

Original Research Article

Genetic Variability for Yield and Quality Characters in Chickpea (*Cicer arietinum* L.) Under Rice Based Cropping System

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ABSTRACT

The experimental material comprised seven lines viz., Vaibhav, Indira Chana-1, JG 315, JG 11, JG 14, JG 16, JG 130 of agronomic base and three testers JG 97, ICCV 96029 and ICCV 96030 for early maturity were crossed as per Line x Tester mating design fashion to develop 21 F₁s during, Rabi 2014-15. These F₁s along with their parents were evaluated two replications in one row plot during, Rabi 2015-16. Under following rice based cropping system viz. E₁: CS-I, E₂: CS-II, and E₃: CS-III. The row to row and plant to plant spacing 30 x 10 cm maintained at Research cum Instructional farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur. The PCV was higher in magnitude than its corresponding GCV for all the characters under study. This indicated the influence of the environment on the expression of these characters. The high values of phenotypic coefficients of variation were recorded for secondary branches plant⁻¹, pod plant⁻¹, hydration index, seed yield plant⁻¹, hydration capacity seed⁻¹, biological yield, primary branches plant⁻¹, Swelling index in all three environment E₁, E₂ and E₃. High heritability estimates coupled with high genetic advance were found for the characters plant height⁻¹, primary branches plant⁻¹, secondary branches, plant⁻¹, pods plant⁻¹, biological yield plant⁻¹, 100-seed weight, seed yield plant⁻¹, seed volume, hydration capacity seed⁻¹, hydration index and swelling index all three environments E₁, E₂ and E₃ indicated the role of additive genetic variance in the expression of these characters. Rest of the characters were having moderate to low heritability coupled in high to low genetic advance as percentage of mean indicated the role of non-additive genetic component in their expression.

Keywords

Genetic variability and chickpea

Introduction

Chickpea [*Cicer arietinum* (L.) 2n = 2x = 16] belongs to genus *Cicer*, tribe Cicereae, family Fabaceae, and subfamily Papilionaceae. It is commonly called gram, bengal gram or garbanzo bean, is the most important cool season food grain legume in the world after common bean (*Phaseolus vulgaris* L.) and pea (*Pisum sativum* L.). Chickpea is the world's third most important food legume crop grown as rained in cool

and dry climate in semi-arid regions. During the last few decades, due to increasing demand of the food for world's growing population depend to a large extent on the conservation and use of world's remaining plant genetic resources. Chickpea covers about 11.7 million ha area and 9.3 million tones production in over 45 countries of the world. India is the largest chickpea producer accounting a share of about 67% in global

chickpea production with about 9.93 million ha area, 9.53 million tones production and productivity of 960 kg/ha. Distribution of chickpea in six states *viz.*, Madhya Pradesh, Rajasthan, Maharashtra, Uttar Pradesh, Karnataka and Andhra Pradesh together contribute 90.2% of the production and 90.8 % of the area of the country. Chhattisgarh covers 0.276 million ha area with production 0.213 million tones and productivity of 771 kg ha⁻¹. (Project Coordinators Report, 2014-15). Genetic variability is the first pre-requisite for any crop improvement programme as it provides opportunity to select an ideal plant type. It helps for choice of better yield attributes either for selection or hybridization. Lacks of exploitation of variability have been implicated as one of the major limitation in improving the productivity of chickpea. The Analysis of variance provides estimates of phenotypic, genotypic and environmental variances, which are used for the estimation of respective coefficients of variation. The relative values of such coefficients of variation give an idea about the magnitude of variability present in a population. They also indicate whether selection for improvement of characters will be rewarding or not. The phenotypic coefficient of variation, genotypic coefficient of variation, genetic advance and heritability play an important role in development of superior chickpea genotypes.

Materials and Methods

The experimental material comprised seven lines *viz.*, Vaibhav, Indira Chana-1, JG 315, JG 11, JG 14, JG 16, JG 130 of agronomic base and three testers JG 97, ICCV 96029 and ICCV 96030 for early maturity were crossed as per Line x Tester mating design fashion (Kempthorn, 1957) to develop 21 F₁s during *rabi* 2014-15. These F₁s along with their parents were evaluated two replication

in one row plot during *rabi* 2015-16. Under following three rice based cropping system *viz.* E₁: Cropping System I: after harvest of early rice variety (Danteshwari) CS-I, E₂: Cropping System II: after harvest of medium rice variety (Mahamaya). CS-II, E₃: Cropping System III: after harvest of late rice variety (Dubraj) CS-III. The row to row and plant to plant spacing 30 x 10 cm maintained at Research cum Instructional farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur The recommended packages of practices were adopted to raise the normal crops. Observations on metric traits were recorded on single plant basis on five randomly selected competitive plant of each genotypes from each replication in each cropping system were as observation on days to 50% flowering, days to maturity, plant height, number of primary branches plant⁻¹, pods plant⁻¹, Biological yield plant⁻¹, harvest index, 100 seed weight, Seed yield plant⁻¹, seed volume, hydration capacity seed⁻¹, hydration index, swelling index and protein content were recorded on plot basis as per the chickpea descriptor developed by ICRISAT-IBPGR- ICARDA (1993). The experimental data was analyzed statistically by the method of analysis of variance for single factor (Gomez and Gomez, 1984) and lastly to find out the significance mean difference between varieties different genetic parameters were estimated. The various genetic parameter *viz.* genotypic and phenotypic coefficient of variation, heritability in broad sense and expected genetic advance were estimated and selection indices were formulated as suggested by Robinson *et al.*, (1966).

Results and Discussion

Analysis of variance in E₁ (CS-I), E₂ (CS-II) and E₃ (CS-III) presented in Table 1 indicated that the mean sum of squares due

genotypes were significant for the all the characters studies which, revealed that there was considerable genetic variability amongst the material under the study, which can be exploited through selection. This is an indicative of existence of sufficient variability among the genotypes for the traits. These findings are in general agreement with the findings of Altnbas (2002), Upadhyay *et al.*, (2002), Parshuram *et al.*, (2003), Brar *et al.*, (2004), Kaur *et al.*, (2004), Jeena *et al.*, (2005), Durga *et al.*, (2007) and Shrivastava *et al.*, (2012).

Genotypic and phenotypic coefficient of variation

Genetic parameter of variation for seed yield and its components among 31 genotypes (Parents and crosses) are presented in Table 2 over all mean and range for yield and its components revealed that there is statistical genetic variability. Genotypic and phenotypic coefficients of variation are simple measure of variability, these measure are commonly used for the assessment of variability. The relative value of these types of coefficients gives an idea about the magnitude of variability present in a genetic population. Thus, the components of variation such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated under present investigation and are presented in table 2. The phenotypic coefficients of variation were marginally higher than the corresponding genotypic coefficient of variation indicated the influence of environment in the expression of the characters under study. Coefficients of variation were estimated at phenotypic and genotypic levels and classified as *per* Burton (1952) as low (< 10%), moderate (10-20%) and high (>20%). Data revealed phenotypic coefficients of variation were in general, higher in magnitude than that of genotypic

coefficients for all the studied characters. The PCV was higher in magnitude than its corresponding GCV for all the characters under study. This indicated the influence of the environment on the expression of these characters. The high values of genotypic coefficients of variation were recorded for secondary branches plant⁻¹, pod plant⁻¹, hydration index, seed yield plant⁻¹, hydration capacity seed⁻¹, biological yield, primary branches plant⁻¹, Swelling index in all three environment E₁, E₂ and E₃. The highest values of genotypic coefficient of variation were recorded for harvest index in E₁ and E₂. Moderate genotypic coefficient of variation was recorded seed volume and 100 seed weight in E₁, E₂ and E₃. The lowest genotypic coefficients of variation were noted for days to 50% flowering, protein content, days to maturity in E₁, E₂ and E₃. The highest values of phenotypic coefficients of variation was recorded for secondary branches plant⁻¹ followed by pod plant⁻¹, hydration index, seed yield plant⁻¹, hydration capacity seed⁻¹, biological yield, primary branches plant⁻¹, Swelling index in all three environment E₁, E₂ and E₃. The highest values of phenotypic coefficients of variation were recorded for harvest index in E₁ and E₂. Moderate phenotypic coefficient of variation was noted for seed volume and 100 seed weight in E₁, E₂ and E₃. Similarly moderate phenotypic coefficient of variation was recorded for harvest index and plant height in E₃.

Mishra and Yadav (1994) reported high genetic variation for plant height, days to 50 % flowering and days to maturity. Jeena and Arora (2001) reported high GCV for 100-seed weight and seed yield plant⁻¹. Kashyap *et al.*, (2003) reported high PCV and GCV for biological yield and pods plant⁻¹. Kaur *et al.*, (2004) reported high PCV and GCV for 100-seed weight and pods plant⁻¹. Pandey and Rastogi (2005) reported high GCV for

seed yield, pods plant⁻¹ and 100 seed weight. Khan *et al.*, (2006) reported high GCV for pods plant⁻¹, 100 seed weight and seed yield. Atta *et al.*, (2008) reported high GCV and PCV for 100 seed weight seed yield plant⁻¹ and pods plant⁻¹. Thakur and Sirohi (2008) reported for high PCV and GCV for seed yield plant⁻¹, biological yield plant⁻¹, pods plant⁻¹ and 100-seed weight. Malik *et al.*, (2009) reported for high GCV for pods plant, 100-seed weight, harvest index, and seed yield plant⁻¹. Alwani and choumane (2010) reported high genetic variation for plant height days to 50 % flowering and days to maturity. Parameshwarappa *et al.*, (2012) reported high GCV for pods plant⁻¹. Jayalakshmi *et al.*, (2011) reported high GCV for seed yield. Malik *et al.*, (2011) reported high PCV observed for 100 seed weight and hydration capacity seed⁻¹. Shrivastava *et al.*, (2012) reported for high genotypic coefficient of variation (GCV) and phenotypic coefficient of variance (PCV) for 100 seed weight, seed yield plant⁻¹, pods plant⁻¹, harvest index and biological yield plant⁻¹.

Heritability

In any crop improvement programme, the most basic information required by a breeder is the extent of the inheritance capacity of the genotype for different characters under consideration. In fact, the variability of biological population is an outcome of genetic constitution of the individual make up of that population in relation to prevailing environments. Such studies enable the breeder to have maximum selection response, if the variance exhibited by the populations is largely due to additive genetic variance. In this investigation, an attempt was made to estimate the broad sense heritability, which involves all types of gene expression, additive as well as non-additive effects, in order to draw some valid

conclusion about the possibilities of the improvement of the various characters. To this reason estimate of heritability and genetic advance should be interpreted together. As the genetic advance estimates are dependent on the unit of characters under measurement, hence genetic advance expressed as percentage of mean was calculated in order to have relative comparison of expected genetic gain for quantitative characters for one generation of selection in hypothetical selection programme. Heritability estimates in broad sense was estimated and categorized as high (> 70 %), moderate (50-70 %) and low (< 50 %) as suggested by Robinson (1966). Heritability in broad sense was calculated for each character among all the 15 characters (Table 2). In E₁ high heritability estimates were noted for the characters hydration capacity seed⁻¹, hydration index, 100-seed weight, swelling index, seed yield plant⁻¹, seed volume, days to 50 % flowering, secondary branches plant⁻¹, biological yield plant⁻¹, pods plant⁻¹, primary branches plant⁻¹, days to maturity and harvest index. Whereas low heritability was observed for plant height and protein content. In E₂ high heritability estimates were observed for the characters hydration capacity seed⁻¹, hydration index, 100-seed weight, days to 50 % flowering, days to maturity, primary branches plant⁻¹, seed yield plant⁻¹, seed volume, swelling index, secondary branches plant⁻¹, biological yield plant⁻¹, pods plant⁻¹ and plant height. Moderate heritability was noted for harvest index and protein content. In E₃ high heritability estimates were recorded for the characters hydration index, hydration capacity seed⁻¹, 100-seed weight, days to 50 % flowering, days to maturity, seed volume, secondary branches plant⁻¹, biological yield plant⁻¹, seed yield plant⁻¹, swelling index, pods plant⁻¹ and plant height. Moderate heritability was observed for primary

branches plant^{-1} and protein content. Whereas, harvest index exhibited low heritability.

Genetic advance

Genetic advance as percentage of mean was estimated and categorized as high ($> 20\%$), moderate (10-20%) and low ($< 10\%$) as suggested by Johnson (1955). Genetic advance was calculated for all the 15 characters (Table 2). In E_1 the higher genetic advance as percentage of mean was observed for secondary branches plant^{-1} , hydration index, seed yield plant^{-1} , hydration capacity seed^{-1} , biological yield plant^{-1} , primary branch plant^{-1} , pods plant^{-1} , harvest index seed volume, swelling index, 100-seed weight. Moderate genetic advance as percent mean was observed days to 50% flowering and rest of the characters observed low for. In E_2 the higher genetic advance as percentage of mean was observed for secondary branches plant^{-1} , seed yield plant^{-1} , hydration index, hydration capacity seed^{-1} , pods plant^{-1} , biological yield plant^{-1} , primary branches plant^{-1} , harvest index, seed volume, swelling index, 100-seed weight and plant height. Moderate genetic advance as percent mean was observed for days to 50% flowering and low for protein content and days to maturity. In E_3 the higher genetic advance as percentage of mean was observed for secondary branches plant^{-1} , hydration index, seed yield plant^{-1} , hydration capacity seed^{-1} , biological yield plant^{-1} , pods plant^{-1} , swelling index, seed volume, primary branch plant^{-1} , 100-seed weight, and plant height. Moderate genetic advance as percent mean was observed for harvest index and days to 50% flowering, rest of the characters reported low.

High heritability coupled with high genetic advance in table 3 which were found for the characters plant height $^{-1}$, primary branches

plant $^{-1}$, secondary branches, plant^{-1} , pods plant^{-1} , biological yield plant^{-1} , 100 seed weight, seed yield plant^{-1} , seed volume, hydration capacity seed^{-1} , hydration index and swelling index all three environments E_1 , E_2 and E_3 indicated the role of additive genetic variance in the expression of these characters. Rest of the characters were having moderate to low heritability coupled in high to low genetic advance as percentage of mean indicated the role of non-additive genetic component in their expression.

Similar finding were also reported earlier by Khan *et al.*, (2006) who reported high heritability days to flowering, days to maturity, pods plant^{-1} , 100 seed weight and seed yield plant^{-1} . Atta *et al.*, (2008) reported high heritability for 100-seed weight, days to 50% flowering, seed yield plant^{-1} , pods plant^{-1} , secondary branches plant^{-1} and plant height. Sidramappa *et al.*, (2008) reported for high heritability for secondary branch plant^{-1} , seed yield plant^{-1} , 100 seed weight and harvest index. Thakur and Sirohi (2008) reported high heritability coupled with genetic advance for seed yield plant^{-1} , biological yield plant^{-1} , 100-seed weight, pods plant^{-1} and plant height. Johnson *et al.*, (2010) and Malik *et al.*, (2009) reported high heritability coupled with high genetic advance for 100 seed weight and days to 50% flowering. Sharma and Saini (2010) reported high heritability for 100 seed weight, pods plant^{-1} , seed yield plant^{-1} and branches plant^{-1} . Malik *et al.*, (2011) observed high heritability and genetic gain for all characters except hydration index. Parmeshwarrappa *et al.*, (2012) reported high heritability coupled with high genetic advance for 100 seed weight and seed yield plant^{-1} . Sewak *et al.*, (2012) and Shrivastva *et al.*, (2012) who observed high heritability coupled with high genetic advance in 100 seed weight, pods plant^{-1} and days to maturity and seed yield.

Table.1 Analysis of variance for yield, its attributes and quality characters under E₁, E₂ and E₃ in chickpea

Source of variation	D.F.	Mean sum of squares														
		Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant ⁻¹	Secondary branches plant ⁻¹	Pods plant ⁻¹	Biological yield plant ⁻¹ (g)	Harvest index (%)	100-seed weight (g)	Seed yield plant ⁻¹ (g)	Seed volume (ml seed ⁻¹)	Hydration capacity seed ⁻¹ (g)	Hydration index	Swelling index	Protein content (%)
E₁: CS-I (After harvest of early rice variety of 90-110 days)																
Replication	1	0.000	0.750	22.350	7.730	45.650	9.600	11.590	16.150	0.000	26.450	0.004	0.0012	0.0005	0.136	0.944
Treatment	30	26.55**	12.190**	40.370**	6.140**	376.02**	9197.4**	881.57**	341.26**	20.60**	301.12**	0.02**	0.0213**	0.0032**	3.920**	2.160**
Error	30	1.000	1.350	16.340	0.510	14.480	366.900	35.060	51.040	0.353	9.55	0.008	0.00068	0.0001	0.0813	0.776
E₂: CS-I I (After harvest of medium rice variety of 111-135 days)																
Replication	1	22.090	17.50	165.05	2.245	45.470	650.43	58.46	157.8	0.230	0.289	0.0014	0.0067	0.00052	0.089	1.896
Treatment	30	32.79**	27.66**	102.14**	4.037**	310.01**	6475.9**	731.99**	239.4**	22.18**	317.15**	0.023**	0.209**	0.0032**	3.45**	1.898**
Error	30	0.880	0.966	14.520	0.433	17.970	526.300	57.380	56.880	0.364	12.31	0.0078	0.009	0.00012	0.165	0.5489
E₃: CS-I II (After harvest of late rice variety of above 135 days)																
Replication	1	0.0035	5.790	54.32	0.505	0.029	69.17	43.78	580.6	0.2382	17.140	0.0041	0.0033	0.00042	0.2061	0.7568
Treatment	30	32.09**	26.587**	60.40**	1.993**	262.75**	684.75**	462.16**	255.53*	23.07**	163.47**	0.019**	0.206**	0.0031**	3.124**	2.3847**
Error	30	0.688	0.632	9.77	0.4587	11.83	83.76	21.69	120.42	0.365	9.88	0.0073	0.0014	0.00001	0.3667	0.5868

*Significant at 5 % level; **Significant at 1 % level of probability

Table.2 Genetic parameters of variation yield, its attributes and quality characters under E₁, E₂ and E₃ in chickpea

Characters	Environment	Mean (\bar{X})	Range		GCV (%)	PCV (%)	Heritability 'h ² (bs)' (%)	Genetic advance (GA)	Genetic advance as percentage of mean (%)
			Min.	Max.					
Days to 50 % flowering	E ₁	55.610	48.500	64.500	6.430	6.670	92.700	7.090	12.750
	E ₂	54.790	45.000	64.000	7.290	7.490	94.800	8.010	14.619
	E ₃	51.300	41.500	59.000	7.210	7.370	95.600	8.030	14.516
Days to maturity	E ₁	103.460	95.000	105.500	2.250	2.520	80.000	4.290	4.147
	E ₂	103.620	89.000	106.000	3.530	3.650	93.200	7.270	7.016
	E ₃	97.200	83.000	99.000	3.430	3.530	94.500	7.090	6.876
Plant height (cm)	E ₁	55.120	46.900	68.400	6.290	9.660	42.400	4.650	8.436
	E ₂	50.610	41.400	68.350	13.080	15.090	75.100	11.820	23.355
	E ₃	41.710	33.200	54.550	12.060	14.200	72.200	8.800	21.098
Primary branches plant ⁻¹	E ₁	4.890	2.300	8.100	34.290	37.260	84.700	3.180	65.031
	E ₂	4.083	2.400	7.550	32.870	36.610	80.600	2.480	60.740
	E ₃	3.716	2.250	5.750	23.570	29.800	62.600	1.430	38.482
Secondary branches plant ⁻¹	E ₁	28.560	7.100	54.000	53.150	55.240	92.600	26.650	93.312
	E ₂	23.390	8.200	50.550	51.660	54.750	89.000	22.490	96.152
	E ₃	20.940	7.450	43.450	53.470	55.930	91.400	19.060	91.022
Pods plant ⁻¹	E ₁	134.800	34.900	265.500	50.070	52.110	92.300	85.750	63.613
	E ₂	118.890	47.000	247.000	45.870	49.770	85.000	85.120	71.596
	E ₃	60.400	33.550	98.600	28.700	32.450	78.200	31.580	52.285
Biological yield plant ⁻¹ (g)	E ₁	58.200	18.400	87.250	35.350	36.780	92.300	40.730	69.983
	E ₂	52.710	24.200	80.600	34.840	37.690	85.500	34.980	66.363
	E ₃	38.370	16.400	64.100	38.670	40.530	91.000	29.170	76.023

Cont...

Characters	Environment	Mean (\bar{X})	Range		GCV (%)	PCV (%)	Heritability 'h ² (bs)' (%)	Genetic advance (GA)	Genetic advance as percentage of mean (%)
Harvest index (%)	E ₁	51.970	36.030	81.780	23.180	26.940	74.000	21.340	41.062
	E ₂	49.410	34.780	83.080	19.340	24.640	61.600	15.450	31.269
	E ₃	58.500	30.470	80.230	14.050	23.440	35.900	10.150	17.350
100-seed weight (g)	E ₁	19.660	13.900	26.150	16.180	16.460	96.600	6.440	32.757
	E ₂	19.390	13.500	26.150	17.320	17.320	96.800	6.690	34.502
	E ₃	19.250	13.240	26.150	17.500	17.780	96.900	6.830	35.481
Seed yield plant ⁻¹ (g)	E ₁	29.080	13.400	71.300	41.510	42.850	93.900	24.100	82.875
	E ₂	25.920	11.200	66.550	49.510	49.510	92.500	24.460	94.367
	E ₃	21.680	9.400	41.750	40.410	42.930	88.600	16.990	78.367
Seed volume (ml seed ⁻¹)	E ₁	0.168	0.110	0.230	19.230	19.960	92.800	0.060	35.736
	E ₂	0.164	0.120	0.230	20.900	20.900	93.300	0.070	42.761
	E ₃	0.165	0.110	0.220	18.530	19.240	92.700	0.060	36.342
Hydration capacity seed ⁻¹ (g)	E ₁	0.274	0.150	0.570	37.690	37.810	99.400	0.210	76.782
	E ₂	0.274	0.080	0.570	37.420	37.420	99.100	0.210	76.698
	E ₃	0.271	0.090	0.570	37.360	37.600	98.300	0.210	77.434
Hydration index	E ₁	0.030	0.010	0.060	42.460	42.600	99.300	0.026	87.248
	E ₂	0.029	0.010	0.060	43.570	43.570	99.300	0.027	92.784
	E ₃	0.030	0.010	0.060	42.270	42.440	99.200	0.027	90.604
Swelling index	E ₁	5.342	3.280	7.890	25.960	26.500	95.900	2.800	52.415
	E ₂	5.355	3.270	7.890	25.100	25.100	90.900	2.520	47.059
	E ₃	5.206	3.250	7.780	22.550	25.380	79.000	2.150	41.299
Protein content (%)	E ₁	15.336	13.460	17.150	5.440	7.910	47.200	1.150	7.499
	E ₂	15.513	13.960	17.260	7.130	7.130	55.100	1.280	8.251
	E ₃	15.334	13.430	17.100	6.180	7.950	60.500	1.520	9.913

* E₁: CS-I (Environment 1), E₂: CS-II (Environment 2) and E₃: CS-III (Environment 3)

Table.3 Summary of heritability and genetic advance for yield, its attributes and quality characters under E₁, E₂ and E₃ in chickpea

Characters	Heritability (h ² b)			Genetic advance (%) of mean		
	E ₁	E ₂	E ₃	E ₁	E ₂	E ₃
Days to 50% flowering	H	H	H	M	M	M
Days to maturity	H	H	H	L	L	L
Plant height (cm)	L	H	H	H	H	H
Primary branches plant ⁻¹	H	H	M	H	H	H
Secondary branch plant ⁻¹	H	H	H	H	H	H
Pods plant ⁻¹	H	H	H	H	H	H
Biological yield plant ⁻¹ (g)	H	H	H	H	H	H
Harvest Index (%)	H	M	L	H	H	M
100-seed weight (g)	H	H	H	H	H	H
Seed yield plant ⁻¹ (g)	H	H	H	H	H	H
Seed volume (ml)	H	H	H	H	H	H
Hydration capacity seed ⁻¹	H	H	H	H	H	H
Hydration index	H	H	H	H	H	H
Swelling index	H	H	H	H	H	H
Seed Protein content (%)	L	M	M	L	L	L

*E₁= CS-I (Environment 1); E₂= CS-II (Environment 2); E₃=CS-III (Environment 3)

Acknowledgement

The Author are great full to All India Coordinated Research Project on chickpea, Research cum Instructional farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur for providing funding and field for the experiment and also thanks full to Major Advisor Dr. R.N. Sharma, Professor/ Principal Scientist, GPB at this university.

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