



ISSN (E): 2277-7695

ISSN (P): 2349-8242

NAAS Rating: 5.23

TPI 2023; 12(3): 381-384

© 2023 TPI

www.thepharmajournal.com

Received: 01-12-2022

Accepted: 05-01-2023

Anish Choudhury

Department of Seed Science and
Technology, Bidhan Chandra
Krishi Viswavidyalaya,
Mohanpur, Nadia, West Bengal,
India

Kanad Mukherjee

Department of Agricultural
Chemicals, Bidhan Chandra
Krishi Viswavidyalaya,
Mohanpur, West Bengal, India

Prabir Chakraborti

Department of Seed Science and
Technology, Bidhan Chandra
Krishi Viswavidyalaya,
Mohanpur, Nadia, West Bengal,
India

Corresponding Author:

Anish Choudhury

Department of Seed Science and
Technology, Bidhan Chandra
Krishi Viswavidyalaya,
Mohanpur, Nadia, West Bengal,
India

Variability in chickpea genotypes considering seed morphology with a few bio-molecules

Anish Choudhury, Kanad Mukherjee and Prabir Chakraborti

DOI: <https://doi.org/10.22271/tpi.2023.v12.i3d.18952>

Abstract

Quality seed production of efficient strains can be valuable which are developed through breeding strategy at parental selection emphasizing the seed morphology and bio-molecular activity at germination initiation. The significant distinct variation in qualitative assessment of seed was observed exploited 20 Chickpea genotypes. The observable factors like seed length; breadth, L/B ratio, seed volume, 1000 seed weight, α -amylase activity as well as α -amylase rising rate were responsible to denote the selection approach. The genotype V₈ (FLIP-171C) demonstrated eminence in seed length, L/B ratio, 1000 seed weight with occurrence of α -amylase rising rate though high genetic changeability was noticed among genotypes for all characters. Coefficient of variation offered a relative measure on variance among diverse characters. GCV was advanced (more than 20%) for seed length, L/B ratio of seed, seed volume, and 1000 seed weight. Greater heritability (H₂ %) combined with better genetic advances (GA %) was detected for seed length, and 1000 seed weight. Furthermore, the considerable characters explained hopeful positive correlation with each other. Hence, these parameters were vital for considerable seed uniqueness and choice based on these qualities would be reliable for chickpea genotypes developed under West Bengal condition.

Keywords: Chickpea, heritability, seed morphology, variability

Introduction

Seeds are vital for purifying the crop output as well as crop standard. Seeds bear genetic uniqueness in successful crop production that may be exploited as quality and healthy seedlings establishment in order to increase crop productivity. The vital determinant of seed quality is the varietal authenticity. Varietal purity showed significant impacts in crop yields. Therefore, the farmers should be conscious about varietal purity in their seeds. The Chickpea (*Cicer arietinum* L.), a leguminous crop, belongs to family *Fabaceae* (2n=16) which is commonly grown as Rabi crop in India where the major growers are Madhya Pradesh, Uttar Pradesh, Maharashtra and Rajasthan for its better productivity. There are two main groups of chickpea on the basis of seed size, colour, thickness, and shape. These are Desi chickpea and Kabuli chickpea. Desi is smaller in size with tan to black in colour and widely cultivated under dryland area. Kabuli type is larger in size with thin coats containing slightly lighter colour.

The seed quality exposed its features primarily in structure and texture, i.e. morphological strictures. Seed quality can also be evaluated through incidence of biochemical parameters specially at seed germination and vigour (Choudhury and Bordolui, 2022a) [4]. During subsequent germination, primed seeds exhibit a faster and more synchronized germinate on and young seedlings are often more vigorous against abiotic stresses than seedlings obtained from unprimed seeds of chickpea (Choudhury and Bordolui, 2022b) [5]. Studies on genotypic variability in respect to different parameters on seed morphology and activity of biomolecules, especially in qualitative aspects may be proper in seed production system in addition to planned exploitation of breeding plan for establishment of added capable strains. Therefore, a selection on prospective genotypes from landraces or high yielding cultivar was considered that may achieve the extensive research in future. The selection and use of advanced genotype with good genetic potential is a steady requirement for the production of better Chickpea. Study on seed potentiality through analysis on genetic variability allowing for different genotypes of Chickpea, the morphological and biochemical traits of seed may be considered as creative criteria to build up a good strain.

Materials and Methods

The seeds of diverse 20 genotypes considering two categories of chickpea were collected from

AB-DSF farm, BCKV, Nadia, West Bengal after proper maturity and these were assessed through morphological and physiological evaluation in Departmental laboratory, Seed Science and Technology, Faculty of Agriculture, BCKV, Mohanpur, West Bengal at 2020-2021. The 10 genotypes of Kabuli are denoted as V₁ (FLIP07-273C-S3), V₂ (FLIP-88-85C-S2), V₃ (FLIP-10-173), V₄ (FLIP-10-81C), V₅ (FLIP-09-308C), V₆ (FLIP-10-252C), V₇ (FLIP-10-122C), V₈ (FLIP-171C), V₉ (FLIP-09-194C), V₁₀ (FLIP-10-218C), and in desi types are denoted as V₁₁ (FLIP-08-254C), V₁₂ (FLIP09-146C-S5), V₁₃ (FLIP-07-314C-S6), V₁₄ (FLIP-88-85C-S2), V₁₅ (XIIth70-S1), V₁₆ (X11th70-S1), V₁₇ (X11th82-S2), V₁₈ (FLIP-10-81C), V₁₉ (X11th83-S) and V₂₀ (X11th78-S6). The measurable morphological parameters of seed were length and breadth of the seed, length and breadth ratio, 1000 seed weight, seed volume etc. The observable biochemical activity was the soluble protein (lowery's method), and Alpha-amylase (colorimetric method with DNS reagent) after 24 hours of seed soaking at germination initiation stage. The enhancement rate of Alpha-amylase with progression of germination up to 5th day (120 hours of seed soaking) was also measured. The statistical analysis was done through completely randomized design considering 3 replications for each character. The consequence was achieved at 1% level of significance through application of software OP STAT. The genotypic and phenotypic coefficient of variation was assessed allowing to the methods of Burton (1953) [3]. Heritability in broad sense was designed as per method of Allard (1960) [1] and Robinson *et al.* (1949) [11]. The expected Genetic Advance as percent of mean was calculated as suggested by Johnson *et al.* (1955) [8].

Results and Discussion

The observation on a few seed morphologies in addition to seed quality displaying bio-molecular action precise for a particular genotype would be important for qualitative up gradation of the produce. Seed is the most vital constituent in plant life cycle as well as crucial input in agriculture while characterization of this constituent in diverse crops was meager. The planned approach on various researches particularly in cultivation practice and breeding programs were extremely reliant to seed specification, where inconsistent nature of seed on a crop genotype should be helpful (Biswas and Chakraborty, 2019) [2]. The present study was an attempt to fulfil the objectives to some extent on a crop, Chickpea. The examination on seed morphology and the action of few bio-molecules may heighten the information in this feature. The initial level on unevenness was observed in seed morphology consisting dissimilar numerical parameters in connection to some noticeable sign though a few distinct characters was measured for current study. The twenty (20) genotypes considering two (2) unlike categories of chickpea cultivars viz. Kabuli genotypes and Desi genotypes showed a variable nature. Considering the two categories, desi genotypes were characteristically lesser in seed length compared to high yielding Kabuli genotypes. The genotypes V₁₇ and V₁₉ showed dominance among diverse genotypes under desi type, where all genotypes of Kabuli genotypes can be influencing indicating the superior value of V₂ and V₈ genotypes. The significant distinction was observed in most of the interpretation allowing for mean values of the genotypes. The morphological quantifiable parameter seed breadth showed marked variability in a significant manner

related to the entire genotypes. The uppermost value was specified in V₁₁ for desi type and V₁₀ followed by V₈ for Kabuli type though the seed breadth was not motivated to seed length considering all values. The significant discrimination was noticed in overall mean values though non-significant trend was also perceive din some cases. The length-breadth ratio of the seed acted as a signal point for the specific seed marker related to distinct cultivar. The ratio was higher in high-yielding genotypes of kabuli types compared to desi land races. The extreme value was observed in V₈ (1.34) for Kabuli types though the high trend of values was only observed in V₁₇ and V₁₈ for desi. The significant differentiation was followed among mean values of all genotypes though a non-significant association was identified within a few genotypes under both Desi and Kabuli cultivars. Seed volume clarified equivalent attitude in presence of genotypes considering at previous seed length. The Desi land races indicated lower seed volume in divergence to the higher seed volume of Kabuli types. The extreme value was observed in V₁₀, V₁, V₂ and V₈ under non-significant mode though other values were significantly distinct among the cultivars. The lowest volume was observed in V₁₁, V₁₂ and V₂₀ under desi category. The maximum seed weight was detected in V₈ followed by V₂ though others Kabuli genotypes displayed a range within 37 to 39 g in approximate. The lower values of desi type indicated range within 26 to 31 g highlighting its topmost value in V₁₉ followed by V₁₈ and V₁₇. The significant distinction was sustained for all genotypes representing a prominent variability of genotypes for the character. The soluble protein was maximum in the seed of V₁₀ followed by V₅ and V₈. In contrast to these, V₆, V₇ and V₃, showed minimum level in estimation of soluble protein. In view of 20 genotypes, the Desi type was better in soluble protein content in dry seed with least variability within genotypes. At initial stage of germination, the speed of imbibition may be valuable to initiate germination process allowing for biochemical action. The activity can accelerate the activity of germination initiating enzyme α -amylase. In present experiment, the α -amylase activity was observed after 24 hours of imbibition seeing 20 chickpea genotypes that was significantly variable to each other in mean values of different genotypes. The maximum activity was observed at V₇ followed by V₉ and V₈ under the group of Kabuli type in addition to V₂₀ of desi type. The α -amylase activity up to 120 hours of imbibition exposed an expanding rate (per day) in enzymatic action. The genotype V₈ and V₁₀ presented maximum rate in progression of α -amylase. The 20 genotypes showed the variable nature in significant manner considering the mean values, where minimum action was observed in V₁ and V₁₄. The genetic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) markedly displayed the genetic pressure on most of the seed parameters. The high heritability (H₂ %) with high genetic advance as percentage of mean (more than 20%) specified these pressures as additive gene action. The biochemical action at the stage of seed germination potentially showed high heritability (H₂%) and high genetic advance (GA %) at seed parameters viz. alpha-amylase activity, soluble protein content expressing the potential genetic effect of these qualities.

The characters under the group of seed morphology considering length, breadth, ratio of length breadth, seed volume, 1000 seed weight etc., where significant variable nature was projecting for all genotypes. The genotype V₈

(FLIP-171C) and V₂ (FLIP-88-85C-S2) were hopeful in length, L/B ratio as well as 100 seed weight under kabuli high-yielding genotypes, but in other cases, there was no specific distinguishing superiority for the Desi and Kabuli group type. In biochemical activities, V₁₀ showed higher values though V₉, V₈ were also capable in some cases. The high genetic variability among diverse genotypes was perceived for most of the characters, where V₈ in both morphological and biochemical contextual in addition to V₉ for biochemical aspect showed the superior values. In biochemical traits, other varieties viz. V₅, V₁₁, and V₁₈ showed their effect and eminence in α -amylase activity. Considering the above consequence, it is anticipated that the different characters sustained an association within them where V₈, V₉, V₁₉ were important. V₈ displayed high value not only in seed morphology but peak achievement of enzymatic action was also detected. The other variety V₁₁ under desi group presented distinction in biochemical activity at the time of imbibition. The genetic variability was assessed in dissimilar cultivars on a specific crop by description of diverse characters related to yield attributing parameters (Parvathi *et al.*, 2011; Seyoum *et al.*, 2012, Singh *et al.*, 2012; Dhanwani *et al.*, 2013, Debbarma *et al.*, 2018) [9, 11, 12, 7, 6], but the opinion on seed traits for assessment of genetic variability was very meagre. The present work highlights these characters for arranging the selection procedure to achieve the goal of breeder for crop upgrading highlighting seed quality

alike to the current view on seed traits in rice (Biswas and Chakraborty, 2019) [2]. A strong positive correlation was detected in all morphological parameters as well as bio-molecular action of seed. Heritability was high for maximum traits however it was middle in seed breadth. High heritability does not the only indicator of top genetic gain in entire situations. Hence, the heritability along with genetic advance should be measured for the study. The results recommended the prospect for progression the seed traits through direct selection of seed. Heritability along with genetic advance covers the competence of selection (Yadav *et al.*, 2010; Debbarma *et al.*, 2018) [13, 6] through assessing the factors of environmental effect as well as additive gene action supportive for prosperous breeding.

A strong positive correlation was observed in all morphological parameters as well as bio-molecular activity of seed. Heritability was high for maximum traits though it was medium in seed breadth. High heritability does not the only indicator of high genetic gain in all situations. Here after, the heritability along with genetic advance should be measured for the investigation. The outcomes advised the possibility for upgrading the seed traits through direct selection of seed. Heritability along with genetic advance extends the competence of selection (Yadav *et al.*, 2010; Debbarma *et al.*, 2018) [13, 6] through evaluating the factors of environmental impact as well as additive gene action supportive for prosperous breeding.

Table 1: Study on genotypic variability of chickpea genotypes considering seed morphology with some bio-molecules

	Variety	SL (mm)	SB (mm)	SL/SB ratio	SV (ml)	100 SW (g)	Soluble protein (m g g ⁻¹)	α -amylase (μ g min ⁻¹ g ⁻¹) at 24hours imbibition	Rising rate of α -amylase day ⁻¹ (up to 5 th day)
Kabuli Type	V1	7.17	5.42	1.32	0.17	38.36	25.58	163.5	25.86
	V2	7.25	5.53	1.31	0.17	42.67	22.47	171.4	48.04
	V3	6.48	5.48	1.18	0.15	39.51	20.92	189.0	46.19
	V4	7.04	5.53	1.27	0.15	38.59	22.36	180.5	26.78
	V5	7.02	5.39	1.30	0.13	36.05	26.60	186.9	45.42
	V6	7.01	5.37	1.31	0.15	38.61	17.89	184.5	36.17
	V7	7.03	5.41	1.30	0.16	37.02	18.48	201.6	48.59
	V8	7.67	5.72	1.34	0.17	43.27	25.48	199.3	57.2
	V9	6.16	5.51	1.12	0.14	39.04	25.24	201.2	34.82
	V10	7.15	5.91	1.21	0.18	49.32	27.86	193.4	56.98
Desi Type	V11	4.92	5.19	0.95	0.10	22.25	18.59	177.8	53.07
	V12	4.62	4.70	0.92	0.10	21.96	23.98	185.8	35.9
	V13	5.70	4.76	1.19	0.12	24.28	25.58	160.9	36.46
	V14	4.92	4.78	1.03	0.11	21.44	26.60	162.7	26.6
	V15	4.50	4.82	0.93	0.11	24.19	26.92	165.6	45.38
	V16	4.55	4.71	0.96	0.11	22.17	24.15	184.3	35.39
	V17	6.39	4.82	1.32	0.13	25.03	22.46	173.9	44.93
	V18	6.03	4.72	1.27	0.11	25.26	25.50	189.7	45.93
	V19	6.11	4.92	1.24	0.12	26.88	22.47	164.6	45.19
	V20	4.55	4.65	0.97	0.10	22.14	18.68	198.4	35.42
	Mean	6.11	5.17	1.08	0.13	31.40	23.39	181.7	41.5
	LSD(0.01)	0.39	0.21	0.05	0.003	0.66	2.94	0.195	9.74
	GA(%)	32.13	5.93	31.94	25.79	31.24	20.73	16.34	30.09
	H ² (%)	95.61	59.85	94.42	83.27	96.25	91.34	97.09	94.51

SL: Seed Length, SB: Seed Breadth, SL/B: Seed length/breadth ratio, 1000SW: 1000 seed weight

Correlation Matrix

Table 2: Correlation study on seed morphology with some bio-molecules

	Seed length	Seed breadth	SL/SB ratio	Seed Volume	100 SW	Soluble protein (mg g ⁻¹)	α -amylase ($\mu\text{g min}^{-1} \text{g}^{-1}$) at 24 hours imbibition
Seed breadth	0.857**						
SL/B ratio	0.978**	0.735**					
SV	0.932**	0.914**	0.859**				
100SW	0.890**	0.835**	0.839**	0.894**			
Soluble protein (mg g ⁻¹)	-0.010 ^{NS}	0.023 ^{NS}	-0.031 ^{NS}	0.043 ^{NS}	0.042 ^{NS}		
α -amylase ($\mu\text{g min}^{-1} \text{g}^{-1}$) at 24hours imbibition	0.253 ^{NS}	0.366 ^{NS}	0.180 ^{NS}	0.272 ^{NS}	0.248 ^{NS}	-0.244 ^{NS}	
Rising rate of α -amylase day ⁻¹ (up to 5 th day)	0.242 ^{NS}	0.349 ^{NS}	0.194 ^{NS}	0.210 ^{NS}	0.341 ^{NS}	-0.031 ^{NS}	0.338 ^{NS}

R-square value: 0.0642

Values indicated in parenthesis are the correlation values under stress condition ** - highly significant, * - significant, NS – Non-significant

The observed result specified the core set of germplasm contain high genetic variability. The broad sense heritability and genetic advance as percentage of mean designated that seed weight, imbibition rate and higher activity of alpha-amylase are the most significant characteristic of seed and selection based on these qualities would be extremely valuable in chickpea genotypes grown under New Alluvial Zone of West Bengal.

References

- Allard RW. Principles of Plant Breeding. John Wiley and Sons Inc., New York; c1960. p. 485.
- Biswas Utpal, Chakraborty Prabir. Variability in aromatic and non-aromatic rice genotypes considering seed morphology with some bio-molecules. International Journal of Chemical Studies. 2019;7(3):3648-3651
- Burton GW, De Vane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal. 1953;45:478-481.
- Choudhury A, Bordolui SK. Seed invigoration treatment with sodium molybdate (Na₂MoO₄) Nutri-priming for improvement of quality performance of Bengal gram (*Cicer arietinum* L.). The Pharma Innovation Journal. 2022a;11(12):3381-3386.
- Choudhury A, Bordolui SK. Inducement of Seed Priming with Potassium Nitrate on quality Performance of Chickpea (*Cicer arietinum* L.). Biological Forum – An International Journal. 2022b;14(4):779-783.
- Debbarma Mampi, Laloo Bingiala, Mandal Jayanta, Chakraborty Prabir. Genetic variability in yield attributes of Lentil genotypes under new alluvial zone. Current Journal of Applied Science and Technology. 2018;30(5):1-6
- Dhanwani RK, Sarwgi AK, Solanki A, Kumar J, Tiwari. Genetic variability analysis for various yield attributing and quality traits in rice (*Oryza sativa* L.) The Bioscan. 2013;8(4):1403-1407
- Johnson WW, Robinson HF, Comstock RE. Genotypic and phenotypic correlation in soybeans and their implications in selection. Agronomy Journal. 1955;47:477-482.
- Parvathi PS, Satyanarayana Rao V, Lal Ahmed M, Anilkumar P. Correlation and path analysis of yield and quality attributes in rice. The Andhra Agricultural Journal. 2011;58(3):310-314.
- Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. Agronomy Journal. 1949;41:353-359.
- Seyoum M, Alamesew S, Bantte K. Genetic variability, heritability correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). Journal of Plant Sciences. 2012;7(1):13-22.
- Singh PK, Dhakad BK, Singh HB, Singh AK. Genetic variability and association analysis in rice (*Oryza sativa* L.) treated with *Trichoderma harzianum*. Crop Research. 2012;44(1&2):141-145.
- Yadav P, Rangare NR, Anurag PJ, Chaurasia AK. Quantitative analysis of rice (*Oryza sativa* L.) in Allahabad agroclimatic zone. Journal of Rice Research. 2010;3:16-18.