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GENETIC ANALYSIS AND INTERRELATIONSHIP OF YIELD ATTRIBUTING TRAITS IN CHICKPEA (*Cicer arietinum L.)*

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ABSTRACT

Twenty chickpea (*Cicer arietinum* L.) genotypes were evaluated for genetic potential, heritability, genetic advance and traits association of yield contributing characters during 2010-2011, at The University of Agriculture, Peshawar**.** The experiment was carried out in a randomized complete block (RCB) design with three replications. Data were recorded on days to 50% flowering, pods per plant, seeds per pod, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, 100-seed weight and seed yield plant^{-1}. Analysis of variance revealed significant ($P<0.01$) variation among genotypes for all the studied characters. Broad sense heritability estimates were highest for pods per plant (0.88), primary branches plant^{-1} (0.83), 100-seed weight (0.82), seed yield plant^{-1} (0.75) and secondary branches plant^{-1} (0.77). Genetic advance was higher for pods per plant (40.14), seed yield plant^{-1} (38.24%), primary branches plant^{-1} (36.64%) and secondary branches plant^{-1} (30.25%). Seed yield plant^{-1} showed highly significant genetic as well as phenotypic correlation with pods per plant, number of primary branches plant^{-1}, secondary branches plant^{-1} and 100-seed weight in positive direction. To conclude, pods per plant, number of primary branches, number of secondary branches and 100-seed weight would be the appropriate selection criteria for better seed yield in chickpea.

Key words: Chickpea, genetic analysis, interrelationship, yield, traits.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is an important food legume providing protein in human diet. It has the ability to fix atmospheric nitrogen and improve soil fertility with low added cost of production (Ali *et al*., 2008). Chickpea ranks third among pulses, and it accounts for 12% of the world pulses production (Khan *et al*., 2011). The Asian region contributes 70% to the total world's chickpea production (Malik *et al*., 2010).

Genetic variability is a prerequisite for any breeding program, which provides opportunity to a plant breeder for selection of high yielding genotypes. However information on the association between yield and its various components provide the basis for the selection of improved varieties (Saleem *et al*., 2005). Information on the relative magnitude of the different sources of variation particularity among different genotypes for several traits helps in measurement of their range of genetic diversity and may provide evidence for identification of their relationship.

The variability of a biological population is an outcome of genetic constitution of the individuals and its interaction with the prevailing environment. A survey of genetic variability with the help of suitable parameters such as genetic coefficient of variation, heritability estimates and genetic advance are absolutely necessary to start an efficient breeding program. Some of the characters are highly associated among themselves and with seed yield. The analysis of the relationships among these characters and their associations with seed yield is essential to establish selection criteria. (Atta *et al*., 2008). Progress in any breeding program depends upon the nature and magnitude of variability present in the base population. Assessment of the extent of genetic variability within chickpea is fundamental for chickpea breeding (Qureshi *et al*., 2004).

Chickpea breeders should consider heritability estimates along with genetic advance because heritability alone is not a good indicator of the amount of usable genetic variability (Noor *et al*., 2003). The concept of heritability explains whether the differences observed among individuals arose as a result of differences in genetic makeup or due to environmental forces. Genetic advance gives an idea of possible improvement of new population through selection, when compared to the original population. The genetic gain depends upon the amount of genetic variability and magnitude of the masking effect of the environment. Information of the genetic variability, heritability and association of various characters provides a basis to the plant breeders to breed the chickpea genotypes possessing higher yield potential. Selection on the basis of grain yield, a polygenic character, is usually not very efficient, but selection based on its component characters could be more efficient.

Keeping in view the utmost importance of genetic variability, heritability, genetic advance and traits association the present investigation was undertaken on 20 genotypes of chickpea.

MATERIALS AND METHODS

Twenty chickpea genotypes obtained from different national and international institutions (Table A) were planted in a randomized complete block design with three replications, in the experimental field of Khyber Pakhtunkhwa Agricultural University, Peshawar, during 2010-11. Each genotype was planted in a separate plot which was consisted of three rows of 4 meter length, with a plant-to-plant and row-to-row distance of 10 and 30 cm, respectively. The plots were separated by a distance of 60 cm. Recommended cultural practices were carried out to maintain healthy crop growth. Number of days to flowering was recorded at the time when at least 50% plants showed the appearance of first flower. At maturity, data were recorded for yield and its various components including, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, 100-seed weight and seed yield plant^{-1}. The data was subjected to statistical analysis by a statistical software SAS (Statistical Analysis System) version 9. The mean values of the genotypes of each parameter were further compared by using the least significant difference (LSD) test at 5% level of probability. Genotypic and phenotypic correlation coefficients were calculated according to the method followed by Singh and Chaudhary (1979).

RESULTS AND DISCUSSION

Genetic variation and heritability: Analysis of variance disclosed highly significant ($p \leq 0.01$) differences among genotypes for all studied traits indicating the presence of adequate genetic variability among all the tested genotypes (Table 1). Saleem *et al*. (2005) and Ali *et al*. (2009) also found significant variability among chickpea genotypes, whilst Atalay and Babaoglu (2012) observed low level of variability, which could be attributed to difference germplasm.

Flowering time of a variety plays an important role in its selection and has a direct relationship with earliness or lateness of a variety, because early flowering varieties usually mature early. Early flowering traits has significant beneficial effects by reducing crop duration in chickpea and escape most of the weather hazards like hill storm, floods, rains and diseases etc. Besides, it vacates the land early for sowing of succeeding crop. Days to flowering is mostly used as basis for determining the maturity. Days to 50% flowering varied from 141.00 to 156.67 among all genotypes (Table 2). The mean values indicated that genotype NKC-5-S17 produced 50% flowering earlier with a mean value of 141.00 days and was also found statistically at par with 15 other genotypes having the range of 141.33 to 146.33 days. The maximum days to 50% flowering were divulged by the genotype SL-05-42 (156.67 days) followed by 10 other genotypes by having the range of 144.00 to 149.00 days. Genotypic and environmental variance for days to 50% flowering was 9.30 and 11.24 (Table 3), respectively. It showed moderate heritability estimates (0.45), which indicated that total variability was due to both, genetic as well as environment influences. Our results are in line with the findings of Anbessa *et al*. (2006), who also reported moderate heritability estimates for this trait. Low value of genetic advance (1.97%) was observed for the said trait, which indicated the influence of epistatic genes on this character. Saleem *et al*. (2005) and Sidramappa *et al*. (2008) also detected low genetic advance for number of days taken to flowering in chickpea genotypes.

The data presented evinced that all genotypes differed highly significantly from one another for number of pods per plant (Table 1). Data for number of pods per plant was in range of 20.99 to 74.55. Maximum (74.55) pods per plant were observed for genotype NKC-5-S15, followed by NKC-10-99 (64.66), NDC-4-20-6 (59.44), NDC-5-S10 (57.22) and NKC-5-S22 (56.53). Minimum number of pods per plant was recorded for SL-05-42 (20.99), which was also found close to two other genotypes NDC-122 (28.44) and NKC-5-S23 (28.99) (Table 2). Genotypic variance for number of pods per plant was 183.26, while environmental variance was 25.20. Genetic variance was extremely higher than the environmental variance indicating greater influence of genotype than environment on the trait. The high heritability (hs) estimate (0.88) and greater genetic advance (40.14%) (Table 3) revealed that this trait shows good response to selection. Our results are supported by investigations of Saleem *et al*. (2005) and Ali *et al* (2009).

Seeds per pod also showed highly significant differences among chickpea genotypes (Table 1), with mean values ranged from 1.10 to 1.89. Highest number of seeds per pod was produced by genotypes NDC-15-4 and NDC-5-S10 with the mean of 1.89, which showed statistical aqualance with five other genotypes, ranged from 1.67 to 1.77. Minimum (1.10) number of seeds per pod was revealed by SL-05-42, followed by seven genotypes, varied from 1.13 to 1.40 (Table 2). Genotypic and environmental variance for number of seeds per pod was 0.04 and 0.03, respectively. Genetic variance was slightly greater than the environmental variance, whereas the heritability estimate was a bit high (0.57). Which shows that of this character is appropriate for selection. Genetic advance (14.09%) revealed moderate value for seeds per pod (Table 3). These results are in conformity to the earlier findings of Bakhsh *et al*. (2007) in chickpea.

Results revealed highly significant differences for number of primary branches per plant that varied from 1.55 to 3.89 (Table 2). Genotype NKC-5-S15 acquired maximum number of primary branches per plant (3.89), followed by genotype NKC-5-S20 (3.66).

However, minimum number of primary branches per plant was recorded for genotype NKC-5-S21 (1.55) which was statistically equal to the range (1.67 to 2.03) of nine chickpea genotypes. Our results are authenticated by the results of Saleem *et al*. (2005) and Ali *et al*. (2009), who also reported highly significant variation for primary branches per plant in chickpea. Genotypic and environmental variances for the said parameter were 0.44 and 0.09, respectively (Table 3). The genetic variance was about five times greater than the environmental variance resulting in higher magnitude of heritability (0.83), which indicated that main proportion of variability was primarily due to genetic causes. Reports of Saleem *et al*. (2005) and Ali *et al*. (2008) strengthened our results. The high genetic advance (36.64%) showed the effect of additive gene action in the determination of primary branches per plant. Our findings are similar to Arshad *et al*. (2004) but contradictory to the outcome of Sidramappa *et al*. (2008), who reported low value of genetic advance for this character in chickpea. The difference in result could be attributed to difference in environmental conditions and genotypes used in study.

Number of secondary branches per plant ranged from 5.56 to 14.67 (Table 2). Genotype NKC-5-S15 produced maximum (14.67) number of secondary branches per plant followed by genotypes SL-03-15 (10.78), NKC-5-S22 (10.00) and NDC-4-20-6 (9.67), whereas genotype NDC-15-1 produced least (5.56) number of secondary branches per plant which is statistically equalant to the range (5.66 to 7.00) of with six other genotypes. Bakhsh *et al*. (2007) also observed significant variation for the said trait in chickpea genotypes. Genetic and environmental variances for this trait were 4.00 and 1.18, respectively (Table 3). The least value of environmental variance as compare to genotypic variance confirms the leading role of genotype in the expression of this character. High heritability estimate (0.77) and genetic advance (30.25%), indicates the success of selection for this trait. Arshad *et al*. (2004) also reported high heritability estimates as well as high genetic advance for secondary branches per plant in chickpea.

The range of 100-seed weight among genotypes was 17.23 to 32.84 g (Table 2). Genotype NKC-5-S15 (32.84 g) was noticed with highest 100-seed weight, followed by NKC-5-S17 (31.17), while genotypes NDC-5-S10 (17.23 g) and Karak 3 (19.09 g) followed by nine other genotypes (22.58 to 25.18 g) revealed least values. These results are authenticated by the reports of Sharma and Saini (2010) and Akhtar *et al*. (2011) in chickpea.. Genotypic and environmental variances for 100-seed weight were 12.95 and 2.81, respectively (Table 3). The superior role of genotypic variance in the character is also clear from the high value of heritability (0.82). This is in accordance with the findings of Dwevedi and Lal (2009) and Sharma and Saini (2010). High heritability estimate indicate that selection for this character will be effective, being less influenced by environmental effects. Genetic advance (18.13%) was moderate, which in agreement to the result of Sidramappa *et al*. (2008) in chickpea.

Analysis of variance divulged highly significant differences among genotypes for seed yield per plant (Table 1). It varied from 5.02 to 23.91 g (Table 2) in which the maximum value was given by NKC-5-S15 (23.91 g) that is statistically equal to the genotype NDC-4-20-6 (20.59 g). Whereas, the lowest seed yield per plant was observed in SL-05-42 (5.02 g) followed by three genotypes viz., NKC-5-S21 (8.08 g), NKC-5-S23 (8.71 g) and NDC-122 (8.95 g). Malik *et al.* (2010), Sharma and Saini (2010) and Khan *et al.* (2011) also reported significant genetic variability for this trait among chickpea genotypes. Genotypic variance was 19.40, while environmental variance was 6.61 (Table 3). The heritability (0.75) and genetic advance (38.24%) were high. High heritability estimates coupled with high genetic advance for the said trait was also reported by Jeena *et al.* (2005) and Atta *et al.* (2008). High heritability for seed yield per plant indicates that large proportion of the total variance was due to genotype and environmental influence is less. Therefore selection for further crop improvement is reliable.

Traits association: Days to 50% flowering showed negative and highly significant correlation with seed yield per plant (r_g = -0.58, r_p = -0.37) and pods per plant (r_g = -0.56) at genetic level. While at phenotypic level its correlation with pods per plant was non-significant and negative (r_p = -0.24). Its association with seeds per pod (r_g = -0.31, r_p = -0.14), primary branches per plant (r_g = -0.26, r_p = -0.18), secondary branches per plant (r_g = -0.19, r_p = -0.07) and 100-seed weight (r_g = -0.06, r_p = -0.01) was non-significant and negative both at phenotypic as well as genotypic levels (Table 4). Similar results were reported by Saleem *et al*. (2005), between seed yield and days to flowering. Yucel *et al*. (2006) also found significant and negative relationships of days to flowering with 1000 seed weight. Whereas Atta *et al*. (2008) confirmed contrasting relationship of days to flowering with primary branches and secondary branches.

At both genotypic and phenotypic levels, number of pods per plant revealed highly significant positive association with number of secondary branches per plant (r_g = 0.72, r_p = 0.60) and seed yield per plant (r_g = 0.97, r_p = 0.84). Number of pods per plant had positive and highly significant relationship with number of primary branches per plant (r_g = 0.44, r_p = 0.40) at phenotypic level, while significant positive at genotypic level. The relationship between number of pods per plant and 100-seed weight (r_g = 0.30, r_p = 0.23) was non-significant and positive at both genotypic and phenotypic levels. The trait had non-significant and negative association with number of seeds per pod (r_g = -0.17, r_p = -0.15) at both genotypic and phenotypic levels (Table 4).

Number of seeds per pod had highly significant and negative genotypic and phenotypic correlation with number of secondary branches per plant (r_g = -0.59, r_p = -0.45). Similarly it exhibited highly significant negative relation (r_g = -0.52, r_p = -0.45) with 100-seed weight only at phenotypic level, while significant negative at genetic level. Its association with seed yield per plant (r_g = -0.14, -0.12) was in negative direction both at genotypic and phenotypic levels. This trait had-non significant positive association with number of primary branches per plant (r_g = 0.17, r_p = 0.05) at both the levels (Table 4).

Number of primary branches per plant revealed significant and positive correlated with number of secondary branches per plant (r_g = 0.47, r_p = 0.39) and seed yield per plant (r_g = 0.52, r_p = 0.42). Non-significant positive correlation was noticed for number of primary branches per plant with 100-seed weight (r_g = 0.09, r_p = 0.07) at both genetic and phenotypic levels (Table 4). Yucel *et al*. (2006) also reported that primary branches are positively correlated with secondary branches and seed yield. Number of secondary branches per plant had highly significant and positive genotypic and phenotypic correlation with 100-seed weight (r_g = 0.73, r_p = 0.57) and seed yield per plant (r_g = 0.71, r_p = 0.64). Saleem *et al*. (2005) also observed that secondary branches per plant is positively correlated with 100 seed weight both at genetic and phenotypic levels. 100-seed weight revealed positive and highly significant correlation with seed yield per plant (r_g = 0.50, r_p = 0.38) at phenotypic level but significant positive at genotypic level (Table 4).

Table A. List of 20 Chickpea genotypes along with their pedigree and origin.

Genotype	Group	Parentage	Origin
NDC-122	Desi	C-44 × ILC-195	NIFA/Pakistan
NDC-15-1	Desi	Pb-91/M	NIFA/Pakistan
NDC-15-4	Desi	Pb-91/M	NIFA/Pakistan
NDC-4-20-6	Desi	C-44/M	NIFA/Pakistan
NDC-5-S10	Desi	JG74 x ICC (12071)	NIFA/Pakistan
Karak 3	Desi	Local selection	Karak/ Pakistan
SL-05-42	Desi	Local selection	Karak/ Pakistan
SL-05-53	Desi	Local selection	Karak/ Pakistan
SL-08-14	Desi	Local selection	Karak/ Pakistan
SL-03-15	Desi	Local selection	Karak/ Pakistan
NKC-10-99	Kabuli	FLIP98-138C × SEL99TH15039	ICARDA/Syria
NKC-5-S12	Kabuli	BAHODIR × SEL99TER5530	ICARDA/Syria
NKC-5-S13	Kabuli	SEL99TH15039 × S98008	ICARDA/Syria
NKC-5-S14	Kabuli	SEL99TH15039 × S98008	ICARDA/Syria
NKC-5-S15	Kabuli	FLIP98-15C × S98033	ICARDA/Syria
NKC-5-S17	Kabuli	S99456 × SEL99TER85314	ICARDA/Syria
NKC-5-S20	Kabuli	FLIP98-138C × SEL99TH15039	ICARDA/Syria
NKC-5-S21	Kabuli	GLK95069 × SEL99TER85530	ICARDA/Syria
NKC-5-S22	Kabuli	CA9783007 × SEL99TER85534	ICARDA/Syria
NKC-5-S23	Kabuli	CA9783007 ×SEL99TER85534	ICARDA/Syria

Table 1. Analysis of variance and CV for various quantitative traits in chickpea

Parameters	**Mean squares**	**CV %**
Days to 50% flowering	39.14^{**}	2.31
Number of pods per plant	574.99^{**}	11.33
Number of seeds per plant	0.17^{**}	12.29
Primary branches plant^{-1}	1.41^{**}	12.70
Secondary branches plant^{-1}	13.18^{**}	13.40
100-seed weight	41.67^{**}	6.67
Seed yield per plant	64.81^{**}	18.37

*, ** = Significant at 5 and 1% probability, respectively, whereas NS = Non-significant

Table 2. Means of different chickpea genotypes for yield and various yield parameters.

Genotypes	Days to 50% flowering	Pods per plant	Seeds per plant	Primary branches plant^{-1}	Secondary branches plant^{-1}	100-seed weight (g)	Seed yield plant^{-1} (g)
NDC-122	146.33bcdef	28.44hi	1.67abcd	1.67fg	7.00efgh	25.18efg	8.95ghi
NDC-15-1	142.67def	35.22gh	1.67abcd	1.83efg	5.56h	23.18fg	12.28efgh
NDC-15-4	147.33bcd	36.44gh	1.89a	2.99b	5.66h	23.22fg	12.39efg
NDC-4-20-6	142.00def	59.44bc	1.43cdefgh	1.67fg	9.67bcd	26.67cde	20.59ab
NDC-5-S10	142.33def	57.22bcd	1.89a	3.11ab	6.05fh	17.23h	15.04ef
Karak 3	144.00abcdef	42.89fg	1.67abcd	2.03defg	5.78h	19.09h	12.07efgh
SL-05-42	156.67a	20.99i	1.1i	2.11def	7.44efg	23.27fg	5.02i
SL-05-53	146.67bcde	50.61def	1.23fghi	1.99defg	8.44cde	28.49bc	15.72ce
SL-08-14	149.00b	47ef	1.47bcdefg	2.00defg	8.11de	28.06cd	14.91ef
SL-03-15	145.00bcdef	54.77cde	1.4defghi	3.00b	10.78b	27.99cd	17.70bc
NKC-10-99	144.00bcdef	64.66b	1.5bcdef	2.44cd	8.58cde	25.02efg	19.43bc
NKC-5-S12	145.00bcdef	43.43fg	1.37defghi	1.67fg	8.11de	22.64g	12.19efh
NKC-5-S13	148.33bc	31.99h	1.77a	1.77efg	7.89de	27.12cde	11.53efgh
NKC-5-S14	142.67def	32.44h	1.4defghi	2.11def	6.89efh	27.23cde	11.26fgh
NKC-5-S15	143.00cdef	74.55a	1.13hi	3.89a	14.67a	32.84a	23.91a
NKC-5-S17	141.00def	45.78f	1.33efghi	1.99defg	8.11de	31.17ab	17.17bc
NKC-5-S20	142.00def	42.33fg	1.55bcde	3.66a	8.53cde	22.96fg	17.76bc
NKC-5-S21	144.00bcdef	32.66h	1.17ghi	1.55g	6.98efh	22.58g	8.08hi
NKC-5-S22	143.33cdef	56.53bcd	1.5bcdef	2.22d	10.00bc	23.76fg	15.05f
NKC-5-S23	141.33def	28.99hi	1.72abc	2.77bce	7.81ef	25.42def	8.71ghi
LSD	5.54	8.30	0.30	0.49	1.79	2.77	4.25

Table 3. Genetic, environmental and phenotypic variances, heritability (bs) and genetic advance for different traits of chickpea during 2011.

Traits	Vg	Ve	Vp	h^{2}	GA (%)
Days to 50% flowering	9.30	11.24	20.54	0.45	1.97
Number of pods per plant	183.26	25.20	208.46	0.88	40.14
Number of seeds per plant	0.04	0.03	0.07	0.57	14.09
Primary branches plant^{-1}	0.44	0.09	0.53	0.83	36.64
Secondary branches plant^{-1}	4.00	1.18	5.18	0.77	30.25
100-seed weight (g)	12.95	2.81	15.76	0.82	18.13
Seed yield per plant	19.40	6.61	26.01	0.75	38.24

Vg = Genetic variance, Ve = Environmental variance, Vp = Phenotypic variance, GA = Genetic advance

Table 4. Genetic correlation (above diagonal) and phenotypic correlation (below diagonal) between various traits of 20 chickpea genotypes.

	DF	PP	SP	PB	SB	SW	SY
DF	----	-0.56^{**}	-0.31	-0.26	-0.19	-0.06	-0.58^{**}
PP	-0.24	----	0.17	0.40^{**}	0.60^{**}	0.30	0.97^{**}
SP	-0.14	-0.15	----	0.05	-0.45^{**}	-0.52^{*}	0.89^{**}
PB	-0.18	0.40^{**}	0.60^{**}	----	0.47^{*}	0.09	0.52^{*}
SB	-0.07	0.05	-0.45^{**}	0.39^{**}	----	0.73^{**}	0.71^{**}
SW	-0.01	0.23	-0.45^{**}	0.07	0.57^{**}	----	0.50^{*}
SY	-0.37^{**}	0.84^{**}	-0.12	0.42^{**}	0.64^{**}	0.38^{**}	----

*, ** = Significant at 5 and 1% probability, respectively

DF= Days to 50% flowering, PP= Pods per plant, SP= Seeds per plant, PB= Primary branches plant^{-1}, SB= Secondary branches plant^{-1}, SW= 100-seed weight, SYP= Seed yield plant^{-1}.

Conclusion: On the basis of these results it was suggested that Pods per plant, primary branched per plant, secondary branches per plant and 100 seed weight may be given more importance while making selection for higher yield potential in chickpea. Genetic potential of genotypes revealed highly significant differences for all the studied traits. The promising genotypes were NKC-5-S15, NKC-10-99, SL-05-53, NKC-5-S22, SL-03-15 and NDC-4-20-6 with high genetic potential for majority of the traits. These genotypes can safely be used in future chickpea breeding programs for further exploitation of their genetic variability.

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