GENETIC EVALUATION OF CHICKPEA (*Cicer arietinum*L.) GERMPLASM FOR GROWTH, SEED YIELD AND IT'S ATTRIBUTING CHARACTERS IN PRAYAGRAJ AGRO-CLIMATIC CONDITIONS.

ABSTRACT

The current study evaluated 13 chickpea genotypes raised in a randomized block design with 3 replications during *Rabi* season of 2020-21 at Experimental research farm of Department of Genetics and Plant Breeding. Naini Agriculture Institute, Prayagraj.The results indicated that the magnitude of higher value of Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) was recorded for seed yield per plot and biological yield per plant respectively.The genotype C-203 recorded highest number of pods per plant, biological yield per plant, seed yield per plant and seed yield per plot. High Heritability coupled with high Genetic advance as percent mean was recorded for seed yield per plot, biological yield per plant and number of primary branches per plant. The analysis of variance indicated that there were highly significant differences among genotypes***.***

Key words*: Chickpea, Genetic advance, Genetic variability, Heritability,*Seed yield, grain legumes,Phenotypic variability,Genetic analysis

1. INTRODUCTION

“Legumes (grain legumes) are an important source of healthy food for humans and animals because they are high in protein as well as other essential minerals, vitamins, and dietary fiber. Legumes increase the viability of agricultural land by restoring soil fertilization through biological nitrogen fixation with the help of *Rhizobium* bacteria” [1]. “Pulses occupy a special place due to their high protein content. It is a self-pollinated crop. Due to its widespread growing nature in subtropical and warm-temperate regions, it is considered the third most important pulse crop after Fababean and Field Pea**.**Madhya Pradesh stands first in total gram area (34.32%) and production (39.47%). followed by Rajasthan (16.64% and 14.99%) and Maharashtra (16.09% and 12.95%). Uttar Pradesh ranges from 0.57 million hectares to 0.73 million tons, with a productivity of 1155 kgha^{-1}”[2].The protein percent in the Chickpea is about 17.72 to 38.5 percent and the carbohydrates are about 56.5 percent besides ash, calcium, phosphorus, and iron[3].Any new features used in Varietal Identification must be clearly defined, approved, and have a standard inspection method and should not be influenced by the environment, and should be accessible to breeders, also associated with lower costs. (According to the International Union for Conservation of New Plant Varieties **(UPOV)**[4]. Genetic variation helps to identify better yield traits for selection, the differential analysis assesses the environmental variation used to estimate phenotypes, genotypes, and related coefficients of variation [19,20]. The status of diversity in a specific population can be determined by the diversity coefficient values. The phenotypic coefficient of diversity, the genetic coefficient of diversity, and heredity help to identify superior genotypes. Inheritance provides information about genetic variation related to genetic variation and is also an important parameter for selecting desired parents. Current experiment was carried out with the objectives of Assessing the Genotypic and Phenotypic variability among Chickpea genotypes for the seed yield under PrayagrajAgro-climatic conditions for the future breeding program.

2. MATERIALS AND METHODS

The experiment was carried out during rabi season 2020-2021, at Field Test Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture

Sciences and Technology, Prayagraj. Soil was Sandy loam in texture with pH level of 7.0 to 8.0. The material comprised of 13 chickpea genotypes sown in a randomized block design with three replications with spacing of 30 X 10 cm.Data was recorded on five randomly selected plants in each plot in each replicationfor the traits except for Field emergence, Days to 50% flowering, Days to 50% pod setting, Days to maturity based on plot basis and remaining parameters were based on plant basis. Data on Field emergence percentage (%). Plant height (cm) @ 60, 90 DAS, Days to 50% flowering, Days to maturity, "Days to 50% pod setting,Number of primary branches per plant, Number of secondary branches per plant, Number of pods per plant, Number of seeds per plant, Seed index, biological yield per plant (g), Harvesting index (%), Seed yield per plant (g), Seed yield per plot (g) was observed. Analysis of Variance was worked out to test the significance of F and T tests" [21]. "It was carried out according to procedure of RBD for each characters as per the methodology suggested byPanseand Sukhatme".[5]. Data analysis was done to estimate Genotypic coefficient of variation (%) and phenotypic coefficient of variation (%) byBurton[6],Heritability (%)by Burton and Devane[7], Genetic advance byJohnson et al.,[8] and Genetic Advance as percent mean.

3. RESULTS AND DISCUSSION

Analysis of Variance revealed high significant difference between 13 genotypes for 15 traits (table 1) viz.Field emergence percentage (%). Plant height (cm) @ 60, 90 DAS, Days to 50% flowering, Days to maturity, Days to 50% pod setting,Number of primary branches per plant, Number of secondary branches per plant, Number of pods perplant, Number of seeds per plant, Seed index, biological yield per plant(g), Harvesting index (%), Seed yield per plant(g), Seed yield per plot(g). The 13 genotypes indicated the significant variation among all the characters.

3.1 Range of Variability

The range of variability (as shown in Table 2) for Field emergence (66.47% to 79.40%), Days to 50% flowering (64.00 days to 74.00 days), Days to 50% pod setting (76.00 days to 97.00 days), Days to Maturity (115.67 days to 129.67 days), Plant height (34.33 cm to 51.43 cm), Number of Primary branches per plant(2.33 to 4.27), Number of Secondary branches per plant(4.27 to 6.60), Number of pods per plant(33.53 to 54.60), Number of seeds per pod (45.67 to 67.60), Seed index (16.87 g to 25.60g), Biological yield per plant (16.48 to 37.47), Harvesting index (23.98 % to 44.37 %), Seed yield per plot (99.17 g to 281.63 g), Seed yield per plant(7.13 g to 11.27 g).

Table 1. Analysis of variance for different characters in Chickpea

S. No.	**Characters/traits**	**Mean Sum of Squares**		
		Replication (df =02)	**Treatments(df = 12)**	**Error(df = 24)**
01	Field Emergence	13.19	64.60**	16.58
02	Plant height @ 60 days	1.00	16.41**	1.37
03	Plant height @ 90 days	0.76	52.54**	1.44
04	Day to 50% flowering	0.92	26.34**	1.45
05	Days to 50% pod setting	10.18	98.02**	22.87
06	Days to Maturity	19.00	61.45**	5.89
07	No. of primary branches per plant	0.08	1.02**	0.04
08	No. of secondary branches per plant	0.10	1.40**	0.05
09	Number of pods per plant	1.24	119.14**	1.14
10	Number of seeds per pod	33.35	160.48**	23.91
11	Seed Index	1.75	20.38**	0.74
12	Biological yield per plant	5.82	102.82**	2.29
13	Harvest Index	21.37	90.04**	7.70
14	Seed yield per plot	134.56	9925.25**	41.91
15	Seed yield per plant	0.04	3.80**	0.15

*** and ** indicates significance at 5% and 1% respectively.**

Table 2. Genetic parameters for 15 traits of Chickpea

Traits	Mean	GCV	PCV	h^2	GA	GAM
Field Emergence	73.13	5.47	7.81	49.12	5.78	7.90
Plant height @ 60 days	21.48	10.43	11.76	78.59	4.09	19.04
Plant height @ 90 days	43.46	9.50	9.89	92.19	8.16	18.78
Days to 50% Flowering	68.92	4.18	4.53	85.12	5.47	7.94
Days to 50% pod setting	88.56	5.65	7.82	52.27	7.45	8.42
Days to Maturity	124.08	3.47	3.98	75.88	7.72	6.22
No. of PBPP	3.39	16.88	17.82	89.73	1.12	32.95
No. of SBPP	5.29	12.69	13.38	90.01	1.31	24.80
Number of pods per plant	45.07	13.91	14.11	97.19	12.74	28.26
Number of seeds per pod	55.32	12.20	15.06	65.56	11.25	20.34
Seed Index	21.70	11.79	12.44	89.86	5.00	23.03
Biological yield per plant	26.32	22.00	22.74	93.60	11.54	43.84
Harvest Index	33.64	15.57	17.62	78.10	9.54	28.35
Seed yield per plot	157.88	36.36	36.59	98.74	117.49	74.42
Seed yield per plant	8.78	12.55	13.32	88.72	2.14	24.35

No of PBPP = no of primary branches per plant, No of SBPP = No of primary branches per plant, PCV: Phenotypic Coefficient of Variation, GCV: Genotypic Coefficient of Variation, GA: Genetic Advance, GAM: Genetic Advance as Percent of Mean.

3.2 Phenotypic and Genotypic coefficient of variation

Even after accounting for the impact of environment on the expression of these traits, it was discovered that the estimated phenotypic coefficient of variation was higher than the equivalent genotypic coefficient of variation. Nonetheless, for every character, a strong correlation was found between the phenotypic and genotypic coefficients of variation. High genotypic coefficient of variation was recorded for seed yield per plot (36.36), Biological Yield per plant (22), and moderate for number of primary branches per plant (16.88) and harvest Index (15.57) and it was Low for days to 50% pod setting (5.65), field emergence (5.47). High phenotypic coefficient of variation was recorded for seed per plot (36.59), biological yield per plant (22.74) and moderate for no of primary branches per plant (17.82), harvest index (17.62),while it was low for days to 50% pod setting (7.82), days to 50% flowering (4.53). On an average high phenotypic and genotypic coefficient of variation was recorded for seed yield per plot, biological yield per plant suggesting variability among these traits. The results are in conformity with the findings of Babbaret al., [9],Reddy et al.**,**[10]and Gediyaet al.,[11].

3.3 Heritability

Lush (1949) gave the concept of heritability [12] which is the ratio of Genotypic Variance (VG) to Phenotypic variance (VP). High heritability was observed for seed yield per plot (98.74), No of pods per plant (97.19),Biological yield per plant(93.6),Plant height at 90 days (92.19), No of secondary branches per plant (90.01), Seed index (89.86), No of primary branches per plant (89.73), seed yield per plant (88.72), days to 50 % Flowering(85.12), Plant height at 60 days (78.59),Days to Maturity (75.88), Harvest Index (78.1), No of seed per pod (65.66) and indicated that this characters are less influenced by environmental effect and selection on the basis of phenotypic performance of genotypes would be more efficient in further improvement of these traits. High to moderate heritability indicated considerable potential for the development of high yielding varieties through desirable selection in succeeding generations. Comparable findings were reported by Desai et al.,[13], Thakur et al.,[14], Kumar et al.,[15].

3.4 Genetic Advance

High genetic advance was recorded for seed yield per plot (117.5) and moderate for number of pods per plots (12.74). biological yield per plant (11.54), No of seeds per pod (11.25) while it was low for harvest index (9.54), plant height at 90 days (8.16), days to maturity (7.72), days to 50% pod setting (7.45), field emergence (5.78), days to 50% flowering (5.47), seed index (5.0), plant height at 60 days (4.09), seed yield per plant (2.14), No of secondary branches per plant (1.31), No of primary branches (1.12). Low genetic advance was observed for the following characters, above which may be attributed to non-additive gene action governing these traits and improvement of such characters is possible through use of hybridization and hybrid vigour and moderate estimates of genetic advance indicating both additive and dominance gene effects, comparable results was reported by Joshi et al., [16].

3.5 Genetic Advance as Percent of Mean

High genetic advance as percent of mean were recorded for seed yield per plot (74.42), biological yield per plant (43.84), No of primary branches per plant (32.95), Harvest index (28.35), No of pods per plant (28.26), No of secondary branches per plant (24.8), seed yield per plant (24.35), seed index (23.03), No of seeds per pod (20.34) while it was low for days to 50% pod setting (8.42), days to 50% flowering (7.94), field emergence (7.9), days to maturity (6.22). similar results were reported by Barad et al.,[17], Mohammed et al.,[18]. From the above results high genetic as percent of mean indicated that these traits are most probably under the control of additive gene action and hence these traits can be fixed by proper selection.

4. Summary

It was summarized that based on mean performance of 13 genotypes of Chickpea. Seed yield per plant was highest in case of C-203 (11.27) and C-1025 (10.53) and C- 1027 (9.73) genotypes. On basis of ANOVA, significant difference was present among genotypes. The magnitude of GCV and PCV was recorded high for seed yield per plot and biological yield per plant. High heritability coupled with high genetic advance as percent of mean was recorded for seed yield per plot, biological yield per plant, number of primary branches per plant, harvest index, number of pods per plant, number of secondary branches per plant, seed yield per plant, seed index and number of seeds per plant.Hence these findings can berecommended to breeders for selection of parents in hybridization and also to farmer for better yield.

5. Conclusion

Based on the mean performance of 13 genotypes of Chickpea, seed yield per plant was highest in case of C-203 (11.27) and C-1025 (10.53) and C-1027 (9.73) genotypes. On the basis of analysis of variance, significant differences were recorded for the seed yield and its components indicating the presence of large amount of variability among the genotypes. The biological yield per plant and seed yield per plot showed the largest GCV and PCV values. In terms of seed yield per plot, biological yield per plant, number of primary branches per plant, harvest index, number of pods per plant, number of secondary branches per plant, number of seeds per plant, and number of seeds, high heritability combined with high genetic advance was noted as a percentage of mean.

Limitations of the Study

I am very thankful to your very important suggestions;very politely I would like to inform you that my educational requirement, The research project was already completed with the guidance of my professor. At this stage again starting the experiment from the beginning may not be possible. I am thankful for your valuable suggestion, I shall definitely consider your valuable suggestion for my research project, further I will take 30genotypes instead of 13 genotypes.

Thank you.

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