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Evaluation of chickpea (*Cicer arietinum* L.) genotypes for seed yield and quality traits

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Abstract

The present study entitled "Genetic divergence for seed yield, morpho-genetic and quality traits in chickpea" (*Cicer arietinum* L.) was carried out at Pulses Research Sub-Station (PRSS), Samba, during *Rabi* seasons 2017-18 and 2018-19. The experimental material comprising of 48 chickpea (*Cicer arietinum* L.) genotypes along with 5 checks were evaluated in Augmented Block Design at two locations *viz*, Advanced Center for Rain-fed Agriculture (ACRA), Rakh Dhiansar and Pulses Research Sub-Station (PRSS), Samba. Analysis of variance indicated the presence of notable genetic variability among chickpea genotypes for yield and quality traits for all the character studied. Estimates of components of variance indicated that genotypic variance contributed maximum to the phenotypic variance thereby, suggesting that the available genetic variability can be exploited through selection and hybridization. The variation present in the chickpea genotypes for breeding high yielding chickpea genotypes.

Keywords: Cicer arietinum L., genotypic variance, phenotypic variance, hybridization

Introduction

India is the world's largest importer of pulses, accounting for about 24 percent of global demand and 27 percent of consumption. Its share of global imports is increasing. Per capita pulse intake in India has decreased from 70 grammes per day in the 1960s to 48 grammes per day in 2019. This is due to rising population and stagnant pulse demand. This is in contrast to the WHO's recommendation of 80 grammes of pulse a day. According to available data, India import pulses to the tune of 2-3 million tonnes per year to meet domestic demands. It is a valuable crop because of its high nutritional value, with 4.5 percent fat, 8 percent crude fibre, 25-29 percent calcium, 41-50 percent starch, and 2.7 percent ash on average. Aside from its nutritious benefit, it is a significant contributor to soil fertility because of its ability to fix nitrogen with the aid of bacteria (Rhizobium sp) (Gul et al., 2013) [6]. Despite its high nutritional value and economic significance, chickpea cultivation in India has a poor and unpredictable average productivity. This may be due to the evolution of cultivars with a limited genetic base, making them more susceptible to constitutional stresses (Bhanu et al., 2017) ^[3]. Soaking characteristics, cooking time, and nutritional value all influence chickpea consistency. Breeding systems haven't paid enough attention to acceptability traits. These characteristics include grain size, form, colour, and appearance, as well as storage stability, cooking properties, product consistency and taste. Legumes with this defect are known to have long cooking time to soften cotyledon and seed cover. They are less desirable and less nutritious for the market. There were some hypotheses to justify the causes of leguminous hardening, but the process is still unexplained. Until intake, the chickpea seeds are transformed into a range of items. The key method for producing a tender edible product for both domestic and industrial scale processes is to soak dried seeds for 14-16 hour at room temperature, followed by cooking in boiling water for 1-2 hour (Manasa et al., 2020)^[9]. These two processes modify the physical and chemical composition of the seeds and control the following processes: water diffusion into the seed, starch gelatinization, geometrical and dimensional modifications, and soluble solid leaching from the seed through the soaking and cooking media, all of which are significant phenomena in chickpea during soaking and cooking. The seed swelling is an important parameter for analyzing and developing and designing the operation, and for designing and building equipment (Sayar et al., 2016)^[13].

Material and Method

The present study was carried out in Augmented Design at two locations, Advanced Center for

Rain-fed Agriculture (ACRA), Rakh Dhiansar and Pulses Research Sub-Station (PRSS), Samba, of SKUAST-Jammu, during Rabi season of 2017-18 & 2018-19. The experiment were sown under rain-fed conditions. The experimental materials used for present study comprised of 48 genotypes of chickpea (Cicer arietinum L.). The genotypes were diverse with respect to morphological and important economical traits. Among 48 genotypes, HC-5, CSJ-515, RSG-888, DKG-964 and BG-372 were undertaken as standard check. The seed materials for present study were received from Pulses Research Sub-Station (PRSS), Samba, of SKUAST-Jammu, during Rabi season 2017-18. The experiment was based on Augmented Design as suggested by Federer (1956, 1975) and Raghava Rao (1975)^[5] with the purpose of evaluating and doing statistical analysis of a large number of new selections. The yield of new selection was adjusted for block differences, which was measured by check varieties in every block. 48 genotypes along with 5 checks were planted in an augmented block design. The five check varieties were HC-5, CSJ-515, RSG-888, DKG-964 and BG-372. Experimental materials were allocated in six blocks in augmented block design with 5 checks distributed randomly in each block.

Observations were recorded for seed yield and quality traits *viz.*, protein content (%), 100 seed volume (cc), water absorption (%) overnight soaking, volume expansion (%) overnight soaking, hard grains (%), cooking time (min.), water uptake (%) at cooking time, volume expansion (%) at cooking time and seed yield as per standard procedures.

Results and Discussion

Analysis of variance was carried out among 48 chickpea genotypes and 5 checks using Augmented Block Design (Federer, 1956) and is presented in table 01. These varieties were found to be highly significant for seed yield and all the quality traits. Block effect were non-significant for all the morphological and quality traits except hard grains. As a result, there are significant underlying genetic variances among check varieties for various traits.

Mean performance and genetic variability

The mean performance for 53 chickpea genotypes for seed yield and 08 quality traits is presented in table 02 respectively. The genetic variability for seed yield and 08 quality traits of 48 chickpea genotypes and 5 checks was determined by genotypic and phenotypic coefficients of variation, heritability (broad sense), and genetic advance as a percentage of mean and the results for some are presented in tables 02 and figures 01, 02 & 03. The table shows that for seed yield and 08 quality traits studied, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV).

Protein content (26.93), 100 Seed volume (27.00), water absorption percent overnight soaking (0.33), volume expansion percent overnight soaking (0.82), hard grains (12.00), cooking time (80.54), water uptake percent at cooking time (0.24), volume expansion percent at cooking time (1.60) and seed yield (15.51) recorded the highest performance for the respective characters. In the present study wide range of variability was observed for almost all the traits studied except seed yield (15.51) water absorption percent overnight soaking (0.17-0.33), volume expansion percent at cooking time (0.07-0.24), volume expansion percent at cooking time (0.18-1.60). The characters protein content (16.55-26.93), 100 Seed volume (11.25-27.00), hard grains (4.00-12.00), cooking time (63.80-80.54) and seed yield (7.87-15.51) showed considerable amount of variability. These finding were in conformity with finding of Honnappa *et al.* (2018) ^[7], Olika *et al.* (2019) ^[11], Manasa *et al.* (2020) ^[9] and Anusha *et al.* (2020) ^[1].

Among the 48 chickpea genotypes along with 5 checks studied RKG-13-460 (protein content), BG-3066 (100 seed volume), GNG-2300 (water absorption percentage overnight soaking), CSJ-824 (volume expansion percentage overnight soaking), PBC-506 (hard grains), BG-3078 (cooking time), GNG-2300 (water uptake percentage at cooking time), CSJ-824 (volume expansion percentage at cooking time), and GNG-2346 (seed yield) recorded the highest performance for the respective characters.

The phenotypic coefficient of variation estimates were significantly higher than the genotypic coefficient of variation estimates, indicating that the variability in these characters was attributed to both genetics and the environment factors. High estimates of phenotypic coefficient of variance was observed for volume expansion percent at cooking time (40.71%) followed by water uptake percent at cooking time (26.47%), hard grains (21.95%), 100 seed volume (19.00%) and seed yield (15.70%). A similar pattern was shown at the genotypic level as well. As a result of the recent investigation, it was discovered that the population has sufficient genetic diversity and that there is a lot of scope for improvement. The difference between phenotypic coefficient of variance and genotypic coefficient of variance was negligible/ low for seed yield (0.30) and volume expansion percent overnight soaking (0.21). This suggests that environmental factors have the least impact on the expression of these traits and that their phenotype is the true representation of their genotype. Moreover, selection depending on specific results would be effective. These results were consistent with previous studies of Mohammed et al. (2019) [10], Sayar et al. (2016) [13], Bakhsh et al. (2011)^[2], Malik et al. (2011)^[8] and Ozer et al. (2010)^[12]. Hence, these characters can be assured, and simple selection can be studied to improve further.

Heritability and genetic advance

The estimate of heritability (bs) is high, the phenotypic appearance provides a similar measure of genotypic importance, allowing a breeder to make selections based on the individuals' as per results. In present investigation high estimates of heritability in broad sense were observed for water absorption percent overnight soaking (94.89%), 100 Seed volume (93.62%), volume expansion percent at cooking time (93.14%), cooking time (92.21%), volume expansion percent overnight soaking (91.76%) and protein content (83.73%). However hard grains (56.93%) showed moderate heritability. Similar findings have been reported by the Anusha *et al.* (2020) ^[1], Mohammed *et al.* (2019) ^[10] and Sayar *et al.* (2018).

For volume expansion (%) at cooking time (78.10%), water uptake (%) at cooking time (48.82%), 100 Seed volume (36.66%), water absorption (%) overnight soaking (31.48%), hard grains (25.74%) and genetic advance as a percentage of mean was high, indicating that these characters were governed by additive genes and that selection would be rewarding for improving these characters. Protein content (18.53%) and cooking time (10.21%) showed moderate genetic advance as a percentage of the mean. Volume expansion (%) overnight soaking (9.66%) had low genetic advance as a percent of mean, indicating that these characters were governed by non-additive genes. Similar findings have been reported by the Tripathi *et al.* (2012) ^[14], Honnappa *et al.* (2018) ^[7], Olika *et al.* (2019) ^[11] and Manasa *et al.* (2020) ^[9]. High heritability with low genetic advance as percentage of

high heritability with low genetic advance as percentage of mean recorded for Protein content, 100 Seed volume, water absorption percent overnight soaking, volume expansion percent overnight soaking, cooking time, water absorption percent at cooking time and volume expansion percent at cooking time. It indicates that non-additive genes play a significant role in the inheritance of these characters, indicating that direct selection based on these characters is ineffective and unreliable. It shows that if character is heavily affected by the environment, selection will be ineffective. Characters including seed yield per plant would be rewarding in the chickpea improvement programme.



Fig 1: GCV and PCV diagram for seed yield and quality traits.



Fig 2: Heritability(bs) diagram for seed yield and qualty traits.



Fig 3: Genetic advance as% of mean diagram for seed yield and quality traits.

Abbreviation: Protein= Protein content (%), SV= 100 Seed volume (cc), WAOS= Water absorption (%) overnight soaking, VEOS= Volume expansion (%) overnight soaking, HG=Hard grains (%), CT= Cooking time (Min.), WUCT= Water uptake (%) at cooking time, VECT= Volume expansion (%) at cooking time, SY= Seed yield (gram).

Source of variation		MSS								
		Protein	SV	WAOS	VEOS	HG	СТ	WUCT	VECT	SY
Blocks (ignoring Treatments)	5	0.16	14.35 **	0.01 **	0.01 **	1.47	13.54 **	0.03 *	0.08 **	1.36
Blocks (eliminating Treatments)	5	0.84	0.84	0.04	0.01	4.21 *	1.28	0.02	0.04	3.44
Treatments (eliminating Blocks)	52	9.81 **	27.90 **	0.04 **	0.03 **	6.06 **	34.77 **	0.04 **	0.22 **	5.42 **
Treatments (ignoring Blocks)	52	9.74 **	29.20 **	0.04 **	0.03 **	5.80 **	35.95 **	0.04 **	0.22 **	5.22 **
Test Entries	47	8.16 **	20.11 **	0.02 **	0.02 **	3.87 **	22.63 **	0.02 **	0.17 **	3.79**
Checks	4	23.53 **	128.45 **	0.02 **	0.01 **	29.80 **	197.63 **	0.02 **	0.48 **	23.28**
Checks vs. Test Entries	1	29.19 **	59.46 **	0.02 *	0.09 **	0.27	15.28 **	0.02**	1.64 **	0.08
ERROR	20	0.92	0.86	0.01	0.01	1.28	1.18	0.004	0.08	1.80

Table 1: Analysis of variance among seed yield and quality traits

*, ** significant at 5% an 1% level, respectively

Abbreviation: Protein= Protein content (%), SV= 100 Seed volume (cc), WAOS= Water absorption (%) overnight soaking, VEOS= Volume expansion (%) overnight soaking, HG= Hard grains (%), CT= Cooking time (Min.), WUCT= Water uptake (%) at cooking time, VECT= Volume expansion (%) at cooking time, SY= Seed yield (g).

S. No.	Characters	Range	Mean	Genetic coefficient variance (GCV%)	Phenotypic coefficient variance (PCV%)	Heritabilit y (bs)%	Genetic advance	Genetic advance as% of mean
1.	Protein content (%)	16.55-26.93	22.22	9.84	10.74	83.73	4.09	18.53
2.	100 seed volume (cc)	11.25-27.00	19.45	18.39	19.00	93.62	7.06	36.66
3.	Water absorption (%) overnight soaking	0.17-0.33	0.25	15.69	16.11	94.89	0.08	31.48
4.	Volume expansion (%) overnight soaking	0.66-0.82	0.74	4.90	5.11	91.76	0.07	9.66
5.	Hard grains (%)	4.00-12.00	7.85	16.56	21.95	56.93	2.02	25.74
6.	Cooking time (min.)	63.25-80.54	72.36	5.17	5.38	92.21	7.40	10.21
7.	Water uptake (%) at cooking time	0.07-0.24	0.15	25.05	26.47	80.54	7.50	48.82
8.	Volume expansion (%) at cooking time	0.18-1.60	0.86	39.29	40.71	93.14	0.64	78.10
9.	Seed Yield (g)	7.87-15.51	11.88	15.40	15.70	35.26	1.29	10.93

Conclusion

All of the characters studied analysis of variance revealed that positive genetic variability among chickpea genotypes for yield and quality traits and components of variance evaluations showed that genotypic variation contributed the most to phenotypic variation, indicating that accessible genetic variability may be utilized through selection and hybridization.

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