DISSECTION OF GENETIC VARIABILITY AND HERITABILITY ESTIMATES OF CHICKPEA GERMPLASM FOR VARIOUS MORPHOLOGICAL MARKERS AND QUANTITATIVE TRAITS

ROZINA KHAN*, FARHATULLAH* and HAMAYOON KHAN**

* Department of Plant Breeding and Genetics, Khyber Pakhtunkhwa Agricultural University, Peshawar – Pakistan.

** Department of Agronomy, Khyber Pakhtunkhwa Agricultural University, Peshawar – Pakistan.

ABSTRACT

An investigation was carried out using forty seven genotypes of chickpea to study the nature and magnitude of genetic variability. The data were recorded on three morphological markers and eight important quantitative traits on the genotypes raised in randomized complete block design having three replications. The study was carried out in the field of Plant Breeding and Genetics, Agricultural University, Peshawar, Pakistan during the chickpea growing season of 2006-07. The germplasm was grouped as desi (pink flower, green with purplish tinge stem and colored seed coat) and kabuli (white flower, green stem and white seed coat) types. Highly significant differences were recorded among genotypes for days to 50% flowering (90-122 days), days to maturity (163-178 days), leaf area (1.73-10.92 cm²), number of leaflets leaf¹ (11.6-16.3), plant height (47-94 cm), 100 seed weight (13-39 g), biological yield plant⁻¹ (14.3-68 g), and grain yield plant⁻¹ (4.1-28.9 g). Grain yield plant⁻¹ had maximum phenotypic and genotypic coefficient of variation (PCV and GCV), followed by biological yield plant⁻¹. Heritability estimates of all the traits were high except leaf area which showed moderate heritability. Highest heritability was recorded for days to 50% flowering (93) followed by biological yield plant⁻¹ (89), plant height (88), 100 seed weight (82), grain yield plant⁻¹, leaflets leaf¹ (75) and days to maturity (68). The genotypes were identified as genetically diverse and can be utilized in future chickpea improvement programs.

Key Words: Chickpea, Genetic Variability, Heritability, Morphological Markers

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INTRODUCTION

Chickpea is one of the world's most important but less-studied leguminous food crop with 740-Mb genome size. Chickpea ranks third among pulses, fifth among grain legumes, and 15th among grain crops of the world. It accounts for 12% of the world pulses production, with a 1.9% annual growth rate of chickpea production during the last 20 years (Upadhyaya, 2003). Chickpea is one of the major pulse crops in West Asian and North African regions. It has great importance as food, feed and fodder. Due to the increasing need for legumes, chickpea is no longer considered a subsistence crop. The rising trend in its trade suggests that the crop is grown increasingly for the market (Saxena *et al.*, 1996). In the developed world it represents a valuable crop for export. It provides a protein-rich supplement to cereal-based diets. Chickpea is valued for its nutritive seeds with high protein content, 25.3-28.9 %, after de-hulling (Hulse, 1991). The characterization of diversity in germplasm collections is important to plant breeders for crop improvement and to gene bank curators for efficient and effective management of collection (Updhaya, 2003). The presence of genetic variability is of utmost importance for any breeding program and for that reason the plant breeders have emphasized the evaluation and characterization of core collection for utilization in breeding programs. Thus the evaluation of germplasm is not only useful in selection of core collection but also for its utilization in breeding programmes.

Chickpea has high variation for various qualitative and quantative traits i.e. grain color and shape, color of flower, podding, seed coat color, earliness, insect pests resistance, like any other crop of different ecological zones, that can help breeders to release better and superior lines and varieties (Dasgupta *et al.*, 1987; Singh, 1997). For maintenance and efficient utilization of germplasm, it is important to investigate the extent of genetic variability and its magnitude for the determination of the success of a breeding program (Smith *et al.*, 1991). An initial step in a breeding program is the assembly of germplasm with a wide range of genetic variability. The utility of a germplasm collection would be enhanced if the unique features of each genotype were to be described and recorded, so that the researcher could choose those genotypes in the collection, which have the genetic characteristics, desired for his specific objectives (Shah, 1999).

Evaluation and characterization of chickpea germplasm has received attention of plant breeders due to increased recognition and its importance (Virmani *et al.*, 1983; Bakhsh *et al.*, 1992). The present study was planned to characterize chickpea genotypes for various morphological markers and to study other quantitative traits in order to estimate genetic variability and heritability of important parameters in the germplasm under study.

MATERIALS AND METHODS

Forty seven local/exotic genotypes obtained from Nuclear Institute for Food and Agriculture (NIFA), Peshawar; Gram research station (GRS), Ahmedwala Karak and International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) India (Table I) were evaluated in the fields of Plant Breeding and Genetics department, Agricultural University Peshawar, during the season of 2006-07. The material was planted in randomized complete block design (RCBD) with three replications. Genotypes were characterized for three morphological markers i.e. flower color (pink/white), stem color (green/green with purplish tinge) and seed coat color (brown/dark brown/ yellow/white). Flower color and stem color were recorded at flowering stage while seed coat color was noted at pod maturity.

Genotype	Parentage	Origin Genotype		Parentage	Origin	
name	1 al entage	Origin	name	1 al cittage	Oligin	
NDC-122	C-44 x ILC-195	NIFA, Pakistan	NKC-10-99	Flip98-138c x Sel99th15039	ICARDA/,Syria	
NDC-727	C-44/M	NIFA, Pakistan	NKC-5-S12	BAHODIR x SEL99TER85530	ICARDA, Syria	
NDC-728-5	C-44/M	NIFA, Pakistan	NKC-5-S13	SEL99TH15039 x S98008	ICARDA, Syria	
NDC-730-2	C-44/M	NIFA, Pakistan	NKC-5-S14	SEL99TH15039 x S98008	ICARDA, Syria	
NDC-15-1	Pb-91/M	NIFA, Pakistan	NKC-5-S15	FLIP98-15C x S98033	ICARDA, Syria	
NDC-15-2	Pb-91/M	NIFA, Pakistan	NKC-5-S16	S99456 x SEL99TER85314	ICARDA, Syria	
NDC-15-3	Pb-91/M	NIFA, Pakistan	NKC-5-S17	S99456 x SEL99TER85314	ICARDA, Syria	
NDC-15-4	Pb-91/M	NIFA, Pakistan	NKC-5-S18	(ILC4291xFLIP98-129C) x S98008	ICARDA, Syria	
NDC-4-15-1	C-44/M	NIFA, Pakistan	NKC-5-S19	(ILC4291xFLIP98-129C) x S98008	ICARDA, Syria	
NDC-4-15-2	C-44/M	NIFA, Pakistan	NKC-5-S20	(FLIP98-138C x SEL99TH15039)	ICARDA, Syria	
NDC-4-15-3	C-44/M	NIFA, Pakistan	NKC-5-S21	GLK95069 x SEL99TER85530	ICARDA, Syria	
NDC-4-20-1	C-44/M	NIFA, Pakistan	NKC-5-S22	CA9783007 x SEL99TER85534	ICARDA, Syria	
NDC-4-20-2	C-44/M	NIFA, Pakistan	NKC-5-S23	CA9783007 x SEL99TER85534	ICARDA, Syria	
NDC-4-20-3	C-44/M	NIFA, Pakistan	NKC-5-S24	CA9783007 x SEL99TER85534	ICARDA, Syria	
NDC-4-20-4	C-44/M	NIFA, Pakistan	HASSAN-2K	ILC-195/M	NIFA, Pakistan	
NDC-4-20-5	C-44/M	NIFA, Pakistan	Karak 1	Local selection	Karak, Pakistan	
NDC-4-20-6	C-44/M	NIFA, Pakistan	Karak 2	Local selection	Karak, Pakistan	
NDC-4-20-7	C-44/M	NIFA, Pakistan	Karak 3	Local selection	Karak, Pakistan	
NDC-5-S10	JG 74 x ICC 12071.	ICRISAT, India	Sheenghar	Local selection	Karak, Pakistan	
NDC-5-S11	JG 74 x ICC 12071.	ICRISAT, India	Lawaaghar	Local selection	Karak, Pakistan	
NIFA-88	6153/M	NIFA, Pakistan	ICC 4993	Rabat	Karnataka, India	
NIFA-95	6153/M	NIFA, Pakistan	ICC 19183	ICC 4993	ICRISAT	
NIFA-2005	PB-91/M	NIFA, Pakistan	ICC 4918	Annigeri	Morocco	
NKC-262-26	ILC-195/M	NIFA, Pakistan	ICC 19181	ICC 435	ICRISAT	
NKC-452-2	(ILC4291 x Flip98- 129c) x S98008	ICARDA, Syria				

 Table I
 Pedigree and origin of genotypes/accessions used in the study

Germplasm was also evaluated for quantitative traits including days to 50% flowering, days to maturity, plant height, number of leaflets leaf¹, leaf area, seed yield plant⁻¹,100 seed weight and biological yield. Ten equally competitive plants were ear marked from each genotype replication⁻¹ for recording data on the quantitative traits. Data were analyzed using statistical software SAS (statistical analysis system) version 9 following the model for a Randomized Complete Block Design (RCBD). Least significant difference (LSD) test at 5% probability level was applied for mean separation (James *et al.*, 1997). The genetic parameters (genotypic and phenotypic variances, and their coefficient of variation) and heritability (broad-sense) were estimated as suggested by Burton (1952) and Hanson *et al.* (1956), respectively.

RESULTS AND DISCUSSION

Characterization for flower color, stem color and seed coat color of all genotypes is presented in Table-II. Significant variation in color of three traits among genotypes was observed. Out of 47 genotypes, 29 genotypes including 23 from NIFA, four from Karak and two from ICRISAT, India (Table II) produced pink flowers, green with a purplish tinge stem and light brown to dark brown or yellowish seed coat color. These markers are typical for Desi type chickpea. Rest 18 genotypes including 15 from NIFA, one from Karak and two from ICRISAT (Table II) produced white flowers with green stem and white seed coat. These characters are distinctive for Kabuli type

chickpea. These markers play a vital role in identification of land races and estimation of out-crossing percentage in chickpea. Upadhyaya *et al.* (2002) also found significant variation in core collection of chickpea for flower and plant color (stem color). In their collection dots on seed testa were also present. Moreover variation in flower and seed color is reported by Farshadfar and Farshadfar (2008) while evaluating 360 chickpea land races. Variability in seed coat and flower color was also observed by Afsari *et al.* (2004) in chickpea germplasm.

Genotype Name	e Name Flower color Stem color		Seed coat color	
NDC-122	Pink	Green with purplish tinge	light brown	
NDC-727	"	- <u>'</u> ''	dark brown	
NDC-728-5	"	"	dark brown	
NDC-730-2	"	"	dark brown	
NDC-15-1	"	"	"	
NDC-15-2	"	"	"	
NDC-15-3	"	"	"	
NDC-15-4	"	"	"	
NDC-4-15-1	"	"	"	
NDC-4-15-2	"	"	"	
NDC-4-15-3	"	"	"	
NDC-4-20-1	"	"	"	
NDC-4-20-2	"	"	"	
NDC-4-20-3	"	"	"	
NDC-4-20-4	"	"	"	
NDC-4-20-5	"	"	"	
NDC-4-20-5	"	"	"	
NDC-4-20-0	"	"	"	
NDC-5-S10	"	"	dark brown	
NDC-5-S11	"	"	vellowish	
NIEA 88	"	"	brown	
NIEA 05	"	"	brown	
NIFA 2005	"	"	vellowish	
NIC 10.00	white	Groop	yellowish	
NKC-10-99 NKC 5 812	winte	Green "	winte	
NKC-5-512 NKC 5-512	"	"	"	
NKC-5-515 NKC 5-514	"	"	"	
NKC-5-514 NKC 5 815	"	"	"	
NKC-5-515 NKC 5-516	"	"	"	
NKC-5-510 NKC 5 817	"	"	"	
NKC-5-51/	"	"	"	
NKC-5-518				
NKC-5-S19				
NKC-5-520				
NKC-5-S21				
NKC-5-S22				
NKC-5-S23				
NKC-5-S24				
HASSAN-2K		~		
Karak I	Pink	Green with purplish tinge	brown	
Karak 2	"	"	"	
Karak 3	"	"		
Sheenghar	"	"	"	
Lawaghar	white	Green	white	
ICC4993	"	"	"	
ICC 19183	"	"	"	
ICC4918	Pink	Green with purplish tinge	brown	
ICC19181	Pink	"	brown	

 Table-II
 Flower color, stem color and seed coat color of evaluated chickpea germplasm

The germplasm was also evaluated for days to flowering, days to maturity, plant height, leaflets leaf¹, leaf area, seed yield plant¹, 100-seed weight, and biological yield. Mean square values and mean values (Table III – IV) for each trait revealed highly significant differences and broad range of variation among genotypes, which is amenable for genetic improvement of chickpea through selection. Plant growth duration (flowering and maturity) plays important role in increasing seed yield of chickpea. Variation in climatic factors like temperature and

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photoperiod in different environments affect maturity of genotypes and so the overall yield. In the present study variability in days to 50% flowering and days to maturity were significant among all the genotypes. Flowering in genotype ICC19183 was earlier (90 days), while in NDC-4-20-6 was late (122). Genotype ICC19181 matured earlier (163 days) while genotype Sheenghar matured later (178 days). Other studies have also confirmed significant variation in days to 50% flowering and days to maturity in Chickpea (Atta *et al.*, 2008; Saleem *et al.*, 2008; Hakim *et al.*, 2006) and soybean (Muhammad *et al.*, 2007).

Character	Range	Mean±SE	Mean square Replication Genotype		
Days to flowering	90-122	112.04±2.09	25.45	186.64**	
Days to maturity	163-178	172.36±2.39	12.27	38.40**	
Plant height (cm)	50-94	67.42±3.81	0.90	260.05**	
Number of leaflets leaf ¹	11.6-16.33	13.8 ± 0.92	0.57	8.61**	
Leaf area (cm ²)	1.73-10.92	7.10±1.49	0.45	9.09**	
Seed yield plant ⁻¹ (g)	4.1-28.9	10.59±2.56	3.64	70.75**	
100 seed weight (g)	13-39	24.7±2.73	1.75	88.02**	
Biological yield ⁻¹ (g)	14.3-68	31.11±3.67	10.82	359.36**	

Table III Ranges, means, standard errors and mean squares for different quantitative traits in chickpea germplasm

Plant height is desirable trait to reduced lodging in crops; similarly, higher seed weight, leaf area and more leaflets leaf⁻¹ contribute to higher seed yield. In the present study an adequate variability for plant height and other yield contributing traits among various genotypes was found. Plants of the accession NDC 5-S11 were the shortest (47 cm) whilst those of NKC-5-S15 were the tallest (94 cm). Leaf area of accession NKC-5-S18 was the largest (10.92 cm²) whereas of genotype ICC4918 was the smallest (1.73 cm²). Genotypes NDC-730-2 and NDC-4-20-2 produced the maximum number of leaflets leaf⁻¹ (16.33) while genotype NDC-5-S11 produced the minimum (11.66) leaflets leaf⁻¹. On average seed yield of Karak 3 was the maximum (28.9 g) while that of NDC-15-2 was the lowest (4.1 g). Weight of 100 seed of NKC-5-S18 was the maximum (39 g) whereas that of NDC-4-20-1 was the minimum (13 g). Earlier reports in chickpea by Atta *et al.* (2008), Hakim *et al.* (2006), Arshad *et al.* (2004), and in soybean by Muhamad *et al.* (2007) also confirm these results. Biomass (total dry weight) plant⁻¹ gives significant information about crops. Significant variation in biomass/biological yield plant⁻¹ was observed among genotypes in the collected germplasm for the current study. NIFA-2005 produced the highest biological yield (68 g) whilst NKC-5-S19 yielded the lowest (14.3g). Similarly Jeena *et al.* (2005) and Arshad *et al.* (2004) also reported significant differences in biological yield plant⁻¹ among their chickpea collection.

Components of variance for entire studied parameters are depicted in Table V. Phenotypic coefficient of variation as well as the genotypic coefficient of variation was lower for days to flowering and days to maturity. Moderate values of PCV and GCV were observed for 100 seed weight, leaf area, leaflets leaf¹ and plant height and their range were high for grain yield plant⁻¹ and biological yield. Saleem *et al.* (2008), Atta *et al.* (2008) and Hakim *et al.* (2006) also reported low PCV and GCV for days to flowering and days to maturity in chickpea. Similar results were registered by Saleem at al. (2008) and Atta *et al.* (2008) for seed yield plant⁻¹, plant height, 100 seed weight and biological yield of chickpea, while Hakim *et al.* (2006) observed high values of PCV and GCV in chickpea for 100 seed weight and seed yield plant⁻¹ but lower for plant height. Burli *et al.* (2004) also observed high PCV and GCV values for seed yield plant⁻¹ but they registered low values for 100 seed weight in chickpea. The difference in result for 100 seed weight could be attributed to difference in environment.

Phenotypic coefficient of variability was greater than genotypic coefficient of variability for all the parameters but the difference is less in all the cases except leaf area and seed yield plant⁻¹ (Table V). Differences among PCV and GCV were low for days to 50% flowering (7.1 and 6.9), days to maturity (2.3 and 1.9), plant height (14.5 and 13.4), leaflets leaf⁻¹(13.4 and 11.16), 100 seed weight (23.3 and 21.1) and biological yield plant⁻¹ (36.4 and 34.5) while only leaf area (29.91 and 21.2) and seed yield plant⁻¹ (49.9 and 43.6) revealed comparatively more difference among PCV and GCV. Little difference between PCV and GCV revealed that the genotypic variance is more than the environmental variance. Heritability estimates (Table V) were high for days to 50% flowering (93%), biological yield plant⁻¹ (89%), plant height (88%), 100 seed weight (82%), seed yield plant⁻¹ (77%), number of leaflets leaf⁻¹ (75%) and days to maturity (68%). Moderate heritability was recorded for leaf area (51%). All traits showed high heritability except leaf area which exhibited moderate heritability. High heritability of all the traits was also reflected by the minor difference in magnitudes of PCV and GCV. High estimates of heritability of the traits under study could be due to the greater genetic variability of the germplasm. Saleem *et al.* (2008), Durga *et al.* (2007), Hakim *et al.* (2006), Ghafoor *et al.* (2004) found similar results and observed high heritability in chickpea for days to flowering, plant height, 100-seed weight, seed yield plant⁻¹ and biological yield plant⁻¹.

Genotype	DF 50%	Days Plant No of Leaf		Leaf	Grain yield 100-seed		Bio v/plt (g)	
Genotype		90% mat	height cm	Leaflets	area	per plant (g)	weight (g)	Dio.y/pit (g)
NDC-122	116	173	70	16	8.37	10	27	39.7
NDC-727	118	167	66	12.66	6.23	7	20.7	32
NDC-728-5	118	168	77	15.66	9.51	7.8	21.7	30.4
NDC-730-2	114	166	73	16.33	8.2	7.4	20.9	36
NDC-15-1	118	171	66	15	7.15	15	23	39.6
NDC-15-2	118	175	76	15.66	7.67	4.1	21.1	20.4
NDC-15-3	118	169	62	16	8.07	5	20.3	23.1
NDC-15-4	118	168	67	15.66	7.88	9	25	22.2
NDC-4-15-1	115	173	64	16	7.74	5.3	20.1	24
NDC-4-15-2	116	171	50	16	9.9	7	23	18.2
NDC-4-15-3	118	172	58	15.33	6.51	5.4	23	24.1
NDC-4-20-1	116	169	70	15.33	6.57	18	13	56.7
NDC-4-20-2	119	170	67	16.33	8.37	6.2	21.3	29
NDC-4-20-3	118	172	65	14.66	8.86	5.3	22.3	22
NDC-4-20-4	117	173	67	16	8.04	5	20.6	24.3
NDC-4-20-5	115	170	67	16	6.82	6	21.7	28
NDC-4-20-6	122	173	63	14	7.54	15.6	25	65.7
NDC-4-20-7	116	172	67	15.66	7.74	5.2	21.5	47.4
NDC-5-S10	105	177	51	12	5.74	9.1	27	24.4
NDC-5-S11	104	176	47	11.66	5.47	9	27	23
NIFA-88	116	175	73	12	7.19	7.5	14.6	20.1
NIFA-95	115	174	67	12	4.46	7	14.1	19.7
NIFA-2005	113	171	64	13	7.24	14.7	22	68
NKC-10-99	116	175	88	12	8.37	7.2	33	43.9
NKC-5-S12	112	176	69	12.33	5.29	13.6	23	34.6
NKC-5-S13	113	176	72	12.33	8.37	15.5	35	39.6
NKC-5-S14	111	175	66	12	7.06	14.5	29	32.3
NKC-5-S15	113	175	94	12	9.03	13.1	32	36.7
NKC-5-S16	97	174	60	16	8.55	12	25	30
NKC-5-S17	110	176	57	14	9.85	13.3	34	34.4
NKC-5-S18	99	175	62	12	10.92	13.2	39	32.1
NKC-5-S19	120	172	65	12.33	7.15	10	26	14.3
NKC-5-S20	101	175	72	13	6.45	13.1	29	27.4
NKC-5-S21	112	176	60	14	5.61	12	25	27.1
NKC-5-S22	107	175	64	13.33	6.41	9.2	25	26.4
NKC-5-S23	107	174	73	13.33	7.17	12.5	28	31
NKC-5-S24	110	173	73	11.66	6.77	15	33	36.2
HASSAN-2K	116	174	68	15.66	5.01	13.2	23	26.3
Karak 1	115	175	69	12	7.21	18.2	22	31.3
Karak 2	117	174	67	12.66	8.153	16.9	24	28.5
Karak 3	114	172	67	13	6.35	28.9	25	27.6
Sheenghar	120	178	70	14.33	7.51	14	22	33.4
Lawaghar	118	176	60	14	7.52	13.7	36	25.3
Rabat	97	165	88	12.33	3.65	7	21	28.7
ICC	90	164	89	11	3 85	6	2.2	24.6
Annigeri	96	168	59	12.33	1 73	84	22	25.1
ICC19181	92	163	60	12.33	4 61	59	26	27.7
LSD (0.05)	3.38	3.89	2.42	1.49	4.18	3.16	2.9	3

 Table IV
 Mean values for days to emergence, germination percentage, days to 50% flowering, days to maturity and plant height chickpea genotypes evaluated at Agricultural University Peshawar during 2007-08

 Table V
 Estimates of genotypic variance (Vg), phenotypic variance (vp), genotypic coefficient of variability (PCV), phenotypic coefficient of variability (GCV) and heritability ($h^2_{(bs)}$) for various agronomic traits

Traits	$\mathbf{V_g}$	$\mathbf{V}_{\mathbf{p}}$	GCV	PCV	% h ² (bs)
Days to 50% flowering	60.76	65.06	6.9	7.18	93
Days to maturity	10.88	15.93	1.9	2.3	68
Plant height	81.84	96.37	13.41	14.56	88
Leaflets leaf ¹	2.58	3.43	11.66	13.42	75
Leaf area	2.28	4.519	21.26	29.91	51
Grain yield plant ⁻¹	21.3	27.9	43.6	49.9	77
100 seed weight	27.34	33.34	21.16	23.37	82
Biological yield plant ⁻¹	115.28	128.78	34.51	36.47	89

CONCLUSION AND RECOMMENDATIONS

The present study concluded that there is a great amount of genetic diversity in the germplasm studied. Majority of traits revealed high heritability and low level of differences among PCV and GCV which indicate less environmental influence on these traits and showed that genotypes had more influential role in the expression of these traits. This suggests a great chance of genetic improvements of these traits in chickpea. Thus the variability found in the germplasm could be utilized successfully in different breeding programs for the betterment of existing genotypes and for the development of desirable genotypes through hybridization.

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