Agric Res J **60** (3) : 355-361, *June* 2023
DOI No. 10.5958/2395-146X.2023.00053.4

INTROGRESSION OF DESIRABLE TRAITS FROM *Cicer reticulatum* INTO CULTIVATED CHICKPEA (*Cicer arietinum* L.)

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ABSTRACT

A set of 100 genotypes including 92 inter-specific derivatives, their six parents and two check cultivars was evaluated during *rabi* 2019-20 and 2020-21. The analysis of variance indicated significant differences between genotypes for all traits evaluated in both the years, as well as for the pooled over analysis. The analysis of variance revealed substantial variations across years; however, the year x genotype interaction was non-significant for all of the variables tested. Transgressive segregants were recovered for seed yield, pods per plant, fruiting branches per plant and 100-seed weight. Nine derivatives namely GLW7225, GLW7242, GLW7246, GLW7247, GLW6241, GLW6359, GLW6360, GLW6361 and GLW6362 were found significantly superior than the respective parents and check cultivars for seed yield. High GCV was observed for seed yield, pods per plant, fruiting branches per plant and 100-seed weight. Seed yield, 100-seed weight, days to 50% flowering, pods per plant and fruiting branches per plant had high heritability. Genetic advance was high for seed yield while it was moderate for pods per plant, fruiting branches per plant and 100-seed weight. Plant height, number of pods per plant, fruiting branches per plant, and 100-seed weight had a strong positive association with seed yield. The current study found that the wild progenitor, *Cicer reticulatum*, contains a large amount of latent diversity for numerous yield augmenting traits that can be introgressed into cultivated chickpea for yield improvement.

Keywords: *Cicer reticulatum*, Interspecific derivatives, Productivity traits, Transgressive segregants.

Chickpea (*Cicer arietinum* L.) or Garbanzo bean is a predominant pulse crop of South Asian nations securing 90% of the total cultivated area (Anonymous, 2019a). Being a leguminous crop, it offers a wealthy source of vegetarian protein (22-25%), higher amounts of carbohydrates (65-67%), fats (4-5%), macro nutrients (Ca, P, Mg), micro nutrients (Fe, Zn), vitamins (A, B complex and K) and ash (Jukanti *et al.,* 2012). Furthermore, due to its high potential for export-import, it has significant impact on the economy of developing countries. India is the largest producer and consumer of chickpea in the world as well as the major importer (Anonymous, 2019b). Keeping in view the population growth, the present production levels are insufficient to fulfil domestic needs of chickpea in the country. Such massively low levels of chickpea production were previously addressed by adopting several yield-enhancing and biotic-abiotic stress-resistant germplasm sources found in the cultivated genepool. Eventually, repetitive exploitation of germplasm within the primary genepool has narrowed down the genetic base of cultivated chickpea leading to its more vulnerability to various yield penalty threats. Since due to past breeding strategies, cultivated chickpea germplasm became unresponsive to yield augmentation. Hence, the only practical option is to explore hidden productivity potential in the wild species. Wild germplasm has also been recorded to impart significant contribution towards yield in many other crops like wheat (Swamy and Sarla, 2008), rice (Gaikwad *et al.,* 2014), barley (Pickering and Johnston, 2005) etc. Besides yield enhancement expected from wild sources, resistance to various biotic and abiotic stresses is also the added advantage in the wild germplasm. As a result, *Cicer reticulatum*, also known as the wild progenitor of chickpea, emerged as the most easily crossable wild species for the transfer of many beneficial morphological, phenological, and yield contributing features. Earlier reports of *C. arietinum* x *C. reticulatum* hybridization indicated the transfer of numerous desired traits into cultivated backgrounds, such as fruiting branches, number of pods, number of seeds per pod, seed weight etc. (Singh *et al.,* 2005; Bhavyasree *et al.,* 2018 a, b). The transfer of such desirable yield enhancing traits magnifies the total impact owing to positive association among each other. Traits positively correlated with the seed yield assist in indirect selections by favouring component traits instead of direct selection for seed yield. As a result, association studies provide a fundamental road map to carry out yield-boosting trait choices. In the present study, efforts were made to evaluate various interspecific progenies, derived from *C. arietinum* x *C. reticulatum* crosses, for

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Date of receipt: 22.02.2022, Date of acceptance: 30.06.2023

various desirable morphological, phenological and yield contributing traits.

MATERIALS AND METHODS

The experimental material involved in the present study composed of 92 inter-specific derivative lines, their six parents and two check cultivars. The derivative lines were developed by crossing two elite cultivars (GPF2 and PBG1) with four accessions (ILWC115R, ILWC21, ILWC237, EC556270) of wild progenitor species *Cicer reticulatum.* The cultivated lines were used as female parents while the wild accessions as male parents to generate six interspecific crosses (Cross-I: GPF2 x IL WC237; Cross-II: GPF2 x ILWC21; Cross-III: GPF2 x ILWC115R; Cross-IV: GPF2 x EC556270; Cross-V: PBG1 x ILWC237; Cross-VI: PBG1 x ILWC21). The F_1s were selfed as well as backcrossed with the respective cultivated female parent to develop the segregating generations using pedigree method. Finally, 46 progenies were chosen from direct crosses (without backcross) and 46 progenies from backcrosses. Four crosses namely Cross-I, Cross-II, Cross-IV, and Cross-V each represented eight progenies while Cross-III and Cross-VI each represented seven progenies.

The experiment was conducted at the Pulses Experimental Field Area of Punjab Agricultural University, Ludhiana located at 30.84' N latitude and 75.48' E longitude for two *rabi* seasons (2019-20 and 2020-21). The experimental material was raised in α-lattice design in two replications. Each replication consisted of 10 blocks with each block having 10 entries. Each entry was accommodated in a plot of 2 rows of 2 m length with 30 cm row to row spacing. Data were recorded on plot basis for days to 50% flowering, days to maturity and seed yield per plot (g). For plant height (cm), number of fruiting branches per plant, number of pods per plant, number of seeds per ten pods, and 100-seed weight (g), five plants were taken randomly to record the data.

The data obtained for various traits were subjected to standard statistical analysis using SAS 9.4 software (SAS 2013) to estimate analysis of variance (ANOVA), parameters of genetic variability, genetic advance (Singh and Chaudhury, 1985), heritability in broad sense (Falconer, 1989) and correlation coefficients (Miller *et al.,* 1958).

RESULTS AND DISCUSSION

Evaluation for phenological, morphological and yield contributing traits

The analysis of variance revealed highly significant differences ($P<0.05$) among the genotypes for all the traits studied during both the years (2019-20 and 2020-21) as well as for pooled over analysis. Analysis of variance unveiled significant differences over the years; however, year x genotype interaction was non-significant for all the traits studied (data not shown). Performance of promising derivatives in comparison to parents and checks for phenological, morphological and yield contributing traits has been presented in Table 1.

In cross-I (GPF2 x ILWC237), the female parent i.e. GPF2 was earlier to the male wild parent, (ILWC237) with more number of pods per plant, plant height, number of seeds per ten pods and seed yield per plot, while the wild parent was superior to the female parent for number of fruiting branches per plant and 100-seed weight. The progenies obtained from direct cross were at par or late in flowering and maturity than the wild parent. In comparison to female parent, none of the progeny was early to flower, however two progenies (GLW7225 and GLW7228) were early maturing. Useful transgressive segregants were obtained for plant height (GLW7226 and GLW7228), number of pods per plant (GLW7225 and GLW7226), seeds per ten pods (GLW7228),100-seed weight (GLW7228) and seed yield per plot (GLW7225 and GLW7226). In case of backcross progenies, three lines (GLW6175, GLW6191 and GLW6207) were early in flowering and maturity (GLW6185, GLW6191 and GLW6207). The variability for plant height, fruiting branches and 100-seed weight was comparable to either of the parents. Few derivative lines viz., GLW6199 for pods per plant, GLW6190 for seeds per ten pods and GLW6179 for seed yield per plot were significantly superior compared to the parents.

The male parent, ILWC21 involved in cross-II (GPF2 x ILWC21), was superior for pods per plant and number of seeds per ten pods, while for rest of the traits, female parent GPF2 was superior. The derivative line, GLW7242 from direct cross took minimum number of days for 50% flowering while three lines viz., GLW7245, GLW7246 and GLW7247 were early in maturity. Two lines viz., GLW7242 and GLW7247 had higher pod number and seed yield per plot. In case of backcross progenies, one progeny, GLW6220, was found to be early maturing and had more seeds per ten pods. Plant height was numerically higher in GLW6215 and GLW6217. Overall, GLW6217 outperformed all other backcross progenies.

The female parent, GPF2 of cross-III (GPF2 x ILWC115R), was superior for all the traits, except for plant height and number of fruiting branches per plant, while the male parent, ILWC115R, was superior for later two traits. Among the direct cross progenies, four derivatives (GLW7248, GLW7249, GLW7250 and GLW7254) took minimum days to50% flowering, while three derivatives (GLW7248, GLW7250 and GLW7252)

Table 1. Transgressive segregants for various traits in different inter-specific crosses of chickpea

Type of Progeny	Progeny	Day to 50% Flowering	Day to Maturity	Plant Height (cm)	No. of Pods/ Plant	No. of Fruiting Branches/ Plant	No. of Seeds/ 10 Pod	100-seed weight (g)	Seed Yield/ Plot (g)
Cross-I: GPF2 x IL WC237									
DC	GLW7225	96.25	160.00	39.75	42.75	17.25	18.25	18.35	233.35
DC	GLW7226	97.50	156.75	50.25	42.00	17.00	16.25	18.45	226.60
DC	GLW7228	95.50	158.75	47.25	26.25	12.25	16.25	19.15	106.85
BC	GLW6179	98.00	159.50	39.75	39.25	14.75	18.75	14.40	203.98
BC	GLW6190	98.00	156.50	45.75	40.75	15.25	19.25	15.45	157.98
BC	GLW6199	96.00	155.50	39.25	44.00	14.50	17.00	14.25	176.35
Cross–II: GPF2 x ILWC21									
DC	GLW7239	95.75	157.50	49.75	40.25	14.75	19.00	20.85	171.43
DC	GLW7242	91.25	160.50	32.25	45.75	23.00	18.25	15.65	290.05
DC	GLW7245	99.00	154.50	33.25	42.50	15.75	15.25	14.00	227.55
DC	GLW7246	93.00	154.75	43.75	40.00	17.50	17.50	14.40	244.05
DC	GLW7247	93.00	155.50	40.75	46.25	16.25	18.00	15.65	249.68
BC	GLW6217	96.00	156.50	49.25	36.50	13.00	14.00	14.45	163.35
Cross–III: GPF2 x ILWC115R									
DC	GLW7248	91.25	153.50	52.75	26.00	12.25	16.50	21.40	145.43
DC	GLW7249	90.75	156.25	49.75	27.00	11.25	12.50	21.80	107.55
DC	GLW7250	92.00	152.50	48.75	33.50	13.75	18.00	18.75	155.05
DC	GLW7251	96.00	157.50	42.75	29.00	16.50	14.00	21.85	169.43
DC	GLW7252	94.00	152.50	47.75	38.75	18.00	18.00	21.15	228.30
DC	GLW7254	92.25	155.50	37.75	27.50	13.50	13.00	19.45	108.55
BC	GLW6241	93.00	155.50	49.75	41.50	19.00	18.75	15.15	234.10
Cross–IV: GPF2 x EC556270									
DC	GLW7272	98.25	154.50	36.75	25.75	7.25	19.75	13.80	89.93
DC	GLW7273	95.00	156.50	39.25	36.50	14.25	19.75	13.45	181.05
BC	GLW6273	97.00	152.50	41.75	27.50	13.50	19.00	14.35	211.05
Cross–V: PBG1 x ILWC237									
DC	GLW7296	93.25	155.75	38.75	22.25	12.25	20.00	14.30	102.60
BC	GLW6330	97.25	160.50	47.75	39.00	18.50	14.50	18.50	197.15
BC	GLW6331	96.00	154.50	47.60	44.00	15.50	14.00	17.20	225.93
BC	GLW6341	96.25	152.50	45.75	42.50	17.75	18.00	14.55	128.83

were early maturing. The progenies recorded similar response to the parents for pods per plant and fruiting branches per plant. However, some of the derivatives were found to be significantly superior for plant height (GLW7248), seeds per ten pods (GLW7250 and GLW7252), seed yield (GLW7252) and 100-seed weight (GLW7248, GLW7249, GLW7251 and GLW7252). In case of backcross derived progenies, two derivatives (GLW6244 and GLW6257) were early maturing and one derivative (GLW6262) recorded maximum plant height. Some of the derivatives were found superior for various traits namely pods per plant (GLW6241), seeds per ten pods (GLW6241 and GLW6250) and seed yield per plot (GLW6241). The progeny GLW6241 was found to be superior among all the backcross progenies of Cross III.

The male parent, EC556270 of cross-IV (GPF2 x EC556270) had higher number of fruiting branches whereas female parent, GPF2 was superior for all other yield augmenting traits. In case of progenies

Table 1. Continued.......

Type of Progeny	Progeny	Day to 50% Flowering	Day to Maturity	Plant Height (cm)	No. of Pods/ Plant	No. of Fruiting Branches/ Plant	No. of Seeds/10 Pod	100-seed weight (g)	Seed Yield/ Plot (g)
Cross–VI: PBG1 x ILWC21									
BC	GLW6359	93.50	154.50	51.00	47.00	19.50	13.00	15.35	275.98
BC	GLW6360	97.50	157.75	49.35	52.50	22.00	15.00	15.35	308.35
BC	GLW6361	98.50	157.50	52.50	47.00	16.50	18.50	15.60	234.85
BC	GLW6362	96.50	156.50	49.00	39.50	18.50	17.00	16.60	251.60
Parent	ILWC115R	96.00	158.50	47.13	35.00	19.00	14.50	18.10	160.85
Parent	EC556270	107.75	157.50	37.25	25.50	18.00	14.50	14.70	128.35
Parent	ILWC237	99.25	158.00	41.75	31.75	19.50	15.50	15.90	136.35
Parent	ILWC21	100.00	160.50	36.75	39.50	19.25	17.50	14.75	124.85
Parent	PBG1	95.00	155.50	48.25	40.25	17.50	17.00	14.75	192.73
Parent	GPF2	93.25	155.75	42.25	36.50	17.50	16.50	15.70	199.93
Check	PBG5	93.25	152.25	48.25	35.25	17.00	17.25	21.65	194.58
Check	PBG7	93.25	154.25	49.75	38.00	19.25	18.00	16.80	214.40
GM		95.43	156.25	41.59	31.33	13.90	16.20	15.47	143.14
CV (%)		1.16	0.77	9.70	9.35	9.94	7.02	4.21	7.30
CD (5%)		1.54	1.68	5.62	4.08	1.92	1.58	0.91	14.55

DC: Direct cross progeny; BC: Backcross progeny

derived from direct cross, two derivatives (GLW7271 and GLW7272) for days to maturity, three derivatives (GLW7267, GLW7270 and GLW7290) for plant height, one derivative (GLW7268) for pods per plant, three derivatives (GLW7271, GLW7272 and GLW7273) for seeds per ten pods and two derivatives (GLW7270 and GLW7290) for 100-seeds weight were found to be superior. None of the derivatives outperformed for fruiting branches and seed yield per plot. As far as backcross derived progenies are concerned, some of the derivatives were found to be promising for days to 50% flowering (GLW6277 and GLW6295), days to maturity (GLW6273 and GLW6280), plant height (GLW6270) and seed yield per plot (GLW6273).

The female parent, PBG1 of cross-V (PBG1 x ILWC21) outperformed w.r.t. plant height and seed yield per plot compared to male parent, ILWC21,superior for fruiting branches and seeds per ten pods. Most of the direct cross progenies were comparable to the parents for plant height, pods per plant, fruiting branches, 100-seed weight and seed yield per plot. However, some of the derivatives were superior for days to 50% flowering (GLW7294, GLW7296, GLW7297 and GLW7299), days to maturity (GLW7294, GLW7298 and GLW7301) and seeds per ten pods (GLW7296). Some of the derivatives derived from backcross progenies were found to be promising for days to 50% flowering (GLW6334, GLW6339 and GLW6351), days to maturity (GLW6334 and GLW6341), pods per plant (GLW6331 and GLW6341), seeds per ten pods (GLW6341 and GLW6351), 100-seed weight (GLW6330, GLW6331 and GLW6339) and seed yield per plot (GLW6331). However, all derivatives were similar to the parents for plant height and fruiting branches per plant.

The wild male parent, ILWC237 of cross-VI (PBG1 x ILWC237) had more fruiting branches and seed weight as compared to female parent, PBG1. None of the derivatives derived from direct cross was found superior for seed yield or its component traits. However, some of the derivatives derived from backcross with recurrent parent were found superior for yield contributing traits. Four backcross progenies viz., GLW6359, GLW6360, GLW6361 and GLW6362 recorded significantly higher seed yield compared to the parents and check cultivars.

Significant variability for various traits such as days to maturity (Singh *et al.,* 2018), plant height (Gupta *et al.,* 2015), pods per plant (Singh *et al.,* 1999), seed yield (Singh and Singh 2009) and 100-seed weight (Verma *et al.,* 1991; Singh *et al.,* 2005) was reported earlier in various inter-specific crosses between cultivated chickpea and related wild species including *C. reticulatum*.

Table 2. Pooled estimates of genetic variability parameters for various traits in chickpea

Traits	GCV (%)	PCV (%)	h^2 (%)	GA (%)
Days to 50% flowering	2.85	3.12	83.41	5.37
Days to maturity	1.37	1.60	74.03	2.44
Plant height (cm)	12.75	16.11	62.63	20.79
Pods per plant	22.89	25.2	82.53	42.84
Fruiting branches per plant	21.88	24.26	81.31	40.64
Seeds/10 pods	13.07	15.05	75.44	23.39
100-seed weight (g)	13.53	14.37	88.67	26.25
Seed yield per plant (g)	10.81	11.01	96.44	21.88
Seed yield per plot (g)	37.40	38.21	95.85	75.43

Evaluation for genetic variability parameters

The results of genetic variability parameters and correlation coefficient analysis were almost similar during both the years as well as for pooled over analysis. Therefore, the results of pooled over analysis were presented (Table 2 and 3) and discussed. In general, the phenotypic coefficient of variation (PCV) values were slightly higher than that of corresponding values of genotypic coefficient of variation (GCV) indicated the least vulnerability of genotypes to various environmental fluctuations (Nandpuri *et al.,* 1973). Hence, phenotype represents the consistent measure of genotype. The GCV was found to be the maximum for seed yield per plot (37.40%) followed by pods per plant (22.89%), fruiting branches per plant (21.88%) and 100-seed weight (13.53%). Days to maturity (1.37%) had the minimum value for GCV. Sidramappa *et al.* (2008) also reported maximum GCV for pods per plant and seed yield and minimum GCV for days to maturity, thereby supporting the results of present investigation. Similar results were obtained for PCV values, the estimates were high for seed yield per plot (38.21%) and low for days to maturity (1.60%). Pods per plant (25.20%) and fruiting branches per plant (24.26%) also recorded high variability. Comparatively lower values of GCV and PCV (<15 %) were observed for plant height, seeds per ten pods and 100-seed weight. The results of the present findings for seed yield, pods per plant, days to 50% flowering and days to maturity were in accordance with the previous study (Jha *et al.,* 2012).

Heritability measures the part of phenotypic variation which is heritable and apt for making effective selection. It basically estimates the degree of inheritance of a particular trait from parent to progenies. In this study, seed yield per plant (96.44 %) was found to have high heritability followed by seed yield per plot (95.85 %), 100-seed weight (88.67%), days to 50% flowering (83.41%), pods per plant (82.53%) and fruiting branches per plant (81.31%). High heritability for days to 50% flowering can assist in selection and utilization of early blooming genotypes as donors. These results were in concurrence with the findings of Bala *et al.* (2015) and Joshi *et al.* (2018). The lowest heritability was found for plant height (62.63%). Other traits viz., days to maturity and seeds per ten pods had moderate to high heritability estimates, therefore, selection for these traits may not be much fruitful.

Table 3. Phenotypic correlation coefficients (pooled) among various traits in chickpea

Traits	Days to 50% flowering	Days to maturity	Plant height (cm)	Pods per plant	Fruiting branches per plant	Seeds per ten pods	100-seed weight (g)
Days to maturity	0.24**						
Plant height (cm)	-0.12	-0.15					
Pods per plant	-0.01	-0.01	0.34**				
Fruiting branches per plant	0.10	0.08	0.35**	0.71**			
Seeds per ten pods	-0.06	-0.01	-0.03	0.04	0.07		
100-seed weight (g)	-0.14	-0.02	0.49**	0.25**	0.31**	-0.05	
Seed yield per plot (g)	-0.08	-0.06	0.39**	0.86**	0.77**	0.11	0.32**

*Significant at 5% and **Significant at 1% level of significance

High or low heritability estimates could be of practical utility only if genetic advance of the target trait is taken into consideration. Hence, genetic advance has significant importance in selection for improving original population for a particular trait (Honnappa *et al.* 2018). Genetic advance under selection is governed by three factors viz., extent of variability found in the original population, heritability of the particular trait and selection intensity. Generally, genetic advance as percent of mean is used by various researchers to estimate effective selection indices based on the heritability estimate of the traits. In this study, genetic advance was recorded to be the highest for seed yield per plot (75.43%), moderate for pods per plant (42.84%), fruiting branches per plant (40.64%) and 100-seed weight (26.25%). Similar findings for seed yield and 100-seed weight were also reported earlier (Meena *et al.,* 2014; Bala *et al.,* 2015). High heritability coupled with high genetic advance for seed yield per plot indicated that direct selections can play a significant role for the improvement of this trait due to the prevalence of additive gene action. Low estimates of genetic advance were recorded for the phenological traits, which were in concurrence with the study of Qureshi *et al.* (2004). Plant height (20.79%) and seeds per ten pods (23.39%) had low genetic advance indicating that upon selection these traits cannot contribute significantly towards population improvement. Hence, owing to the prevalence of dominance or epistatic genetic control, breeding strategies involving hybridization followed by selection would be useful for improvement of such traits.

Correlation coefficient analysis

Estimates of correlation coefficient analysis indicated significant positive correlation of seed yield per plot with plant height, number of pods per plant, fruiting branches per plant and 100-seed weight (Table 3). The findings in the present investigation were supported by the previous studies (Thakur and Sirohi, 2009; Salgotra, 2016; Chopdar *et al.,* 2017). The phenological traits viz., days to 50% flowering and days to maturity were found to be significantly positively associated with each other however; their association with the seed yield per plot was negative as reported by Chopdar *et al.* (2017). The other traits like plant height, pods per plant, fruiting branches per plant and 100-seed weight were significant and positively correlated with each other. These results were also propounded by the studies of Thakur and Sirohi (2009). In the present investigation, seed yield per plot showed significant correlation with pods per plant (0.86**) and fruiting branches per plant (0.77**), hence these two traits can be considered as best selection indices for carrying out indirect selections for yield enhancement.

The current study revealed that the wild progenitor, *Cicer reticulatum*, contains considerable hidden diversity for phenological, morphological, and yield enhancing features that are yet to be investigated. Genetic variability and correlation studies revealed critical traits such as pods per plant, fruiting branches, and seed weight that were highly heritable and strongly correlated to seed yield. Hence, may be utilised as indirect selection indices for yield improvement in chickpea.

Authors' contribution

Conceptualization of research work and designing of experiments(SS,IS, SB, TN); Execution of field/ lab experiments(TN, JK, SB); Analysis of data and interpretation (TN, SS, SB, SaS, SoS); Preparation of manuscript(TN, SS, SB, IS, BSG).

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