Original Research Article

STUDIES OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE IN YIELD COMPONENT TRAITS IN CHICKPEA (*Cicer arietinum* L.)

ABSTRACT

20 diverse genotypes of chickpea including three checks viz., GNG 158, GNG 1488, PNG 469-checks, were carried out under Agriculture Research farm, Department of Genetics of Plant Breeding, Lovely Professional University, Phagwara (Punjab). This experiment was conducted in RBD with three replications, during rabi 2021-2022. To estimate genetic variability, heritability and genetic advance percent of the mean. analysis of variance for the design of experiments has been present for all the twelve traitsThe analysis of variance estimation demonstrated that the mean sum of squares attributed to genotypes were significant for all of the characters, suggesting that there was enough genetic diversity among the genotypes. The current study found that the phenotypic coefficient of variation was greater than the corresponding genotypic coefficient of variation for all traits, which could be attributed to genotype-environment interaction to some degree or another, explaining environmental factors influencing the expression of these characters. In the present study, moderate PCV, GCV were observed in No. of secondary branches per plant, 100 seed weight, No. of primary branches per plant, Harvest index, biological yield per plant, No. of pods per plant, Plant height and Seed yield per plant. Low value of PCV and GCV were recorded in No. of seeds per pod, protein content, Days to maturity and Days to 50% flowering, shows the magnitude of PCV and GCV were low and indicating limited scope for improvement. The genotypic correlation coefficient was higher in magnitude than their corresponding phenotypic one, indicating there by strong inherent association between different traits studied. The phenotypic expression of correlation was less due to multiple influences of environmental components in the view of correspondence selection on phenotypic basis would be effective.

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Keywords: Genetic variability,PCV, GCV, chickpea, heritability, genetic advance

1. INTRODUCTION:

Pulses, which are high in protein, are an essential part of the Indian diet. Pulses are generated with the least number of resources; hence they are less expensive than animal protein. In compared to other vegetables, pulses are high in protein, less costly, and may be utilized in a variety of cropping systems without interfering with the primary cereal crops. Aside from being a good source of protein, they are also beneficial to agriculture since they improve soil health and fertility by fixing nitrogen organically. Chickpea (Cicer arietinum L.), also referred as gram, Bengal gramme, chhola, and garbanzo bean, was one of the first grain legumes produced by humans. (Van der Maesen, 1972It is

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a self-pollinated crop from of the Papilionaceae subfamily of the Family Fabaceae (Bentham and Hooker, 1970). Chickpeas are diploid with 2n=16 chromosomes. Chickpeas is the most important pulse crop, with extensive acceptance and use. During the rabi, chickpea is typically farmed in marginal rainfed regions. It is a temperate and subtropical bean plant that flourishes in both tropical and temperate regions. Chickpea is classified into two market types: desi and Kabuli (Pundir*et al.,* 1985). The desi types, which account for around 85 percent of chickpea area, are distinguished by small, angular-shaped, dark-colored seeds with a rough surface, pink flowers, anthocyanin pigment on the stem, and either a semi-spreading or semi erect growth habit.India is the world's leading producer of chickpeas, both in terms of land and output. It might be attributed to a variety of causes, including a favorable environment, high-yielding seeds, increased farmer acceptance, and a wide market. More than half of India's chickpea output is produced in states such as Madhya Pradesh, Maharashtra, and Rajasthan. Chickpeas account for over 70 percent of total of India's pulse exporting (Vikram, P.K. 2021). Chickpeas are split and eaten as dal, as well as whole fried or boiled seeds. As a source of nourishment, animals eat husk and dal bits. Green, immature chickpeas are eaten as a vegetable in India and Pakistan, while chickpea flour is frequently used in snacks and sweets. Animals love the nourishment that straw provides. The lack of genetic variety for the majority of agronomic attributes is a major barrier to the development of pulse crops. Currently, it is simple to transfer genes from (C. *reticulatum*) chickpea to (C. *arietnum*L) chickpea. However, important genes from other species of the genus Cicer cannot be utilized because of incompatibility issues. Using novel techniques like embryo rescue and somatic hybridization, beneficial genes from other cicer species may be introduced into the domesticated chickpea, Cicer arietinum (Altaf and Ahmed, 1990).

2. MATERIALS AND METHODS:

The present investigation entitled “Study of Genetic Variability, heritability and genetic Advance in Chickpea (Cicer arietinum L.)” was conducted during Rabi, 2021-2022. In the experiment twenty 20 diverse genotypes including three checks viz., GNG 158, GNG 1488, PNG 469- checks of chickpea, were carried out under Agriculture Research farm, Dept of Genetics of Plant Breeding, Lovely Professional University, Phagwara (Punjab). This experiment was conducted in RBD with three replications. All Observations recorded for twelve characters. The details of the genotypes used in this study are presented in (Table 1). The experimental materials consisting of twenty diverse genotypes of chickpea were sown in randomized block design in three replications. Each entry was planted in a plot size of 50 x 6 m accommodating 4 rows of 2m length, keeping row to row and plant to plant distance of 45 x 30, respectively. All the recommended package of practices was followed to raise a good and healthy crop. In each plot, five randomly selected competitive plants were tagged to record observations except for days to 50% heading and days to maturity which were recorded on plot basis. By taking the average, the mean value for the treatment was computed. Observations recorded for twelve characters viz., Days to 50 per cent flowering, Days to maturity, Plant height (cm), Number of primary branches per plant, Number of secondary branches per plant, Number of pods per plant, Number of seeds per pod, 100-seed weight (g), Biological yield per plant (g), Harvest index (%),

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Protein content (%) and Seed yield per plant (g).The data acquired was subject to genetic variability, Heritability and Genetic Advance. The Analysis of variance (Panse and Sukhatme, 1962), Heritability (Hanson *et. al.,* 1956), Genetic advance (Johnson *et. al.,* 1955) were estimated.

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3. RESULTS AND DISCUSSION:

Analysis of variance of experiment has been present in Table 2 for all the twelve characters. Analysis of variance indicated that the mean sum of square (MSS) due to genotypes were highly significant for all the characters at 1% and 5% level of significance and it indicated the presence of consisted amount of genetic variability for all the traits. Similar kind of results were also found by Meena *et al.* (2021), Gautam *et al.* (2021).The estimates of Genetic variability, Broad sense heritability and genetic advance per cent of mean is given in Table 4. In the present study, moderate PCV, GCV were observed in No. of secondary branches per plant (19.58, 18.97), 100 seed weight (16.07, 16.02), No. of primary branches per plant (16.5, 15.88), Harvest index (13.26, 13.12), biological yield per plant (11.68, 11.51), No. of pods per plant (10.76, 10.72), Plant height (10.14, 10.11) and Seed yield per plant (10.13, 10). Low value of PCV and GCV were recorded in No. of seeds per pod (8.59, 7.16), protein content (5.07, 5.06), Days to maturity (2.04, 2.02) and Days to 50% flowering (1.94, 1.88), shows the magnitude of PCV and GCV were low and indicating limited scope for improvement.Similar kind of results were also found by Singh *et al.*(2018), Kumar*et al*. (2019), Meena *et al.*(2021).High heritability coupled with high genetic advance as percentage of mean observed in traits viz., for No. of secondary branches per plant (93.8%, 37.86) 100 seed weight (99.3%, 32.87), No. of primary branches per plant (92.5%, 31.46), Harvest Index (97.8%, 26.2), Seed yield per plant (97.4%, 23.38), Number of pods per plant (99.1%, 21.98), Plant height (99.3%, 20.76), and biological yield per plant (97.2%, 20.33) thus these characters show additive gene action in their expression. High heritability with moderate genetic advance as percentage of mean was recorded for Number of seeds per pod (69.5%, 12.3) and Protein content (99.8%, 10.41). High heritability with Low genetic advance as percentage of mean was recorded for days to maturity (98.4%, 4.13), and days to 50% flowering (94.6%, 3.78) indicates presence of non-additive gene effects and selection may be ineffective. Similar kind of results were also found by Singh *et al.*(2018), Kumar *et al.*(2019) Meena *et al.* (2021), Gautam *et al.* (2021).

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Table 1 - List of genotypes used in the study.

S. No	Name of genotype	S. No	Name of genotype

1.	GL25016	11.	CSG 515
2.	ICCL 86111	12.	ICC 3020
3.	GNG 1581	13.	JAKI 9218
4.	GNG 1488	14.	C 18443
5.	PNG 469-	15.	GNG 1958
6.	GNG 2171	16.	ICC- 5434
7.	PBG- 5	17.	PDG- 4
8.	ICC 5335	18.	Vijay
9.	SADABAHAR	19.	MDG 15-1
10.	RSG 945	20.	PBG- 7

Table-2. Mean Sum of Squares

Source of Variation	d.f	Days to 50% Flowering	Days to Maturity	Plant Height	No. ofPrimary Branches Plant-1	No. ofSecondary Branches Plant-1	Number of Pods Plant-1
Replication	2	6.82**	2.87**	0.31	0.12	0.22	6.35**
Genotypes	19	13.27**	23.78**	31.99**	2.27**	4.67**	82.44**
Error	38	0.71	0.38	0.21	0.17	0.29	0.72
CV		0.78	0.44	1.43	7.81	8.41	1.75

Table-2. Mean Sum of Squares

Source of Variation	d.f	Number of Seeds Plant-1	100-grain weight	Biological yield per plant	Seed yield per plant	Protein Content	Harvest index
Replication	2	0.07*	0.09	1.67	0.87**	0.01	4.74*
Genotypes	19	0.07**	9.04**	25.84**	3.12**	3.90**	48.68**
Error	38	0.02	0.06	0.67	0.09	0.01	1.08
CV		8.21	2.35	2.83	0.43	3.42	3.38

****=significantat5% and1%levelofprobability, NS = non-significant.**

Table-3. Mean values for chickpea genotypes

S. No	Genotype	DFF	DM	PH	NPB	NSB	NPP	NSP	HSW	BY	PC	HI	SY
1.	GL25016	106	135	30.23	4.00	6.33	42.60	1.80	11.76	28.37	21.80	29.99	8.51
2.	ICCL 86111	108	136.33	35.03	6.00	6.33	42.07	1.60	10.77	32.03	21.25	24.63	7.89
3.	GNG 1581	105	142.33	35.57	4.00	4.33	49.43	1.87	11.44	28.27	23.12	32.65	9.23
4.	GNG 1488	108	135	29.83	5.00	8.33	52.77	1.80	11.83	27.46	20.15	30.85	8.48
5.	PNG 469	103.67	137	33.80	6.67	7.67	55.55	1.93	10.24	29.40	23.62	37.40	11
6.	GNG 2171	111	141	32.97	5.00	5.33	49.66	1.63	14.03	25.48	22.62	37.07	9.45
7.	PBG- 5	112	139	26.43	4.00	5.33	47.65	1.87	11.89	28.01	23.12	31.23	8.74
8.	ICC 5335	111	139.33	28.00	5.67	6.00	45.08	1.50	8.07	27.53	22.62	31.71	8.73
9.	SADABAHAR	106.33	140	30.73	5.33	5.00	49.72	1.80	9.41	28.44	22.62	27.99	7.94
10.	RSG 945	107.33	135	33.97	4.33	4.33	53.68	1.80	8.00	32.98	23.87	26.20	8.64
11.	CSG 515	108.67	134.67	30.83	6.33	6.33	48.22	1.63	11.00	28.49	24.37	30.54	8.7
12.	ICC 3020	108.67	142	29.23	5.67	5.67	44.87	1.47	10.81	28.44	20.62	31.01	8.82
13.	JAKI 9218	108.33	141.33	30.97	4.33	6.33	58.73	1.83	11.93	26.79	23.75	35.38	9.48
14.	C 18443	109	137	28.73	6.00	7.33	40.30	1.80	11.54	29.04	22.50	26.99	7.84
15.	GNG 1958	109	135	32.90	6.33	7.00	52.97	1.87	8.00	31.47	23.75	27.07	8.52
16.	GL 25016	109.33	137	30.53	4.33	5.67	44.53	1.70	9.21	23.03	22.00	36.79	8.47
17.	PDG- 4	110.33	136	37.90	5.33	6.67	49.25	1.67	9.53	31.93	21.56	23.89	7.63
18.	Vijay	109.33	142	32.63	6.00	8.33	56.50	1.87	11.27	36.39	22.50	30.78	11.2
19.	MDG 15-1	110.33	141	34.30	5.00	6.33	41.42	1.60	11.03	26.07	21.27	26.28	6.84
20.	PBG- 7	110	135.33	39.27	6.00	8.67	49.00	2.07	14.20	29.54	23.12	28.98	8.56
Mean		108.57	138.07	32.19	5.27	6.37	48.70	1.76	10.80	28.96	22.51	30.37	8.73
C.V.		0.78	0.44	1.43	7.81	8.41	1.75	8.21	2.35	2.83	0.43	3.42	3.38

DFF = Days to 50% flowering, **DM** = Days to maturity, **PH** = Plant height, **NPB** = Number of primary branches per plant, **NSB** = Number of secondary branches per plant, **NPP** = Number of pods per plant, **NSP** = Number of seeds per pod, **HSW** = 100 seed weight, **BY** = Biological yield/plant, **PC** = Protein content, **HI** = Harvest index, **SY** = Seed yield/plant.

Table -4: Genetic parameters of variation for seed yield and its components in Chickpea

S. No	Characters	Range		Mean	Co-Variance		Heritability	Genetic	GA%
		Min.	Max.		GCV	PCV	Broad Sense (%)	Advance	Mean
1.	Days to 50% flowering	103.67	112	108.57	1.88	1.94	94.6	4.1	3.78
2.	Days to maturity	134.67	142.33	138.07	2.02	2.04	98.4	5.71	4.13
3.	Plant height (cm)	26.43	39.27	32.19	10.11	10.14	99.3	6.68	20.76
4.	No. of primary branches per plant	4	6.67	5.27	15.88	16.5	92.5	1.66	31.46
5.	No. of secondary branches per plant	4.33	8.67	6.37	18.97	19.58	93.8	2.41	37.86
6.	Number of pods per plant	40.3	58.73	48.7	10.72	10.76	99.1	10.7	21.98
7.	Number of seeds per pod	1.47	2.07	1.76	7.16	8.59	69.5	0.22	12.3
8.	100 seed weight (g)	8	14.2	10.8	16.02	16.07	99.3	3.55	32.87
9.	Biological yield per plant (g)	23.03	36.39	28.96	11.51	11.68	97.2	5.89	20.33
10.	Seed yield per plant (g)	6.84	11.2	8.73	10	10.13	97.4	2.04	23.38
11.	Protein content (%)	20.15	24.37	22.51	5.06	5.07	99.8	2.34	10.41
12.	Harvest Index (%)	23.89	37.4	30.37	13.12	13.26	97.8	8.11	26.72

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