Estimation of ~~Analyzing the~~ genetic ~~variation~~ variabilityfor yield and its ~~attributing~~ componenttraits in Chickpea (*Cicer arietinum* L.)

ABSTRACT

Chickpea (Cicer arietinum L.) is a legume crop ~~belonging~~ which belongsto the family Leguminosae (Fabaceae). The genetic reconstruction of plant is required for developing high yielding varieties by incorporatingthe desirable traits and improving the characters of chickpea yield.The current investigation was conducted with 12chickpea genotypes, raised in randomized block design with three replications during the *Rabi* season 2023 to understand the nature and magnitude of the genetic component of variation for yield and yield traits in chickpea. The genotypes were evaluated to assess the genetic variability, heritability and genetic advance among yield and its components. Analysis of variance revealed that the mean square for genotypes was highly significant for all the traits studied, indicating the presence of a sufficient amount of genetic variability among the ~~variety~~ genotypes for all the 11 characters ~~studiedgenotypes~~under study.~~*viz*.,~~ The genotypes RSG-44 and Aruna were superior not only for seed yield per plant but also related traits like 100-seed weight, biological yield per plant, number of pods per plant and number of primary branches per plant. There is a scope to use These diverse genotypes ~~can be used~~ in future ~~breeding~~ hybridizationprogramme of chickpea.

Key words: Chickpea, genotypes, genetic variability, heritability, genetic advance, seed yield

INTRODUCTION~~INTRIDUCTION~~

Chickpea (*C. arietinum* L.) belongs to the family Fabaceae, within the tribe Cicerae. Chickpea (*Cicer arietinum* L.) also as called gram, garbanzo bean, Indian pea, cerci bean, etc. Bengal gram is a self pollinating, diploid (2n=2x=16) with genome size 1C=740 Mbp. Chickpea (*Cicer arietinum* L.) is the third pulse crop, 5th food legume and 15th grain crop of the world among various grain legumes.The global production of chickpea is nearly 11million tonnes and India is the major producer accounting for 64% of the total chickpea production. It is currently grown on about 11 m ha, with 96%cultivation in the developing countries. Chickpea production has increased during the past 30 years from 7.3 mt (average of 1977- 1979 trienniums) to 8.4 mt (average of 2004-06 triennium) because of increase in productivity from 693 to 786 kg ha^{-1} during this period.

Comment [n1]: Include recent data

It is a major source of high quality protein in human diet and also provides high quality crop residues for animal feed.Among the temperate pulses, chickpea is the most tolerant crop to heat and drought stress and is suitable for cultivation in low fertility soils. Chickpea also helps to maintain soil fertility through biological nitrogen fixation and contributes to the sustainability of cropping systems in the cereal-legume crop rotations. Chickpea crop meets 80% of its nitrogen (N) requirement from symbiotic nitrogen fixation and can fix up to 140 kg N ha^{-1} from air. It leaves a substantial amount of residual nitrogen for subsequent crops and adds plenty of organic matter to maintain and improve soil health. Because of its deep tap root system, chickpea can withstand extended periods of drought by extracting water from deeper layers of the soil.So, the present study was conducted with the objective to estimate the total genotypic variability and determine the heritability of specific agronomic parameters along with superior~~important~~ traits for selection criteria for improving yield in chickpea under normal sown condition.

MATERIALS AND METHODS

The field experiment was conducted at Organic Research Farm, Karguanji, Institute of Agricultural Sciences, Bundelkhand University, Jhansi (U.P.) India. The experimental material used in the present study comprised of the 12 genotypes. The experiment was laid-out in randomized block design with three replications of the plant geometry was maintained at 30 cm x 10 cm. the material was shown with the onset of monsoon on 1st Nov. 2023.Data were recorded on eleven different yield attributing characters *viz.,*~~including~~ days to 50% flowering, days to maturity, plant height, numbers of primary and secondary branches per plant, numbers of pods per plant, numbers of seeds per pod, 100-seed weight, harvest index, biological yield per plant and seed yield per plant. Five plants from each replication were randomly selected from eachgenotypefor recording observations~~ for all the traits~~.

Comment [n2]: Mention plot size

Genotypic (GCV) and phenotypic coefficient of variation (PCV) was calculated as per formula given by Burton (1952) [2], heritability in the broad sense (h2) as suggested by Burton and De (1953) [3] and genetic advance as per the method described by Johnson et al. (1955) [6].

RESULTS AND DISCUSSION

The analysis of variance presented significant differences for all the characters studied (Table 2) viz., days to 50% flowering, days to maturity, plant height, numbers of primary branches and secondary branches per plant, numbers of pods per plant, numbers of seeds per pod, 100 -seed weight, harvest index, biological yield per plant and seed yield per plant. This substantial variability provides a good prospect for improving traits of interest in chickpea breeding programmes. In some of the previous studies conducted by Dehal et al. (2016) [4] and Kumar et al. (2014) [7] similar findings have been reported for genetic variability in chickpea.

Comment [n3]: Try to provide recent findings i.e after 2020

Genetic parameters of yield and its attributing traits are presented in Table 3. Results revealed that PCV% was higher than GCV% for all the traits underestimation~~studied~~. High PCV and GCV were documented for biological yield per plant followed~~tracked~~ by numbers of pods per plant and 100-seed weight. Similarly, the moderate estimates of PCV and GCV were recorded for numbers of seeds per pod followed by numbers of primary and secondary branches per plant, harvest index, plant height and seed yield per plant, while the least estimate of PCV and GCV was recorded for days to 50% flowering and maturity. These results are ~~similartofinding~~revealed the findings of Yadav et al. (2015) [16], Kumar et al. (2018) [8] and Kumar et al. (2020) [9].

Higher estimates of heritability in broad sense were documented for plant height, numbers of pods per plant, biological yield per plant, day to maturity, 100-seed weight, numbers of primary and secondary branches per plant, harvest index, yield per plant, numbers of seeds per pods and day to 50% flowering. These results were in close conformity with the findings of Malik et al. (2010) [10] for 100- seed weight, harvest index, numbers of secondary branches per plant and yield per plant, Babbar et al. (2012) [1] for days to 50% flowering, days to maturity, plant height, 100- seed weight and yield per plant, Pandey et al. (2013) [12] for days to 50% flowering, numbers of seeds per pod, plant height and numbers of pods per plant, Monpara and Gaikwad (2014) [11] for seed yield per plant, 100-seed weight, plant height and numbers of primary branches per plant, Sowjanya et al. (2017) [14] for most of the traits and Honnappa et al. (2018) [5] for numbers of seeds per pod, biological yield per plant, 100-seed weight and yield per plant.

The higher genetic advance documented for biological yield per plant tracked by numbers of pods per plant, 100- seed weight, numbers of primary and secondary branches per plant, harvest index, plant height, numbers of seeds per pod and yield per plant. Whilst moderate estimate of genetic advance as percent of means was recorded for days to maturity and low estimate for days to 50% flowering. These results were in close agreement with the findings of Solanki et al. (2019) [13], Tsehaye et al. (2020) [15] and Kumar et al. (2020) [9].

Comment [n4]: Specify which traits are amenable for selection in favourable direction based on genetic advance

Table 1 Analysis of variance (ANOVA) for yield and its component traits in chickpea genotypes

Source of variation	Degree of freedom (df)	Mean sum of squares										
		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches/ plant	No. of secondary branches/ plant	Number of pod per plant	Number of seeds per pod	100 – seed weight	Harvest index	Seed yield per plant	Biological yield
Replications	2	2.52	9.69	18.38	0.69	6.77	0.02	0.10	8.54	3.28	6.98	42.76
Genotypes	11	20.86**	53.78**	62.05**	1.32*	11.36**	210.08**	0.32*	13.27**	105.66**	63.51**	346.73**
Error	22	3.376	13.11	5.90	0.51	3.08	28.72	0.13	2.89	16.28	4.80	18.63

*, ** Significant at 5% and 1% levels, respectively

Table 2: Mean values of 12 genotypes for 11 characters in chickpea genotypes

Genotypes	DF 50	DM	PH	NPB	NSB	NPP	NSP	100-SW	HI	SYP	BY
CSG-515	52.66	107.66	54.80	3.00	10.67	63.00	1.33	22.21	48.71	21.66	44.34
RSG-44	49.33	104.66	50.33	3.33	16.00	70.00	2.00	29.37	48.71	30.81	63.34
RSG-931	47	105.33	45.00	4.33	12.00	48.00	1.20	25.40	68.79	25.61	37.47
RSG-963	46.66	105.33	58.33	2.67	14.33	57.33	1.67	24.93	49.21	19	38.87
RSG-888	45	111.33	45.00	2.33	12.33	69.00	1.47	25.88	49.43	19.92	40.20
CSJK-6	52.33	100.66	50.67	3.33	14.33	58.00	1.67	22.69	48.33	25.75	53.33
ARUNA	47.33	107.00	55.00	4.67	15.00	71.00	2.07	27.15	47.09	29.48	62.63
GNG-2144	53	113.00	52.33	3.00	14.00	50.00	1.53	23.90	47.12	23.65	50.10
GNG-1969	48.33	108.33	45.33	3.33	9.67	64.00	1.27	26.42	52.98	16.50	31.27
GNG-1958	49.33	115.00	55.00	3.33	15.67	72.00	1.93	27.70	48.19	28.00	58.37
SAMRAT	51	103.66	51.33	2.67	12.67	70.67	1.20	24.77	48.58	25.61	52.87
VARDAN	51.33	111.66	56.00	3.33	13.67	68.67	2.00	23.67	49.54	18.55	37.42
GM	**49.44**	**107.80**	**51.59**	**3.27**	**13.36**	**63.47**	**1.61**	**25.34**	**50.55**	**23.71**	**47.51**
SE	**1.06**	**2.09**	**1.40**	**0.41**	**1.01**	**3.09**	**0.21**	**0.98**	**2.36**	**1.26**	**2.49**
CD 5%	**3.11**	**6.13**	**4.11**	**1.21**	**2.97**	**9.07**	**0.62**	**2.88**	**6.94**	**3.71**	**7.30**
CV	**3.72**	**3.36**	**4.71**	**21.84**	**13.14**	**8.44**	**23.06**	**6.71**	**8.11**	**9.24**	**9.08**

Table 3: Genetic variability parameters for yield and its attributing traits in chickpea genotypes

Characters	**DF 50**	**DM**	**PH**	**NPB**	**NSB**	**NPP**	**NSP**	**100-SW**	**HI**	**SYP**	**BY**
Maximum	54.0000	118.0000	60.0000	5	18.0000	75.0000	2.4	31.5000	79.2464	33.4000	66.7000
Minimum	44.0000	98.0000	42.0000	2	8.0000	40.0000	1	20.2300	44.5148	15.3200	30.2000
Grand Mean	49.4444	107.8056	51.5944	3.2778	13.3611	63.4722	1.61	25.3414	50.5551	23.7147	47.5169
SEm	1.0609	2.0911	1.4027	0.4134	1.0134	3.0943	0.214	0.9820	2.3666	1.2652	2.4921
CD 5%	3.1114	6.1331	4.1141	1.2124	2.9721	9.0754	0.629	2.8801	6.9409	3.7106	7.3091
CD 1%	4.2289	8.3360	5.5917	1.6478	4.0397	12.3350	0.855	3.9145	9.4339	5.0434	9.9344
ECV	3.7162	3.3597	4.7090	21.8434	13.1368	8.4439	23.06	6.7118	8.1080	9.2404	9.0841
GCV	4.8837	3.4152	8.3853	15.8585	12.4343	12.2498	15.36	7.3420	10.7657	18.6552	22.0087
PCV	6.1368	4.7908	9.6171	26.9927	18.0883	14.8781	27.71	9.9475	13.4774	20.8183	23.8097
Heritability (Bs)	63.33	50.82	76.02	34.52	47.25	67.79	30.74	54.48	63.81	80.30	85.44
GA	3.9585	5.4068	7.7708	0.6291	2.3526	13.1875	0.2828	2.8289	8.9560	8.1666	19.9136
GA % mean	8.0060	5.0153	15.0613	19.1929	17.6078	20.7768	17.55	11.1632	17.7153	34.4368	41.9084

CONCLUSION

Analysis of variance revealed that the mean square for genotypes was highly significant for all the traits, indicating the presence of a sufficient amount of genetic variability among the variety for all the 11 characters studied genotypes *viz*., RSG-44 and Aruna were superior not only for seed yield per plant but also related traits like 100-seed weight, biological yield per plant, number of pods per plant and number of primary branches per plant. Thus, selection of any trait can increase the other one, consider these traits for constricting plant type for higher yield, hence, for enhancement of yield these traits may be selected directly.

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