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Estimation of genetic divergence for nutritional quality traits of *desi* chickpea (*Cicer arietinum* L.) under late sown condition

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Abstract
The chickpea (*Cicer arietinum* L.), recognized for its high-quality protein suitable for both human and animal consumption, serves as an excellent source of carbohydrates and protein. Its protein quality surpasses that of other pulses. To assess genetic variability in nutritional quality, 45 advanced breeding lines of desi chickpea underwent analysis. The mineral nutrient composition of these 45 desi chickpea genotypes exhibited significant variations for each nutrient studied. For Fe, Zn, Cu, and Mn, the variability across genotypes ranged from 1.45 mg/100g to 9.28 mg/100g, 0.39 mg/100g to 2.03 mg/100g, 0.30 mg/100g to 1.85 mg/100g, and 0.43 mg/100g to 1.70 mg/100g, respectively. The average protein content stood at 20.77%, with a range of 19.11% to 22.39%. Analysis of variance demonstrated the high significance of genotypes for all studied traits. The Fe exhibited the highest Phenotypic Coefficient of Variation (PCV) and Genetic Coefficient of Variation (GCV), followed by Cu, Mn, Zn, and Reducing Sugar (%), indicating substantial phenotypic variation in these traits. The heritability was notably high for Cu, followed by Fe, Carbohydrate%, Mn, Crude Fiber%, Zn, Reducing Sugar%, and Protein%. Examining the percentage contribution to genetic divergence by twelve characters, Cu emerged as the primary contributor, followed by Carbohydrate (%), Fe, Mn, Crude Fiber%, Reducing Sugar%, Fat%, Ash%, Zn, Non-Reducing Sugar%, Total Sugar%, and Protein%. The 45 genotypes were categorized into 6 clusters, with intra-cluster distances ranging from 0.00 to 9.20. The most significant inter-cluster divergence was observed between genotypes of Cluster III and Cluster VI.

Keywords: Nutritional quality, divergence, chickpea, clusters

Introduction
Chickpea (*Cicer arietinum* L.) holds significance as a vital pulse crop cultivated and consumed globally, particularly in Afro-Asian countries. Recognized for its nutritional richness, chickpeas serve as an essential source of carbohydrates and protein, boasting a protein quality superior to other pulses. Its major storage carbohydrate is starch, accompanied by dietary fiber, oligosaccharides, and simple sugars like glucose and sucrose. Notably, chickpeas are abundant in nutritionally valuable unsaturated fatty acids, while also containing essential minerals such as Ca, Mg, P, and particularly K.

Chickpeas contribute to a diverse array of potential nutritional and health benefits, making them crucial in addressing challenges like the growing population, food security, nutrient security, urbanization, climate change, and evolving food preferences. The demand for high-yielding and nutritionally acceptable chickpea varieties is essential in this context. Given that legumes share a nutrient profile with both vegetables and protein foods, they often fulfill requirements for both food groups. Studies on micronutrients and protein accumulation in pulse crops, such as lentils, have reported the influence of genotype, geographical location, temperature, and soil factors.

Cultivated chickpeas come in two distinct types: Desi and Kabuli. Desi types feature pink flowers, anthocyanin pigmentation on stems, and a colored, thick seed coat. On the other hand, Kabuli types exhibit white flowers, lack anthocyanin pigmentation on stems, and have white or beige-colored seeds with a ram's head shape, a thin seed coat, and a smooth seed surface. The nutritional value of chickpeas has fueled a growing demand, particularly in semi-arid tropics, where chickpeas play a crucial role in the diets of individuals who cannot afford animal proteins or those who choose a vegetarian lifestyle.

Chickpea stands out as a notable provider of carbohydrates and protein, constituting approximately 80% of the total dry seed mass, surpassing other pulses (Chibbar *et al*., 2010) [10]. Remarkably, chickpea is cholesterol-free and offers a rich supply of dietary fiber, vitamins,

and minerals (Wood & Grusak, 2007) [11]. Among pulses, it excels as a source of complex carbohydrates, proteins, dietary fiber, and energy (Ereifez *et al*., 2001; Wang *et al*., 2010) [12, 13]. Additionally, it plays a crucial role as a reservoir of micronutrients such as Fe, Zn, Mg, and Cu (Ereifez *et al*., 2001; Abbo *et al*., 2000) [12, 14]. Given that cereals and pulses form a primary dietary staple for billions of people, focusing on chickpeas could contribute significantly to addressing malnutrition concerns.

Globally, chickpea production reached 145.6 lakh ha, with India leading at 70% of the total (FAO, 2021) [15]. In India alone, chickpea cultivation spans 99.96 lakh ha, yielding 119.11 lakh tonnes Mt, boasting an average productivity of 1192 kg/ha. India holds the top position in both production and consumption of chickpeas globally, followed by countries such as Pakistan, Mexico, Turkey, Canada, Iran, Australia, Tanzania, Ethiopia, Spain, and Burma. In India, major cultivation areas include Madhya Pradesh and Southern states like Andhra Pradesh, Telangana, and Karnataka. Madhya Pradesh, covering 21.60 lakh ha, stands out with a production of 32.14 lakh tonnes and the highest average productivity of 1192 kg/ha among various pulse crops (Directorate of Pulse Development Report, 2020-21) [42].

Chickpea, much like other crops, lacks comprehensive studies on nutrient content levels in Indian subcontinent conditions. Having access to such information holds the potential to formulate a robust breeding strategy aimed at augmenting the nutrient profile of chickpea. Consequently, the current study is initiated with the goals of assessing nutrient levels across various genotypes of desi for different traits and pinpointing suitable parent plants with the potential to contribute to the development of improved genotypes with customized traits. The accomplishment of these objectives represents a significant stride toward cultivating high-nutrition cultivars, fostering healthier living, and enhancing food security for the population.

Materials and Methods

Forty-five advanced breeding lines of desi chickpea underwent analysis for genetic variability in nutritional quality content, including iron (Fe), zinc (Zn), copper (Cu), manganese (Mn), reducing sugar (%), non-reducing (%), total sugar (%), fat (%), ash (%), crude fiber (%), carbohydrate (%), and protein (%). The selected genotypes were cultivated using a randomized block design with three replications during the rabi season of 2017-18 at the Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur (M.P.). The soil at the JNKVV, Jabalpur seed breeding farm is characterized as dark brown and sandy loam with a neutral pH of 7.2.

Matured dry seeds from each variety were harvested in each replication, and powdered seed samples were utilized for nutrient estimation, including iron, zinc, copper, manganese, reducing sugar, non-reducing sugar, total sugar, fat, ash, crude fiber, carbohydrate, and protein content. The micronutrient content (iron, zinc, copper, and manganese) of chickpea seeds was analyzed using Atomic Absorption Spectroscopy (AAS), measuring absorbance at their resonance wavelengths. One gram of oven-dried powdered seeds underwent digestion with a 10 ml triacid mixture (HNO3: H2SO4: HCLO4 @ 9:4:1). The digested samples were made up to 100 ml, and the filtered extract was used for concentration measurement using analytical grade solutions of the elements of interest (Tandon, 1993) [16].

Protein content was estimated by analyzing nitrogen in seed samples through a single digest (sulfuric acid selenium digestion). Aliquots of digests were used for nitrogen determination via sodium hydroxide using the Kjeldahl distillation method (Kjeldahl, 1883) [17]. The total nitrogen content in powdered seeds was multiplied by a factor of 6.25 to determine seed protein content (%), following the method outlined by Jones (1941) [18]. Fat, carbohydrate, and ash content were determined using procedures described in AOAC (Association of Official Analytical Chemists, 1984) [41], while sugar content was determined following the method outlined by Ranganna (1991) [4].

Genetic variability parameters, including coefficients of variation, heritability, and genetic advance as a percentage of the mean, were estimated according to Singh and Chaudhary (1977) [1]. Genetic divergence analysis was conducted following the methods of Mahalanobis (1936) [2] and Rao (1952) [3].

Results and Discussion

The nutrient values of seeds, encompassing iron, zinc, copper, manganese, reducing sugar, non-reducing sugar, total sugar, fat, ash, crude fiber, carbohydrate, and protein content across 45 desi chickpea genotypes, underwent analysis of variance. The results, as depicted in Table 1, unveiled highly significant differences for all the evaluated traits.

Addressing micronutrient malnutrition is more effectively achieved by incorporating essential nutrients into commonly consumed foods rather than relying solely on dietary supplements. Besides being a rich source of protein, chickpeas offer a spectrum of nutrients including carbohydrates, dietary fiber, and a range of minerals (molybdenum, manganese, copper, phosphorus, iron, and zinc) as well as vitamins (riboflavin, niacin, thiamin, folate, and the vitamin A precursor beta-carotene) (Jukanti *et al*., 2012) [19].

The mineral nutrient composition of 45 desi chickpea genotypes exhibited significant variations for each nutrient under investigation (Table 1). The diversity among these genotypes in terms of Fe, Zn, Cu, and Mn content ranged from 1.45 mg/100g (RVSSG 60) to 9.28 mg/100g (GNG 2369), 0.39 mg/100g (RG 2015-05) to 2.03 mg/100g (PG 187), 0.30 mg/100g (RG 2011-04) to 1.85 mg/100g (GL 14015), and 0.43 mg/100g (BG 372) to 1.70 mg/100g (GL 14015), respectively. These findings align with the conclusions of other researchers in the field. For instance, Diapari *et al*. (2014) [21] and Kahraman *et al*. (2017) [22] reported mean copper, iron, zinc, and manganese content of 1.22, 4.48, 3.53, and 1.68 mg/100g, respectively, supporting the results obtained in this study.

The average protein content was 20.77% with the range of 19.11% (JG 2016-1614)-22.39% (PG 187) were observed in desi advanced breeding lines. Out of 45 *desi* chickpea genotypes, the following genotypes namely DC 16-116, GL 14015, JG 36, BRC 302, JG 2016-1614, PG 187, BG 3091, GNG 2367, JSC 56 and BG 372 found the high value of protein content. The result are in closed harmony with Awasthi *et al.,* (1991) [23], Khan *et al., (*1995) [25], Mcintosh and Topping (2000) [26], Sood *et al.,* (2002) [27], Kutos *et al.,* (2003) [28], Singh *et al.,* (2006) [29], Maheri-sis *et al.,* (2008) [30], Alwawi *et al.,* (2010) [31], Falco *et al.,* (2010) [32], Sharma *et al.,* (2013) [33] and Nobile *et al.,* (2013) [34]. As a source of

high quality protein, chickpea enriches the cereal based diet of the people and improves their nutritional balance. Since there are limited breeding efforts in enhancing protein content in chickpea, identification of adapted chickpea lines with higher protein content will help in food fortification and also in utilizing promising lines in further breeding programmes.

Average carbohydrate content was 58.29% varied from 51.37% (JG36) to 64.89% (JG 11 X JG 14) in *desi* advanced breeding lines under investigation with incongruity with Singh *et al.,* (2006) [29] and Kabuo *et al.,* (2015) [35]. High carbohydrate content was estimated in the genotypes *viz.,* JG 11XJG 14, JG 63XICC 4958, ICC 96029X JG 315, JSC 56, Phule G 1012-10-9, RG 2011-04, GNG 2367, PG 187, JG 12X JG 16-1 and H 12-22.

Desi chickpea lines exhibited average fat content 4.66% varied from 3.13% (BG 372) to 6.24% (IPC 2010-14) and high fat content were noted in advanced breeding lines. This result was in agreement with Khan *et al.,* (1995) [25] reported fat content was 5.1%. Agrawal and Singh (2003) [24] estimated the average mean of fat content 3.79% with the range of 3.02-4.69%. Besides this, Falco *et al.,* (2010) [32] analyzed fat content 4.04-6.19%. The range of crude fiber content was 4.43% (ICC96029 X ICC11551) to 8.35% (GNG 2367) with mean value of 6.33%. High crude fiber content was noted in the genotypes *viz.,* JG 36, ICCV 15118, JG 14, JG 12, BG 372, GNG 2367, JG 2017-50, JG 72 X ICCV 4958, RG 2011-04 and JG 63X ICC 4958 of *desi* chickpea. Similar results were found by Gopalan *et al.,* (1995) [36] and Sood *et al.,* (2002) [27]. The mean average of total sugar content was 7.45%, ranging from 6.40% (JG 14) to 8.69% (GL 14015). Among the 45 desi chickpea genotypes, several, including JG 11X JG 14, JG 2017-50, GL 14015, ICC 96029X JG 315, H 12-22, PG 187, BG 372, JG 12, NDG 15-5, and JSC 56, exhibited notably high total sugar content. According to Sanchez-Mata *et al*. (1999) [37], the total soluble sugar content in chickpea varieties ranged from 5.89 to 8.21g per 100g, while the mean total sugar content observed in this study was 8.51%, with a range of 5.34-11.82%. Similar results regarding sugar content were noted in studies conducted by Gupta *et al*. (2006) [38].

In terms of reducing sugar content in desi chickpea, the maximum was recorded at 0.91% (JG74 X ICCV4958), and the minimum at 2.72% (JSC 55, RVG 202), with an average value of 1.53%. Genotypes such as ICC 96029X JG 315, JSC 55, JG 2017-50, IPC 2010-14, GNG 2367, BRC 305, JG 11X JG 14, JSC 56, NDG 15-5, and GL 14015 exhibited elevated levels of reducing sugar content.

The average non-reducing sugar content was estimated at 6.06%, ranging from 4.86% (JG 14) to 8.69% (GL 14015). Genotypes such as JSC 56, PG 187, JG 12 X JG 16-1, GL 14015, H 12-22, JG 2017-50, JG 11X JG 14, NDG 15-5, and RG 2011-04 displayed elevated levels of non-reducing sugar content. In contrast, Agrawal and Singh (2003) [24] and Gupta *et al*. (2006) [38] reported an average mean for non-reducing sugar content at 7.27%, with a range of 4.46-9.86%. Similarly, Kakati *et al*. (2010) [39] observed non-reducing sugar contents ranging from 7.10 to 7.11mg per 100g.

Providing accurate estimates is crucial for devising an efficient selection strategy for quality traits in breeding programs. These studies serve as a valuable resource for identifying high-quality exotic and indigenous advanced lines of chickpea.

Nutritionally rich elite lines of desi chickpea offer a wealth of protein, carbohydrates, dietary fiber, minerals (Fe, Zn, Ca, and Mg), and other essential nutrients vital for human health and development. There is potential for further enhancing the nutritional quality of chickpea, emphasizing the importance of developing varieties with improved nutrition. This approach ensures that consumers receive higher amounts of protein and other nutrients from the same quantity of chickpeas.

Understanding the extent of genetic variability and diversity in breeding material, along with the anticipated progress through selection, is pivotal in initiating well-planned breeding programs focused on enhancing protein and other quality traits.

The magnitude of genetic variability within a population holds significant importance for a plant breeder initiating a thoughtful breeding program. Analysis of variance revealed that genotypes were highly significant for all the studied traits. Variability can result from differences either in the genetic constitution of individuals within a population or in the environment in which they grow. Various parameters, including mean, range, coefficient of variation, heritability, and genetic advance (as a percentage of the mean), were estimated to assess genetic variability. These parameters aid breeders in enhancing quantitatively inherited traits, directly impacting yield.

Both the Genotypic and Phenotypic Coefficient of Variation (GCV and PCV) express the influence of genotype along with the environment and their interaction. The degree of GCV and PCV was higher than the corresponding genotypic coefficient of variation for all the studied characters. The higher magnitude of phenotypic coefficient of variation compared to its genotypic counterpart for all the characters suggests minimal influence of the environment on the expression of these traits (Borate *et al*., 2010) [40].

Elevated PCV and GCV were recorded for Fe, followed by Cu, Mn, Zn, and reducing sugar (%), indicating substantial phenotypic variation for these traits. Selecting for these traits could be effective for chickpea improvement. Crude fiber (%) and fat (%) exhibited moderate GCV and PCV. Traits such as non-reducing sugar (%) followed by total sugar (%), ash (%), carbohydrate (%), and protein (%) showed low phenotypic and genotypic coefficient of variation, indicating limited scope for further improvement in these traits through a selection approach (Table 2).

Heritability, estimated as the ratio of genotypic variance to total phenotypic variance, includes both additive and non-additive gene actions. It aids in assessing the merits and demerits of selecting a particular trait, guiding the breeder in choosing the appropriate selection procedures for a given situation. The heritability (H2bs) is classified into three classes: low (<50%), medium (50-70%), and high (>70%), following the categories suggested by Burton (1952) [7].

In the current investigation, high heritability was estimated for Cu, followed by Fe, carbohydrate%, Mn, crude fiber%, Zn, reducing sugar%, and protein%. These elevated heritability values suggest that the observed variation is primarily under genetic control and is less influenced by the environment. This enhances the potential for significant improvement in these traits through simple selection. Moderate heritability was observed for fat% and total sugar%, while low heritability was estimated for non-reducing sugar% and ash%. The highest genetic advance as a percentage of the mean was recorded for Fe. Moderate genetic advance as a percentage of the mean was observed for reducing sugar%,

followed by Zn, Mn, and Cu. Low genetic advance as a percentage of the mean was noticed for crude fiber%, fat%, total sugar%, non-reducing sugar%, carbohydrate%, protein%, and ash% (Table 2).

Heritability estimates, along with genetic advance, are more informative in predicting genetic gain under selection than heritability estimates alone (Burton, 1952) [7]. However, the presence of high heritability does not necessarily guarantee high genetic advance. If high or moderate heritability aligns with high or moderate genetic advance, it indicates additive gene action in the inheritance of the traits, making selection effective. On the other hand, high or moderate heritability with low genetic advance, or vice versa, suggests the predominance of non-additive gene action. In this study, an attempt was made to estimate broad-sense heritability, with Fe showing both high heritability and high genetic advance as a percentage of the mean. Therefore, direct selection would be effective for this trait, emphasizing its importance in developing promising genotypes in the future (Table 2). These findings align with the results of Aliu *et al*. (2016) [5], Ray *et al*. (2014) [20], and Bueckert *et al*. (2011) [6].

Notably, no traits under study exhibited high heritability with low genetic advance as a percentage of the mean, indicating that non-additive genes do not play a major role in the inheritance of these characters. Hence, direct selection based on these traits would be appropriate and reliable.

The primary objective of the present study was to analyze the genetic divergence among forty-five genotypes and identify key parental genotypes for the development of a hybridization program. Mahalanobis (D2) statistics, widely employed by plant breeders, served as a robust tool to quantify the degree of genotypic divergence.

In the context of selection, characters contributing a higher percentage to divergence are considered crucial. The analysis of twelve characters revealed that Cu contributed the most to genetic divergence, followed by carbohydrate (%), Fe, Mn, crude fiber%, reducing sugar%, fat%, ash%, Zn, non-reducing%, total sugar%, and protein% (Table 3).

The desi chickpea genotypes were grouped into different clusters based on genetic distance. The study, encompassing 45 recently developed desi chickpea genotypes assessed for the nature and magnitude of genetic divergence in quality traits, resulted in six clusters. The genotypes were categorized into these clusters based on D2 values, with intra-cluster distance ranging from 0.00 to 9.20. Cluster I and IV exhibited the maximum intra-cluster D2 value, while clusters II, III, V, and VI showed zero value for intra-cluster distance (Table 4). Similarly, recent studies by Aliu *et al*. (2016) [5] on genetic diversity in Kosovan chickpea genotypes for nutritive traits revealed a wide range of variation, grouping the genotypes into four clusters.

The highest inter-cluster divergence was observed between genotypes of cluster III and cluster VI, followed by cluster II and cluster VI, cluster I and IV, cluster III and IV, cluster II and IV, cluster I and IV, cluster V and VI, cluster IV and V, cluster IV and VI, cluster I and III, cluster I and II, cluster III and V. The cluster distance was lowest between cluster II and cluster III (Table 5). The ascending order of magnitude in intra-cluster divergence indicated more diversity between genotypes within these clusters. The results suggested that incorporating genotypes from distant clusters into the crossing program in chickpea is likely to yield useful recombinants in subsequent generations, as diverse parents could generate a significant amount of genetic variability. Four clusters were monogenotypic in nature, indicating some homology between closely situated clusters.

A diverse range of variation was observed for all the studied characters. For Fe, cluster IV exhibited the maximum value, while cluster III had the minimum. Regarding Zn, cluster VI showed the maximum, and cluster III had the minimum cluster mean values. Cu reached its maximum in cluster IV and minimum in cluster I. Cluster VI showed the highest Mn value, while cluster III had the minimum. For reducing sugar %, cluster V had the maximum, and cluster III had the minimum mean values. Non-reducing sugar % displayed the maximum in cluster VI and the minimum in cluster III. Total sugar's cluster mean value was highest in cluster III and lowest in cluster V. Fat % recorded the maximum mean value in cluster II and the minimum in cluster VI. Ash % had the maximum mean value in cluster III and the minimum in cluster VI. Crude fiber % recorded the maximum mean values in cluster V and the minimum in cluster IV. Carbohydrate % exhibited the maximum cluster mean value in cluster VI and the minimum in cluster V. Protein % reached its maximum in cluster V and minimum in cluster II (Table 6). Superior genotypes based on these traits can be selected and used as donor parents in hybridization programs. Inter-crossing these genotypes from different clusters can be practiced to induce variability in the respective characters, facilitating their rational improvement for increased seed yield.

Based on divergence analysis, the forty-five genotypes of desi chickpea were grouped into six clusters. Cluster I was the largest, comprising thirty-one genotypes, while cluster IV had four genotypes. Clusters II, III, V, and VI each had one genotype: IPC 2010-14, JG 12, JG 36, and Phule G 1018-9-6, respectively (Table 4).

The study in chickpea revealed significant genetic variability for nutrient contents, with promising genotypes such as PG 187, GL14015, JSC 55 (RVG 202), RG12-205, GNG 2367, JG11 X JG14, and BRC 305 showing higher nutrient concentration in Cluster I. To expedite bio-fortification in chickpea, systematic hybridization, followed by studies on combining ability, should be initiated among these promising and diverse genotypes for the genetic improvement of protein and micronutrients.

Table 1: Mean performance of quality traits of different genotypes of chickpea

S No	Genotypes	Fe	Zn	Cu	Mn	Reducing sugar %	Non reducing %	Total sugar %	fat %	Ash %	Crude fibre %	Carbohydrate %	Protein %
1	Phule G 1018-9-6	6.91	2.03	0.71	1.70	2.20	6.72	7.03	3.98	4.01	6.73	60.68	20.45
2	GNG 2369	9.28	0.99	1.51	0.66	1.62	6.00	7.49	3.84	3.87	6.09	57.84	21.29
3	BG 3091	3.08	0.77	0.58	1.30	1.60	5.63	7.36	5.73	5.29	5.99	56.20	19.86
4	PG 187	1.99	2.03	1.38	0.52	2.60	6.77	8.22	4.79	4.16	5.56	60.20	22.25
5	BRC 305	2.28	0.79	0.52	0.43	1.50	6.24	7.32	5.54	4.05	5.54	61.58	22.39
6	JSC 55	2.50	0.70	0.40	0.57	2.35	6.19	7.89	4.50	4.09	6.52	58.62	19.83
7	H 12-22	1.64	1.27	1.55	0.66	1.46	7.21	7.99	3.75	3.96	5.59	60.90	21.06
8	RG 2011-04	2.90	0.74	0.30	1.38	1.45	7.07	8.61	4.57	5.27	7.12	60.91	21.01
9	RG 12-205	2.14	0.75	0.40	0.60	1.38	8.04	7.94	3.30	4.11	7.07	54.75	20.50
10	RKG 13-205	1.85	1.38	1.47	0.78	1.58	5.87	7.17	4.75	4.78	6.59	59.89	21.70
11	JG 2017-50	2.05	0.74	0.35	0.57	2.42	6.18	8.35	4.83	3.75	7.31	54.55	21.46
12	CSJ 887	2.14	0.53	0.44	1.37	1.92	6.02	8.01	4.30	3.39	6.47	60.20	20.03
13	IPC 2010-14	1.78	1.31	1.58	0.67	1.66	5.88	7.91	6.24	4.47	6.84	59.97	20.06
14	GNG 2367	1.82	1.03	0.56	0.73	1.88	5.74	7.22	4.49	4.00	8.35	60.88	22.36
15	JG 2017-49	3.12	0.80	0.45	0.61	1.38	5.51	7.13	4.55	3.77	6.56	58.29	21.10
16	RKG17-01	1.99	0.87	1.50	0.49	1.67	5.40	6.54	5.09	3.94	5.97	58.11	22.08
17	BRC 302	2.96	0.59	0.47	1.33	2.27	5.49	7.69	5.00	4.54	4.51	55.16	21.57
18	JSC 56 (RVG 203)	2.14	1.23	0.47	0.72	1.98	6.40	8.31	3.78	4.62	6.05	57.88	21.43
19	GJG 1503	6.17	0.79	1.60	0.75	1.58	6.14	7.03	4.22	3.76	5.42	57.13	20.99
20	RVSSG 60	1.45	0.83	0.47	1.64	1.70	5.79	6.43	5.08	4.28	6.29	58.00	20.79
21	NDG 15-5	4.04	0.77	0.42	0.55	2.46	7.09	7.82	5.33	3.92	4.76	59.89	20.86
22	BG 372	1.89	1.69	1.53	0.43	1.64	5.75	7.01	3.13	4.44	5.65	59.47	21.49
23	DC 16-116	2.24	0.72	0.58	0.52	1.71	5.76	7.10	5.18	4.09	7.58	58.15	21.71
24	PG 205	1.95	0.61	0.49	0.64	1.47	5.09	6.95	4.76	4.54	6.36	56.15	20.73
25	GL 14015	7.88	1.36	1.85	1.70	2.45	6.84	8.69	5.53	4.00	6.01	59.43	21.54
26	CSJ 956	1.51	0.57	0.49	0.62	1.63	5.71	6.80	3.81	4.25	6.51	56.18	20.35
27	RG 2015-05	2.00	0.39	0.33	0.75	1.43	6.47	7.00	5.33	4.44	5.50	59.61	20.62
28	Phule G 1012-10-9	2.22	0.76	1.57	0.56	2.27	6.52	7.29	5.09	3.98	6.24	60.84	20.87
29	BG 3092	1.76	0.55	0.50	0.50	1.58	5.64	7.03	4.62	3.80	5.80	59.29	20.36
30	BG 372	2.19	1.54	0.49	1.59	1.62	6.05	8.27	4.80	3.95	7.19	57.45	20.60
31	RKG 13-515-1	1.62	0.71	1.44	0.69	1.21	5.97	6.83	4.24	3.83	5.47	59.51	20.17
32	JSC 56 (RVG 203)	2.51	0.86	0.40	0.44	1.56	6.46	6.86	4.95	4.51	6.33	60.96	19.86
33	JSC 55 (RVG 202)	7.88	1.67	1.47	0.59	2.72	5.65	6.82	6.16	5.37	5.63	55.35	22.32
34	JG 11 X JG 14	2.93	0.73	0.35	0.65	1.43	6.46	8.22	3.84	4.12	5.59	64.89	19.85
35	ICC96029 X ICC11551	3.80	0.52	0.46	1.51	0.93	5.36	6.65	3.94	4.48	4.43	56.08	20.01
36	JG 2016-1614	2.58	1.30	1.40	0.52	1.02	5.95	7.04	4.48	3.78	6.50	55.36	20.87
37	JG63 X ICC4958	1.86	0.59	0.34	1.47	1.29	6.65	7.01	4.26	4.62	6.85	63.86	19.11
38	JG12 X JG 16-3	1.68	0.64	0.51	0.62	2.44	5.02	7.44	4.01	4.44	6.64	54.45	22.01
39	JG12 X JG16-1	2.57	1.53	1.50	0.69	1.63	6.49	7.84	5.00	3.86	6.59	59.79	20.45
40	JG74 X ICCV4958	2.01	0.55	0.46	0.69	0.91	6.11	7.21	4.01	4.02	6.93	58.54	21.10
41	ICC96029 X JG315	1.67	0.84	0.42	0.67	1.59	6.06	8.09	6.08	3.84	5.59	60.19	22.11
42	ICCV15118	2.23	1.29	0.48	1.38	2.32	5.03	6.82	4.16	3.89	7.89	53.85	20.65
43	JG 12	1.49	0.51	1.58	0.57	1.43	5.20	7.94	4.74	4.56	6.87	56.36	21.45
44	JG 14	1.62	0.70	0.50	0.59	1.03	4.86	6.40	4.75	3.82	7.59	54.35	20.52
45	JG 36	2.53	1.70	1.52	1.39	2.43	6.48	6.47	5.24	4.41	8.02	51.37	21.56
	Mean	2.82	0.96	0.84	0.84	1.74	6.06	7.40	4.66	4.20	6.33	58.29	20.96
	Min	1.45	0.39	0.30	0.43	0.91	4.86	6.40	3.13	3.39	4.43	51.37	19.11
	Max	9.28	2.03	1.85	1.70	2.72	8.04	8.69	6.24	5.37	8.35	64.89	22.39
	C.V.	12.37	10.99	8.67	12.22	10.64	11.56	7.92	12.77	12.76	7.40	2.01	5.58
	S.E.	0.43	0.21	0.09	0.14	0.24	0.50	0.41	0.42	0.38	0.33	0.83	0.83
	C.D. 5%	1.21	0.60	0.26	0.41	0.69	1.41	1.18	1.20	0.98	0.94	2.37	1.15

Table 2: Genetic parameters of variability for quality traits in *desi* chickpea genotypes

S. No.	Characters	Mean	Range		GCV (%)	PCV (%)	Heritability (%) (Broad sense)	Genetic advance as % of mean 5%
			Min	Max				
1	Fe	2.82	1.45	9.28	63.64	65.41	94.71	38.45
2	Zn	0.96	0.39	2.03	38.66	44.43	75.70	32.54
3	Cu	0.84	0.30	1.85	61.80	62.78	96.92	25.86
4	Mn	0.84	0.43	1.70	45.20	48.34	87.43	28.74
5	reducing sugar %	1.74	0.91	2.72	23.05	26.91	73.47	33.75
6	non reducing %	6.06	4.86	8.04	6.87	10.68	41.40	9.11
7	Total sugar %	7.40	6.40	8.69	6.26	8.40	55.61	9.61
8	fat %	4.66	3.13	6.24	12.47	15.39	65.62	20.79

9	Ash %	4.20	3.39	5.37	4.79	10.21	22.26	4.63
10	Crude fibre %	6.33	4.43	8.35	12.72	13.75	85.52	24.24
11	Carbohydrate %	58.29	51.37	64.89	4.47	4.69	90.80	8.78
12	Protein %	20.96	19.11	22.39	1.01	3.82	69.21	5.46

Table 3: Percent Contribution quality traits towards divergence of *desi* chickpea genotypes

Source	Contribution %
Fe	12.73
Zn	1.31
Cu	38.48
Mn	10.81
reducing sugar %	3.84
non reducing %	1.01
Total sugar %	0.61
fat %	2.93
Ash %	2.22
Crude fibre %	9.39
Carbohydrate %	16.16
Protein %	0.51
Total	100

Table 4: Distribution of genotypes in different clusters using D^2 in *desi* chickpea

Cluster No.	No. of genotypes	Name of the Genotypes
I	37	BG 3091, PG 187, BRC 305, JSC 55, H 12-22, RG 2011-04, RG 12-205, RKG 13-205, JG 2017-50, CSJ 887, GNG 2367, JG 2017-49, RKG17-01, BRC 302, JSC 56 (RVG 203), RVSSG 60, NDG 15-5, BG 372, DC 16-116, PG 205, CSJ 956, RG 2015-05, Phule G 1012-10-9, BG 3092, BG 372, RKG 13-515-1, JSC 56 (RVG 203), JG, 11 X JG 14, ICC96029 X ICC11551, JG 2016-1614 , JG63 X ICC4958, JG12 X JG 16-3, JG12 X JG16-1, JG74 X, ICCV4958, ICC96029 X JG315, ICCV15118, JG 14
II	1	IPC 2010-14
III	1	JG 12
IV	4	GNG 2369, GJG 1503, JSC 55 (RVG 202), GL 14015
V	1	JG 36
VI	1	Phule G 1018-9-6

Table 5: Inter and intra cluster D^2 values of different clusters in *desi* chickpea

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	9.20	11.86	11.95	16.12	12.95	14.99
Cluster II		0.00	5.33	15.00	12.33	19.06
Cluster III			0.00	15.75	11.66	20.52
Cluster IV				7.84	13.84	12.73
Cluster V					0.00	14.98
Cluster VI						0.00

Table 6: Cluster mean values for quality traits in *desi* chickpea

Clusters	Fe	Zn	Cu	Mn	reducing sugar%	non reducing%	Total sugar%	fat %	Ash%	Crude fibre %	Carbohydrate %	Protein %
Cluster I	2.24	0.89	0.70	0.80	1.68	6.05	7.40	4.59	4.18	6.31	58.51	20.91
Cluster II	1.77	1.31	1.58	0.67	1.65	5.88	7.91	6.24	4.47	6.84	59.97	20.06
Cluster III	1.49	0.50	1.58	0.57	1.43	5.20	7.93	4.74	4.55	6.87	56.35	21.44
Cluster IV	7.80	1.20	1.61	0.92	2.09	6.15	7.51	4.93	4.25	5.78	57.44	21.53
Cluster V	2.53	1.70	1.52	1.39	2.43	6.48	6.47	5.24	4.41	8.02	51.37	21.56
Cluster VI	6.91	2.03	0.71	1.70	2.20	6.72	7.03	3.97	4.01	6.73	60.67	20.44

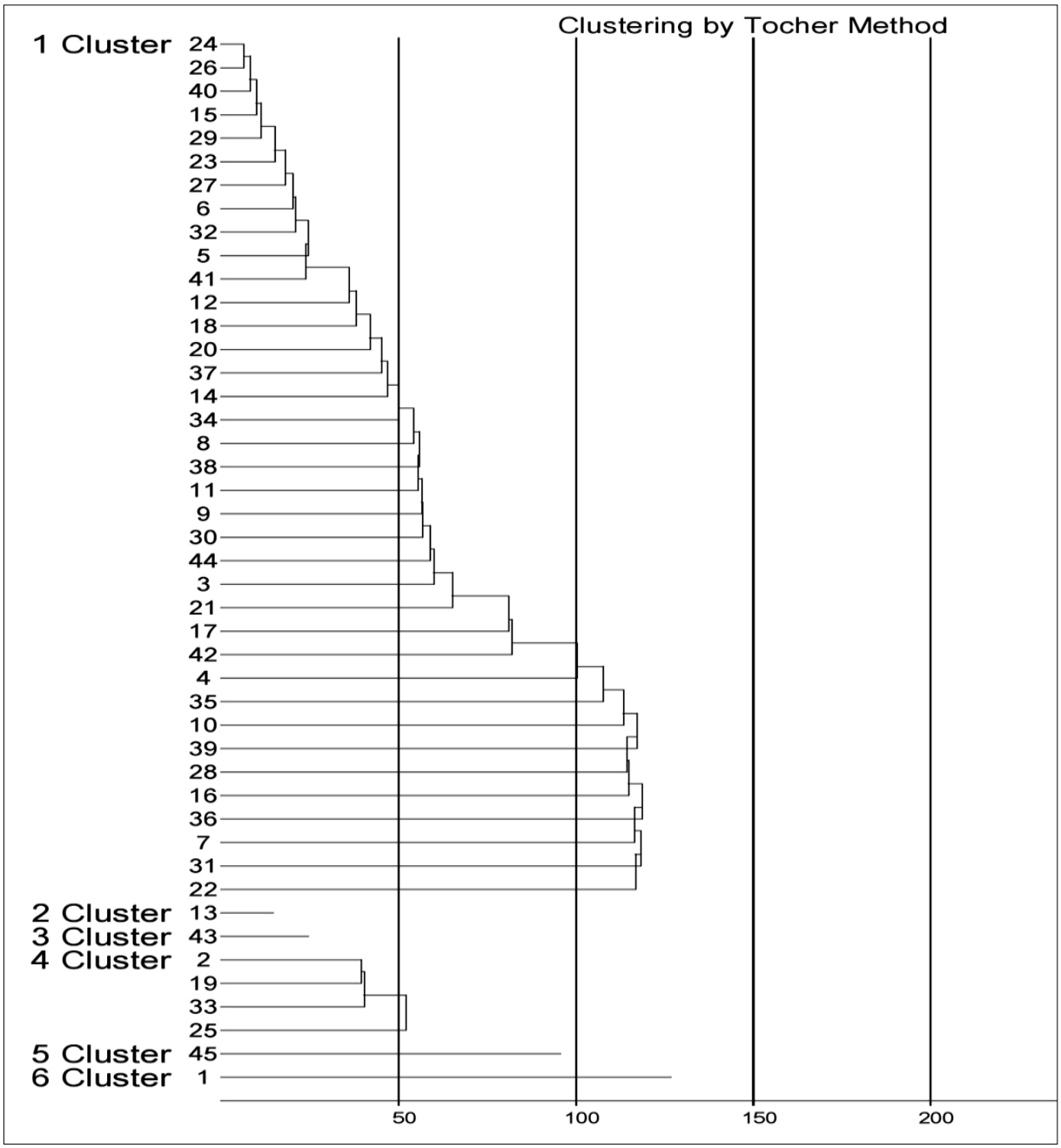

Fig 1: Distribution of *desi* chickpea genotypes in different clusters by Tocher Method

Conclusion

The findings indicated that the diversity among these genotypes in terms of Fe, Zn, Cu, and Mn content ranged from 1.45 mg/100g (RVSSG 60) to 9.28 mg/100g (GNG 2369), 0.39 mg/100g (RG 2015-05) to 2.03 mg/100g (PG 187), 0.30 mg/100g (RG 2011-04) to 1.85 mg/100g (GL 14015), and 0.43 mg/100g (BG 372) to 1.70 mg/100g (GL 14015) respectively . The study in chickpea revealed significant genetic variability for nutrient contents, with promising genotypes such as PG 187, GL14015, JSC 55 (RVG 202), RG12-205, GNG 2367, JG11 X JG14, and BRC 305 showing higher nutrient concentration in Cluster I. To expedite bio-fortification in chickpea, systematic hybridization, followed by studies on combining ability, should be initiated among these promising and diverse genotypes for the genetic improvement of protein and micronutrients.

References

1. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Kalyan Publishers, New Delhi, 1977, 252.
2. Mahalanobis PC. On the generalized distance in statistics. Proc. National Acad. Sci., India. 1936;2:49-55.
3. Rao CR. Advanced statistical methods in biometrical research. John Wiley and sons Inc. New York, 1952, 236-272.
4. Ranganna G, Lokesh G, Gajendragad MR, Chandrakant G, Harshendra K, Ars AK, *et al*. Studies on Infiltration Characteristics of Pavanje River Basin in Dakshin Kannada District in Karnataka. Hydrological Journal. 1991;14:33-40.
5. Aliu S, Kaul HP, Rusinovci I, Shala-Mayrhofer V, Fetahu S, Zeka D. Genetic diversity for some nutritive traits of Chickpea (*Cicer arietinum* L.) from different regions in Kosova. Turkish J Field Crops.

2016;21(1):156-161.
6. Bueckert R, Thavarajah D, Thavarajah P, Pritchard J. Phytic acid and mineral micronutrient in field grown chickpea (*Cicer arietinum* L.) cultivars from western Canada. European Food Res. and Tech. 2011;233:203-212.
7. Burton GW. Quantitative inheritance in grasses. Proc. 6th Int. Grassland Cong. 1952;1:277-283.
8. Moreno M, Cubero JI. Variation in *Cicer arietinum* L. Euphytica. 1978;27:465-485.
9. Thavarajah Dil, Thavarajah P, Asoka Wejesuriya, Michael Rutzke, Raymond P, Glahn, Gerald F, Combs Jr, Albert Vandenberg. The potential of lentil (*Lens culinaris* L.) as a whole food for increased selenium, iron, and zinc intake: preliminary results from a 3 year study. Euphytica. 2011;80:123-128, DOI 10.1007/s10681-011-0365-6.
10. Chibbar RN, Ambigaipalan P, Hoover R. Molecular diversity in pulse seed starch and complex carbohydrates and its role in human nutrition and health. Cereal Chem. 2010;87:342-352.
11. Wood JA, Grusak MA. Nutritional value of chickpea. In Chickpea breeding and management, [SS Yadav, R Redden, W Chen and B Sharma, editors]. Wallingford, UK: CAB International, 2007, 101-142.
12. Ereifez KI, Al Karaki GN, Hammouri MK. Seed chemical composition of improved chickpea cultivars grown under semi arid mediterranean conditions. Int.l J. Food prop. 2001;4(2):239-246.
13. Wang N, Hatcher DW, Tyler RT, Toews R, Gawalko EJ. Effect of cooking on the composition of beans (*Phaseolus vulgaris* L) and chickpeas (*Cicer arietinum* L) Food Res. Int. 2010;43:589-594.
14. Abbo S, Gruask MA, Tzu T, Reifen R. Genetic control of seed weight and calcium concentration in chickpea seed. Plant Breed. 2000;119(5):427-431.
15. FAO Stat. FAO statistical year book. Food and Agriculture organization of the United Nations; c2021. Available from: http://www.faostat.fao.org.
16. Tandon HLS. Methods of analysis of soils, plants, waters and fertilizers. Fertilizers development and consultation organization, New Delhi, India, 1993, 144.
17. Kjeldahl J. New method for the determination of nitrogen in organic substances. Zeitschrift für analytische Chemie. 1883;22:366-383.
18. Jones DB. Factors for converting percentages of nitrogen in foods and feeds into percentages of protein. U.S. Department of Agriculture, Cirular, 1941, No. 83.
19. Jukanti AK, Gaur PM, Gowda CLL, Chibbar RN. Nutritional quality and health benefits of chickpea (*Cicer arietinum* L.): A review. British J Nutri. 2012;108:S11-S26.
20. Ray H, Bett K, Tar'an B, Vandenberg A, Thavarajah D, Warkentin TD. Mineral micronutrient content of cultivars of field pea, chickpea, common bean and lentil grown in Saskatchewan, Canada. *Crop Sci*. 2014;54:1698-1708.
21. Diapari M, Sindhu A, Bett K, Deokar A, Warkentin TD, Tar'an B. Genetic diversity and association mapping of iron and zinc concentrations in chickpea (*Cicer arietinum* L.). Genome. 2014;57(8):459-68.
22. Kahraman C, Keshavarz Ghorabaee M, Zavadskas EK, Cevik Onar S, Yazdani M, Oztaysi B. Intuitionistic fuzzy EDAS method: an application to solid waste disposal site selection. Journal of Environmental Engineering and Landscape Management. 2017;25(1):1-12.
23. Awasthi CP, Abidi AB, Choudhary AR. Studied on the nutritional quality of different varieties of chickpea. Indian Journal of Agricultural Research. 1991;25:21-26.
24. Agrawal K, Singh G. Physico- chemical and milling quality of some improved varieties of chickpea. Journal of Food Science and Technology. 2003;40:439-442.
25. Khan MA, Akhtar N, Ullah I, Jaffery S. Nutritional evaluation of desi and kabuli chickpea and their products commonly consumed in Pakistan. International Journal of Food Sciences and Nutrition. 1995;46(3):215-223.
26. Mcintosh GH, Topping DL. Food legumes in human nutrition in proceeding of Third International Food Legume Research Conference (Knight, R.ed) Linking Research and Marketing Opportunities for Pulses in the 21st Century Netherlands, 2000, 655-660.
27. Sood M, Malhotra SR, Sood BC. Effect of processing and cooking on proximate composition of chickpea (*Cicer arietinum* L.) varieties, Journal of Food Science and Technology. 2002;39:69-71.
28. Kutoš T, Golob T, Kač M, Plestenjak AD. Fibre content of dry and processed beans. Food Chemistry Journal. 2003;80(2):231-235.
29. Singh U, Subrahmanyam N, Kumar J. Cooking quality and nutritional attributes of some newly developed cultivars of chickpea (*Cicer areitinum* L). Journal of the Science of Food and Agriculture. 2006;55(1):37-46.
30. Maheri-Sis N, Chamani M, Sadeghi AA, Aghazadeh AM, Golshani AA. Nutritional evaluation of kabuli and desi type chickpeas (*Cicer arietinum* L.) for ruminants using *in vitro* gas production technique. African Journal of Biotechnology. 2008;7(16):2946-2951.
31. Alwawi HM, Choumane MW. Genotype-environment interaction and genetic parameters in chickpea (*Cicer arietinum* L.) landraces. Journal of Agriculture Sciences. 2010;2(1):154-161.
32. Falco ED, Imperato R, Landi G, Nicolais V, Piccinelli AL, Rastrelli L. Nutritional characterization of *Cicer arietinum* L. cultivars with respect to morphological and agronomic parameters. Emirates Journal of Food and Agriculture. 2010;22(5):377-387.
33. Sharma S, Yadav N, Singh A, Kumar R. Nutritional and antinutritional profile of newly developed chickpea (*Cicer arietinum* L) varieties. International Food Research Journal. 2013;20(2):805.
34. Nobile CGM, Carreras J, Grosso R, Inga M, Silva M, Aguilar R, *et al*. Proximate composition and seed lipid components of kabuli-type chickpea (*Cicer arietinum* L.) from Argentina. Agriculture Science. 2013;4(12):729-737.
35. Kabuo NO, Dialoke SA, Omeire GC, Bedi EN, Peter-Ikechukwu AI, Irekpita TE. Comparison of proximate composition of some cultivars of chickpea (*Cicer arietinum* L.) cultivated in Owerri, Imo State, Nigeria. Food Science and Quality Management. 2015;37:103-9.
36. Gopalan C, Ramasastri BV, Balasubramanian SC. Nutritive value of Indian Foods, Indian Council of Medical Research, Hyderabad, India, 1995, 48.
37. Sánchez-Mata MC, Hurtado MC, Dıez-Marqués C. Effect of domestic processes and water hardness on soluble sugars content of chickpeas (*Cicer arietinum* L.). Food Chemistry. 1999;65(3):331-8.

38. Gupta O, Babbar A. Identification of desi and kabuli chickpea genotypes for multiple disease resistance against soil borne diseases. Indian Journal of Pulses Research. 2006;19(1):129-130.
39. Kakati P, Deka S, Kotoki D, Saikia S. Effect of traditional methods of processing on the nutrient contents and some antinutritional factors in newly developed cultivars of green gram (*Vigna radiata* L.) and black gram (*Vigna mungo* L.) of Assam, India. Int. Food Res. Jr. 2010;17:377-384.
40. Borate VV, Dalvi VV. Correlation and path analysis in chickpea. Journal of Maharashtra Agricultural University. 2010;35(1):43-46.
41. AOAC (Association of Analytical Chemists). Standard Official Methods of Analysis of the Association of Analytical Chemists. 14th Edition, S.W Williams, Washington DC, 1984, 121.
42. Anonymous. Directorate of Pulses Development. Vindhyachal Bhavan, Bhopal (MP); c2021-22. https://dpd.gov.in/Annual%20Report%20(2021-22).pdf