Indian J. Genet., 79(3) 622-625 (2019)
DOI: 10.31742/IJGPB.79.3.13

Short Communication

Hybridity testing and heterosis in relation to genetic divergence in chickpea (*Cicer arietinum* L.) under rice based cropping system

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(Received: March 2019; Revised: June 2019; Accepted: July 2019)

Abstract

The present investigation was carried out to determine the genetic purity of the crosses in chickpea using SSR markers. The application of molecular markers SSR21 and SSR22 in F_1 hybrids and their parental lines produced two bands indicating similarity among the hybrids and parental lines. The mixtures and off-types did not show similar banding pattern as compared to hybrids. The D^2 analysis showed high amount of genetic diversity among parents and parental lines. The value of heterosis in a cross, JG 315 x ICCV 96029 was positive significantly higher for days to 50 % flowering, days to maturity, secondary branches plant^{-1}, pods plant, biological yield and seed yield plant^{-1}, however, it was significantly negative only for 100 seed weight.

Key words: Genetic variability, parental diversity, hybridity, rice based cropping system and chickpea

Chickpea [*Cicer arietinum* (L.) 2*n* = 2*x* = 16], a cool season food grain legume commonly known as gram, Bengal gram or garbanzo bean belongs to genus *Cicer,* tribe Cicereae, family Fabaceae, and subfamily Papilionaceae. Chickpea production and productivity varies in different agro-climatic zones in the world. To enhance the production and the productivity of chickpea, it is necessary to identify diverse parents for hybridization and selection of superior genotypes. Isolating transgressive segregants from a diverse crosses and handling of heterotic progenies through pedigree may lead to improve the crop yield. Jinks (1983) outlined the importance of heterosis breeding in self pollinated crops to extract pure breeding lines equaling or outperforming the best F_1s. Nature and magnitude of heterosis is useful while selecting a cross for further evaluation and selection. In any genetical study producing genetically pure seeds of the hybrid is of paramount importance as it may vitiate the F_2 segregation. In hybrid breeding also the contaminated seed may influences the yield of the hybrid (Mao et al. 1996). Usually genetic purity of hybrid seed is detected visually on the basis of morphologiacal and floral traits. A study was, therefore, conducted to estimate heterosis for yield and physiological traits in chickpea crosses. Hybridity test to establish the genetic purity of hybrids was also done using molecular markers.

The experimental material comprised of eight lines, namely, JG 315, JG 130, JG 11, INDIRA CHANA-1, VAIBHAV, JG 14, JG 16 and JG 315 and three testers, JG 97, ICCV 96029 and ICCV 96030 for early maturity. Line x Tester mating design (Kempthorn, 1957) was followed to develop 21 F_1 crosses and these F_1s along with their parents were evaluated under three rice based cropping systems *viz.,* Cropping System I (CS-I) after harvest of early rice variety, Danteshwari (E_1); Cropping System II (CS-II) after harvest of medium rice variety, Mahamaya (E_2) and Cropping System III (CS-III) after harvest of late rice variety, Dubraj (E_3). The observations were recorded on ten morphological traits, namely, days to 50% flowering, days to maturity, plant height (cm), primary branches/plant, secondary branches plant^{-1}, no. of pods plant^{-1}, biological yield (g), harvest index (%), hundred seed weight (g) and seed yield plant^{-1}.

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Published by the Indian Society of Genetics & Plant Breeding, A-Block, F2, First Floor, NASC Complex, IARI P.O., Pusa Campus, New Delhi 110 012; Online management by www.isgpb.org; indianjournals.com

Table 1. Pooled heterosis over the environments for seed yield and its attributes in relation to parental diversity in chickpea

Parents		D^2 Value	Cross Combinations	Heterobeltiosis									
P_1	P_2			1	2	3	4	5	6	7	8	9	10
High diversity													
JG 315	ICCV 96029	4814.93	JG 315 x ICCV 96029	11.526**	14.420**	3.827	10.477	16.754**	59.850**	35.551**	-9.512	-15.580**	108.518**
JG 130	ICCV 96029	3908.23	JG 130 x ICCV 96029	22.664**	12.964**	-5.814	45.038**	28.001**	31.794**	29.027**	-26.033**	-17.899**	90.203**
JG 11	ICCV 96029	3532.51	JG 11 x ICCV 96029	24.110**	15.154**	13.953	15.145	10.819**	22.015	49.984**	-33.252**	-21.607**	53.400**
Indira Chana-1	ICCV 96029	3503.54	INDIRA CHANA-1x ICCV 96029	8.634**	15.329**	3.552	50.934**	39.352**	35.800**	45.045**	-19.939**	-41.388**	69.755**
VAIBHAV	ICCV 96029	3209.46	VAIBHAV x ICCV 96029	21.584**	14.606**	-2.114	17.347	16.298**	32.200**	40.837**	-20.114*	-15.477**	60.669**
JG 14	ICCV 96029	2930.52	JG 14 x ICCV 96029	22.664**	12.417**	11.272**	53.807**	16.418	37.942**	65.181**	-32.293**	-24.059**	112.097**
JG 16	ICCV 96029	2554.72	JG 16 x ICCV 96029	15.843**	15.154**	21.987**	29.113**	-6.639*	1.628	37.528**	-29.935**	-17.589**	49.225**
JG 16	JG 97	1879.13	JG 16 x JG 97	3.681**	3.634**	15.353**	20.406*	-24.172**	35.752**	30.964**	-14.123	-34.379**	121.513**
JG 16	ICCV 96030	1207.29	JG 16 x ICCV 96030	20.479**	13.649**	-2.397	26.620**	-24.261**	24.143**	23.119*	-23.283**	-37.315**	37.861**
JG 315	ICCV 96030	1020.46	JG 315 x ICCV 96030	14.938**	12.927**	3.808	18.435	1.879	47.526**	27.750**	-7.421	-35.759**	103.442**
Medium diversity													
JG 130	ICCV 96030	838.53	JG 130 x ICCV 96030	10.417**	40.224**	-5.405	26.431**	27.105**	41.778**	59.371**	-19.760*	-35.175**	70.068**
JG 315	JG 97	644.42	JG 315 x JG 97	9.203**	1.812**	16.780**	52.805**	55.377**	58.059**	42.311**	-10.147	-39.350**	124.658**
JG 11	JG 97	623.95	JG 11 x JG 97	0.920	3.634**	9.554*	20.406*	12.026	36.841**	27.929*	-17.217*	-36.864**	105.274**
JG 130	JG 97	614.18	JG 130 x JG 97	-4.602**	3.792**	2.284	51.240**	-0.842	72.143**	26.647**	27.653**	-30.478**	168.919**
JG 11	ICCV 96030	562.95	JG 11 x ICCV 96030	7.979**	13.465**	0.696	80.064**	47.282**	38.168**	34.061**	2.080	-29.144**	86.417**
Indira Chana-1	JG 97	542.95	INDIRA CHANA-1xJG-97	14.233**	2.644**	2.021	49.903**	24.739**	80.493**	32.032**	-35.339**	-21.185**	62.147**
JG 14	JG 97	502.19	JG 14 x JG 97	7.571**	1.485**	12.849**	39.749**	49.737**	41.710**	66.731**	20.712*	-8.566	150.685**
Low diversity													
VAIBHAV	ICCV 96030	446.58	VAIBHAV x ICCV 96030	20.479**	13.293**	1.660	21.939*	14.180**	25.404*	42.589**	-26.950**	-47.237**	37.812**
VAIBHAV	JG 97	443.10	VAIBHAV x JG 97	-3.976**	1.812**	1.494	54.255**	4.940	36.456**	29.625**	-21.241*	-30.593**	43.891**
Indira Chana-1	ICCV 96030	409.61	INDIRA CHANA-1x ICCV 96030	17.021**	12.033**	5.823	97.213**	52.874**	64.601**	49.667**	-22.310**	-8.327**	136.380**
JG 14	ICCV 96030	341.10	JG 14 x ICCV 96030	17.354**	12.216**	4.661	25.381**	-14.883	27.217**	33.976**	-32.777**	-28.560**	18.193*

1. Days to 50% flowering 2. Days to maturity 3. Plant height (cm) 4. Primary branches plant^{-} 5. Secondary branches plant^{-1}

6. Pods plant^{-1} 7. Biological yield (g) 8. Harvest index (%) 9. 100-seed weight (g) 10. Seed yield plant^{-1}

Twenty one SSR markers were utilized for testing hybrid purity of F_1 hybrids. Standard procedure was followed to analyse genetic diversity and to estimate heterosis.

Heterosis in relation to genetic divergence

The data was subjected to Mahalnobis D^2 analysis to compute genetic diversity among 10 parents. Pooled estimates of heterobeltiosis over the environments in relation to parental divergence for seed yield and its attributes in chickpea are given in Table 1. The D^2 value ranged from 341.10 to 4814.93 among the parents and the crosses, JG 315 x ICCV 96029 had the highest parental diversity (4814.93). High amount of genetic diversity has also been reported earlier in other studies (Chaudhary et al. 2012). The magnitude of heterobeltiosis was significantly positive for the days to 50% flowering, days to maturity, secondary branches plant$^{-1,}$ pods plant, biological yield and seed yield plant^{-1} and significantly negative heterosis was recorded for 100 seed weight. Data on parental diversity in relationship of heterosis revealed no definite relation of diversity and heterosis for the traits studied. However, a few crosses displayed, grouped under high diversity, also produced high heterosis for majority of traits except, plant height (Table 1). Two crosses showed high heterosis for no. of pods plant^{-1} while high harvest index was noticed in three crosses. Similarly, the crosses grouped under medium diversity, high to medium heterotic F_1s were obtained for most of the characters except three crosses showed only for plat height. Two crosses displayed high heterosis for secondary branches. One cross each had high harvest index and 100 seed weight for which heterosis was non-significant. However parent grouped under low diversity also yielded low to high heterotic crosses in the present study. It appears from the present study of parental diversity in relation to heterosis the higher diversity leads to high heterosis in chickpea. The present results were supported by earlier findings published by many researchers (Kumar 1997; Katiyar et al. 1993; Jeena and Arora 2000; Kumari and Prasad 2003; Parameshwarappa et al. 2012). However, the materials studied in the present investigation were different and so was the environment. Only a few studies have been conducted under the conditions considered in this research.

Hybridity testing

To determine the parental polymorphism in parents (7 lines and 3 testers) 25 SSR markers with known sequences were taken for the study, out of which two polymorphic markers, SSR21 and SSR 22 were identified. Determining the genetic purity of hybrid seed is an essential requirement for its commercial use, since there is always a chance of contamination in the hybrid seed production plot because of pollen shedders, out crossing and physical mixtures during the subsequent handling of the harvested material. SSR markers are co-dominant and the polymorphism detected between the parental lines was used to establish hybridity. Twenty one crosses along with their respective parents were also analyzed with 25 most informative chickpea specific SSR markers, only two markers, as mentioned above showed polymorphism and identified the pure hybrids**.**

Molecular markers, SSR 21 and SSR 22, which showed parental polymorphism between parents, distinguished the F_1 hybrids, Vaibhav x JG 97 and JG 11 x JG 97 for markers and JG 315 x ICCV 96029 and JG 14 x ICCV 96029, respectively. The present findings have been supported by Quadir et al. (2007), Saeed et al. (2011) and Varshney et al. (2014) in chick pea, while similar reports on testing hybrid purity have been published earlier by several workers (Garg et al. 2006; Moorthy et al. 2011; Bora et al. 2016) in other crops. The present results also suggested that molecular markers are simple, precise and quick option over other methods and visual observation for testing purity of hybrids in short span of time (Singh et al. 2017). The present finding indicated that the selected molecular markers (SSR21 and SSR22) are indeed highly informative and useful in marker based seed genetic purity assessments in chickpea hybrids.

Authors' contribution

Conceptualization of research (PLJ); Designing of the experiments (PLJ, RNS, HCN); Contribution of experimental materials (PLJ, RNS); Execution of field/ lab experiments and data collection (PLJ, RNS); Analysis of data and interpretation (PLJ, RNS, HCN); Preparation of manuscript (PLJ, RNS, HCN).

Declaration

The authors declare no conflict of interest.

Acknowledgement

The authors are grateful to All India Coordinated Research Project on Chickpea, Indira Gandhi Krishi Vishwavidyalaya, Raipur for providing funding and field for the experiment.

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