plant at the time of maturity. Harvested material was weighed for total biomass then were threshed and grains were separated and weighed. Harvest index was calculated according to the formula: harvest index (%) = grain yield / biomass yield × 100. Seed yield was taken from the specified area harvested and 100 seed weight was taken from the hundred random seeds and weighed in gram. The means of all the quantitative characters were subjected to statistical analysis using CROP-STAT (v. 8.5) statistical package. Pearson's correlation matrix among the traits was generated by employing GenSTAT v. 16.1. The factorial and clusters analysis based on morphological traits was done by using DARwin5 software 5.0.158.

Results

Morphological observations

Significant morphological variation was observed for most of the investigated characters. Range, mean, variation, standard deviation and coefficient of variation were highly significant for all the characters studied in the genotypes (tables 1 & 2). Days to flowering ranged from 60–90 days with a mean of 75 days. Standard deviation was 8.57 and coefficient of variation was 11.37% for the genotypes under investigation. Similarly, plant height ranged from 46–77 cm with a mean of 59.53 cm, standard deviation was 7.39 and the coefficient of variation was 12.41%. Days to maturity ranged between 104 and 124 days with a mean of 114.46 days, standard deviation was 7.21 and the coefficient of variation was 6.30%, biomass ranged from 800–2050 g with the mean of 1428 g. Standard deviation was 352.75 and the coefficient of variation was 24.70%. Yield varied from 168–1250 g with a mean of 561 g. Standard deviation was 244.22 and the coefficient of variation was 43.52% (figure 1). 100-seed weight ranges from 22–42 g, with a mean of 30.61 g. Standard deviation was 4.49 with the coefficient of variation of 14.45%. Harvest index ranges from 19–92% with a mean of 38.08%. Standard deviation was 11.38 with the coefficient of variation of 29.88%.

Pearson's correlation among the traits

Pearson's correlation matrix clearly shows that days to maturity was positive and significantly correlated with days to flowering. Biomass is negative and significantly correlated to days to flowering and with days to maturity. Yield is negative and significantly correlated to days to flowering and with days to maturity which means that if the genotype matures late it will produce less. Also, the yield is positive and significantly correlated with biomass. 100-seed weight was positive and significantly correlated with days to flowering, plant height and days to maturity but negatively correlated with biomass and plot yield. Harvest index was positive and significantly correlated with the biomass and plot yield (table 3).

Dendrogram generated from an unweighted pair group method analysis (UPGMA) for all the morphological characters

The means of all the quantitative characters were statistically analysed and Euclidean distances were calculated for all the morphological characters and the genotypes were grouped as per their characters (figure 2). Two distinct groups (A and B) are formed. The group A was fruther divided into two subgroups (group-AI and AII) showing most early and high yielding genotypes including JGK3 (check) (table 4). Group B containing groups BI and BII are having lines differing from the group A based on morphological characters such as days to flowering, days to maturity, plant height, biomass, 100-seed weight and plot yield.

Principal component analysis (PCoA) for morphological characters

A data matrix plot based on all the morphological characters was subjected to PCoA for estimating the genetic differentiation among the 64 genotypes of chickpea. The scatter plot based on these components disclosed a pattern of mainly two groups which are distinctively separated based on yield and maturity. The plot showed that the high yielding genotypes make a group with JGK3 which were high yielding as well as early maturing genotype (figure 3).

Table 1. List of 64 ICARDA chickpea genotype under study.

	Entry name	Pedigree
1	FLIP09-16C	X06TH57/FLIP97-110XFLIP02-36
2	FLIP09-229C	S00794(30 KR)-13
3	FLIP07-228C	X02TH97/FLIP98-130C X Sel01ter 73613.
4	FLIP09-62C	X04TH202/FLIP 84-182 XFLIP 98-229
5	FLIP09-328C	X05TH96/FLIP02-36CXFLIP00-17
6	FLIP09-104C	X05TH99/FLIP02-41CXFLIP97-85
7	FLIP09-222C	S00789(30 KR)-19
8	FLIP09-361C	X06TH113/FLIP03-138XFLIP03-80
9	FLIP09-373C	S00789(30 KR)-18
10	FLIP09-308C	X04TH164/FLIP 87-59CXFLIP99-34
11	FLIP09-406C	X04TH180/FLIP97-205XFLIP97-229
12	FLIP09-432C	X04TH179/FLIP97-165XFLIP97-205
13	FLIP09-247C	S00789(45 KR)-35
14	FLIP09-369C	X06TH75/SelTH10099XFLIP03-120
15	FLIP09-381C	S00789(30 KR)-9
16	FLIP09-199C	X06TH61/FLIP98-128XFLIP00-65
17	FLIP09-250C	S01135(30 KR)-11
18	FLIP09-401C	X04TH139/FLIP98-106XFLIP95-68
19	FLIP09-304C	X04TH159/S01230XFLIP98-230
20	FLIP88-85C	X85 TH143/ILC 629 x FLIP 82-144C
21	FLIP09-122C	X05TH130/FLIP98-16XFLIP98-178
22	FLIP09-133C	X05TH139/FLIP00-14XSel03TH6296
23	FLIP09-436C	X06TH49/FLIP02-28XFLIP00-70
24	FLIP09-346C	X06TH2/X05TH83XFLIP02-84
25	FLIP09-112C	X05TH115/FLIP98-131XFLIP00-17
26	FLIP09-337C	S00789(30 KR)-18
27	FLIP09-171C	X06TH13/X05TH142XT.market
28	FLIP09-422C	X04TH126/FLIP98-229XFLIP96-154
29	FLIP09-326C	X05TH96/FLIP02-36CXFLIP00-17
30	FLIP09-347C	X06TH9/X05TH114XFLIP03-138
31	FLIP07-254C	X03TH157/FLIP97-220CXFLIP97-217C
32	FLIP07-126C	X03TH-58/[FLIP 98- 28C X (RETI) sel01th 12124]XFLIP 98-22C
33	FLIP07-260C	X03TH176/FLIP98-130CXLmarket
34	FLIP07-6C	X03TH51/(S00787Xsel01ter73616)XFLIP98-22C
35	FLIP07-322C	X03TH153/FLIP98-133CXFLIP98-117C
36	FLIP07-218C	X03TH-154/FLIP 97-185CXFLIP98-200C
37	FLIP08-257C	X03TH146/FLIP98-130CXFLIP 97-25C
38	FLIP09-308C	X04TH164/FLIP 87-59CXFLIP99-34
39	FLIP09-287C	X04TH144/FLIP00-10XFLIP97-229
40	FLIP09-181C	X06TH53/FLIP03-128XFLIP01-25
41	FLIP09-301C	X04TH157/S01227XFLIP98-137
42	FLIP07-220C	X03TH156/FLIP98-128CXFLIP 97-118C
43	FLIP09-214C	X06TH80/ILC10766XFLIP03-110
44	FLIP07-280C	X03TH27/(S00879 XFLIP97-25C)XICCV2
45	FLIP08-200C	X03TH-147/FLIP 97-131CXFLIP 97-26C
46	FLIP07-261C	X03TH182/FLIP98-133CXLmarket
47	FLIP09-191C	X06TH54/FLIP03-138XFLIP01-26
48	FLIP03-77C	X00TH 28/FLIP98-15CXS98588
49	ILC482	Long term check
50	FLIP09-194C	X06TH55/FLIP03-73XFLIP01-29
51	FLIP07-335C	X02TH 5/FLIP98-130C X FLIP97-219C
52	FLIP07-63C	X03TH20/(S00784 X FLIP 97-281C)XICCV2
53	FLIP07-70C	X03TH21/(S00791 X FLIP 98- 023C)XICCV2
54	FLIP05-80C	X2000TH 17/FLIP97-25CXS98588
55	FLIP08-72C	X03TH146/FLIP98-130CXFLIP97-25C
56	FLIP09-220C	S00789(30 KR)-5
57	FLIP93-93C	X89TH258/ (FLIP 85-122CXFLIP 82-150C)XFLIP 86-77C
58	FLIP07-183C	X03TH-138/FLIP98-130CXFLIP99-34C
59	FLIP08-254C	X01TH14/(FLIP97-28CXFLIP98-129C)XS99569
60	FLIP09-290C	X04TH147/FLIP00-17XFLIP98-230

Table 1. *(contd)*

	Entry name	Pedigree
61	FLIP09-294C	X04TH147/FLIP00-17XFLIP98-230
62	FLIP06-19C	X2002TH 21/S00787 X FLIP97-261C
63	FLIP07-187C	X03TH-146/FLIP98-130CXFLIP 97-25C
64	JGK-3	LOCAL CHECK

Table 2. Range, mean, standard deviation and coefficient of variation of the genotypes.

	DTF (days)	PH (cm)	MAT (days)	BIOM (g)	YLD (g)	100 SW (g)	HI
Range	60–90	46–77	104–124	800–2050	168–1250	22–42	19–92
Mean	75.42	59.53	114.46	1428.13	561.13	30.61	38.08
SD	8.57	7.39	7.21	352.75	244.22	4.49	11.38
CV (%)	11.37	12.41	6.30	24.70	43.52	14.45	29.88

DTF, days to flowering; PH, plant height; MAT, days to maturity; BIOM, biomass; YLD, plot yield; 100 SW, hundred seed weight; HI, harvest index.

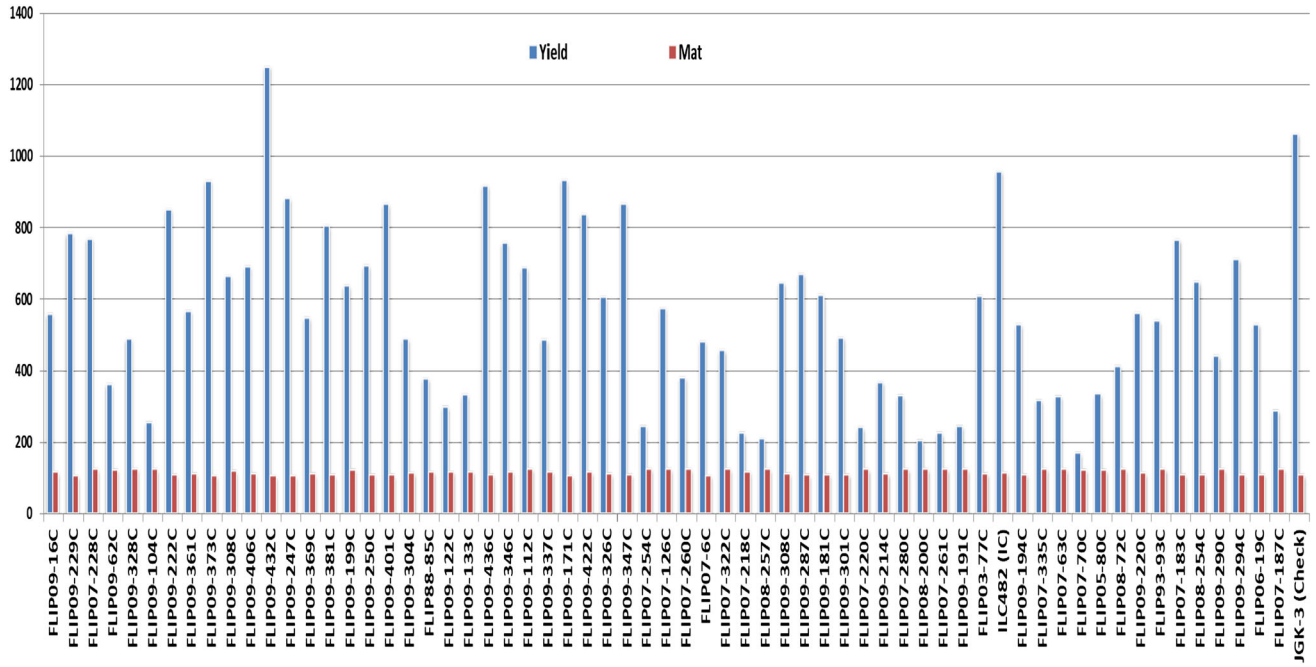

Figure 1. Graphical representation of the early and high yielding genotypes with the comparison of check.

Table 3. Pearson's correlation matrix among the traits under observation.

	DTF	PH	MAT	BIOM	YLD	100 SW	HI
DTF	1						
PH	0.297	1					
MAT	0.701**	0.237	1				
Biomass	−0.355**	0.125	− 0.346**	1			
Yield	−0.578**	0.006	− 0.599**	0.815**	1		
100 SW	0.356**	0.289**	0.416**	− 0.274*	− 0.389*	1	
HI	0.249	0.364	0.253	0.451*	0.589**	0.235	1

*And ** is the significance at 5% and 1%, respectively; DTF, days to flowering; PH, plant height; MAT, days to maturity; BIOM, biomass; YLD, plot yield; 100 SW, hundred seed weight; HI, harvest index.

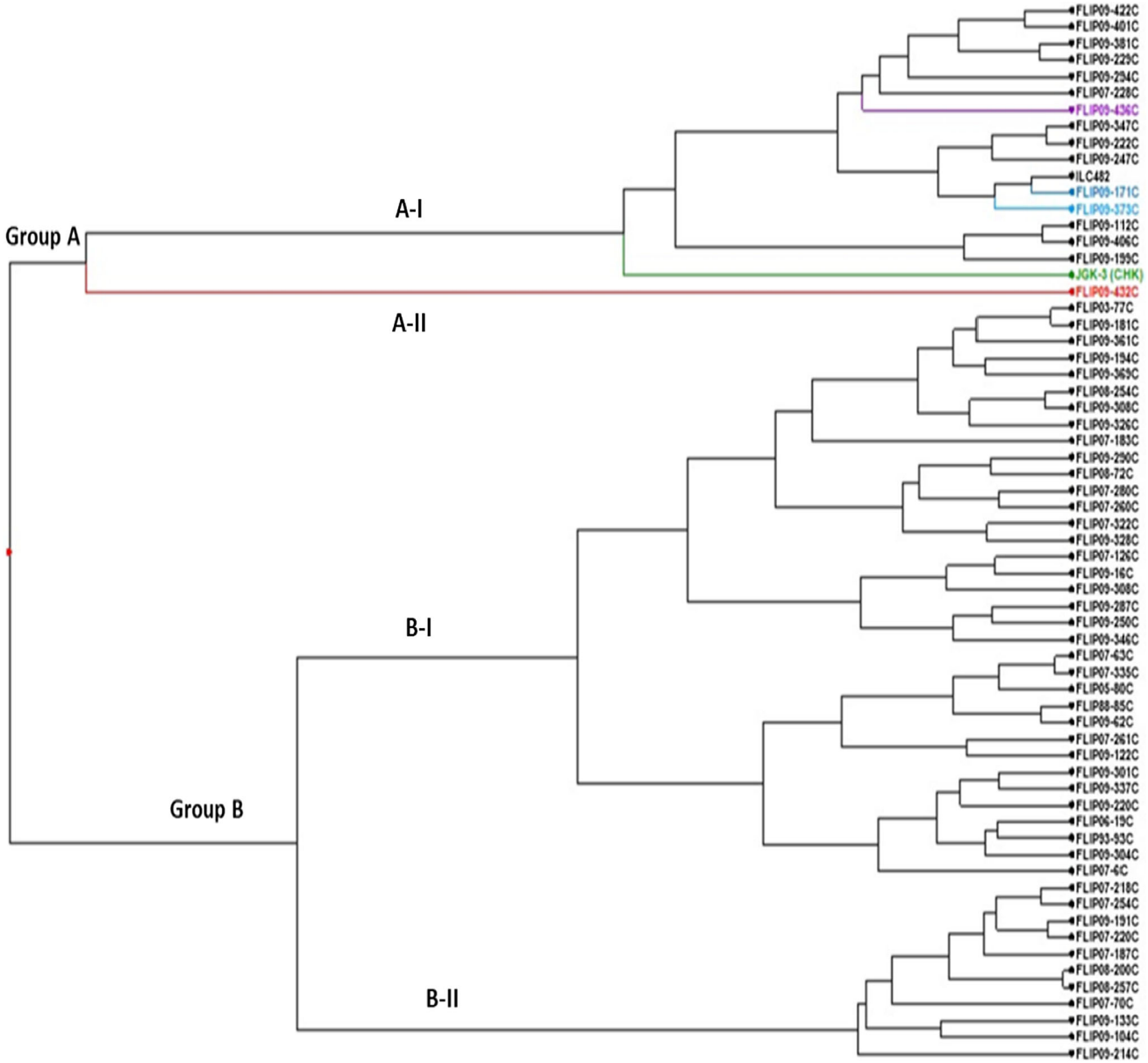

Figure 2. Dendrogram generated from an unweighted pair group method analysis (UPGMA) cluster analysis based on all the morphological characters under study. First two clusters form group A, shows all early and high yielding genotypes.

Discussion

Earlier chickpea was mainly cultivated in the northern part of India, where the cropping season is long and cool. Due to the long and cool cropping season, the crop is vulnerably susceptible to many biotic and abiotic stresses which constraint chickpea production and productivity in northern India. In contrary, the duration for chickpea cultivation is very short in the central and southern parts of India. During its reproduction stage, the crop becomes vulnerable to drought and terminal heat stress which ultimately affetcs its seed yield and productivity. Chickpea crop suffers heavy yield losses up to 40–50% due to drought and terminal heat as it is largely grown under rainfed restricted irrigated conditions on residual soil moisture (Toker and Cagirgan 1998; Leport *et al.* 1999).

Significant variation was observed for most of the investigated characters. It is concluded from the results that FLIP09-432C out-yielded the check JGK-3 which is a well-known early maturing and high yielding variety in the central zone of India. The other genotypes FLIP09-436C, FLIP09-171C, FLIP09-373C and FLIP09-247C were also found promising for earliness combined with high yield. Previous studies in chickpea have also reported a positive and significant correlation of seed yield with biomass yield, days to maturity and harvest index (Ahmad et al.2012; Padmavathi

Table 4. Clustering based on UPGMA for all the morphological characters.

Major cluster	Minor cluster	Number of genotypes	Name of genotypes
Group A	A-I	17	FLIP09-422C, 401C, 381C, 229C, 294C, FLIP07-228C, FLIP09-436C, 347C, 222C, 247C, ILC482, FLIP09-171C, 373C, 112C, 406C, 199C and JGK3
	A-II	01	FLIP09-432C
Group B	B-I	35	FLIP09-77C, 181C, 361C, 194C, 369C, FLIP08-254C, FLIP09-308C, 326C, FLIP07-183C, FLIP09-290C, FLIP08-72C, FLIP0-280C, 260C, 322C, FLIP09-328C, FLIP07-126C, FLIP09-16C, 308C, 287C, 250C, 346C, FLIP07-63C, 335C, FLIP05-80C, FLIP88-85C, FLIP09-62C, FLIP07-261C, FLIP09-122C, 301C, 337C, 220C, FLIP06-19C, FLIP93-93C, FLIP09-304C, FLIP07-6C
	B-II	11	FLIP07-218C, 254C, FLIP09-191C, FLIP07-220C, 187C, FLIP08-200C, 257C, FLIP07-70C, FLIP09-133C, 104, 214C

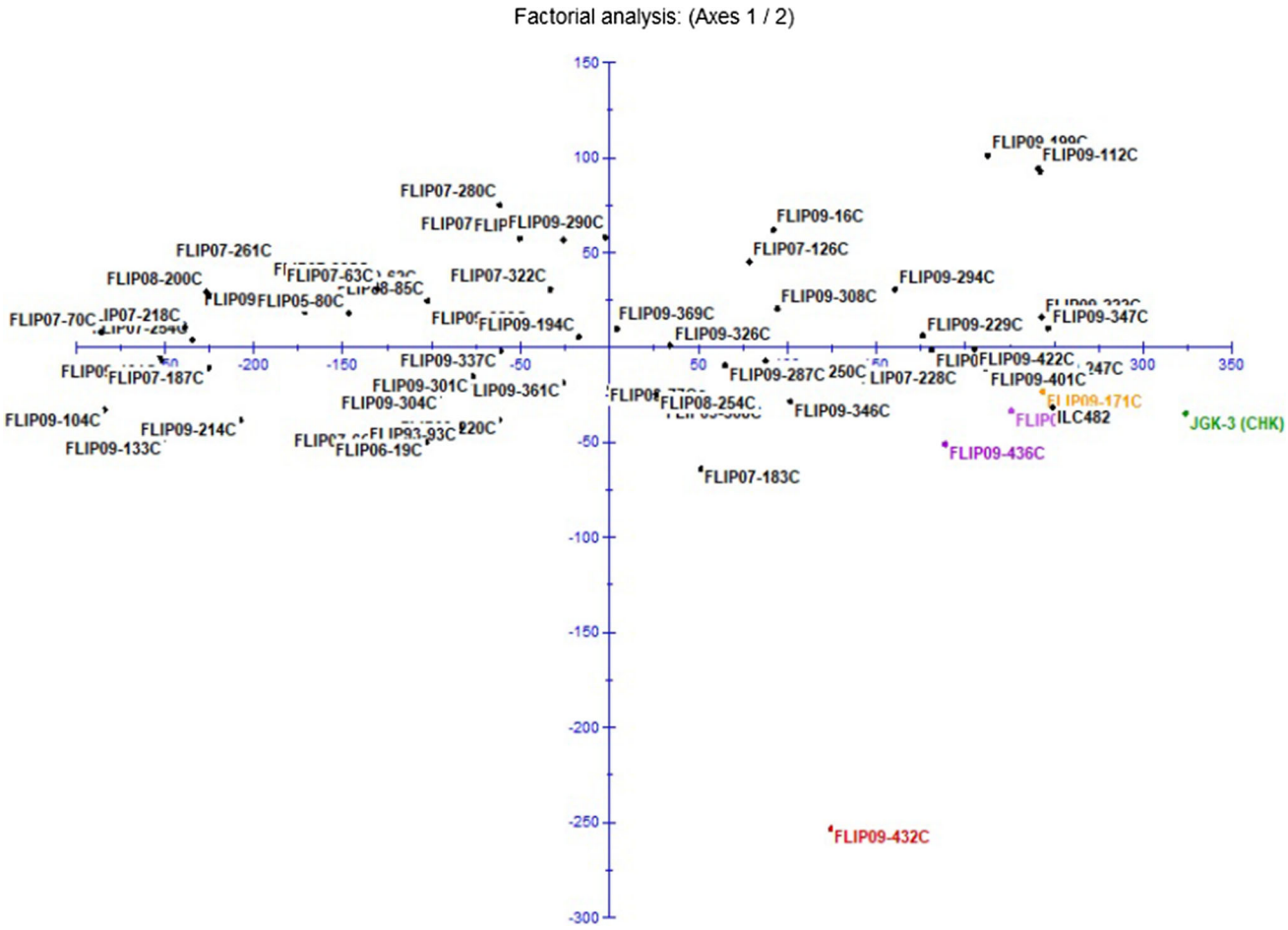

Figure 3. Representation of 1–2 plane of factorial analysis based on morphological traits of 64 chickpea genotypes.

et al. 2013). There is a nonsignificant correlation of seed yield with plant height (Ali *et al.* 2011). Tesfamichael *et al.* (2015) also reported a negative correlation of seed yield with 100-seed weight and with biomass yield in chickpea. A positive and significant correlation between seed yield and biomass yield indicated that both economic characters could be improved at the same time (Tesfamichael *et al.* 2015). All the characters that are positive and significant correlation with yield can be utilized in the hybridization programmes for developing chickpea varieties (Qureshi *et al.* 2004).

The genetic base of cultivated chickpea is narrow due to excessive use of the favourable characters of limited

genotypes for the genetic improvement of chickpea through breeding efforts. Earlier studies have indicated that chickpea from Indian subcontinent had a narrow genetic pool which is limiting the genetic improvement of chickpea through conventional breeding efforts (Singh *et al.* 2008, 2016; Bharadwaj *et al.* 2011b). Plant genetic resources from Mediterranean region are the reservoirs of natural genetic variation in introgression of useful variation present in the exotic germplasm to broaden the genetic base for enhancing chickpea production (Haussmann *et al.* 2004; Bains *et al.* 2012; Sharma *et al.* 2013; Kumar *et al.* 2018).

Genotypes from west Asia and Mediterranean may play a very important role in the development of varieties for early maturity as well as high yielding for the Indian sub-continent. Exploring the extent of natural variation among cultivated chickpea accessions for earliness combined with high yield is very important (Kumar *et al.* 2015). In the central Indian condition, early-maturing varieties with high seed-yield can escape the heat and drought stress during pod filling stage and can produce a good yield. These selected lines have a high potential for yield, earliness, growth and adaptability for central Indian conditions and can be utilized for genetic improvement programmes through hybridization and as a direct introduction of desired traits in chickpea.

Conclusion

Central and southern parts of India are emerging as major kabuli chickpea growing regions in India. The growing season is short and the crop is vulnerable to terminal heat and drought stresses. The present study provides genotypes to select phenologically-adapted genotypes with high seed yield. Farmer prefer early maturing and high yielding varieties which can fit into the short season of central and southern Indian environments, and also can escape the drought and terminal heat during pod filling stage. India is the largest producer as well as importer of chickpea and now emerging as an exporter of large-seeded kabuli chickpea. The screened genotypes will be very important for kabuli chickpea production in India. These genetic materials will be shared with national institutions for testing in All India Coordinated Research Programme, and will be utilized in breeding programmes.

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