

Research Article

Genetic Variability, Heritability and Expected Genetic Advance of Yield and Yield Related Traits in Desi Type Chickpea (*Cicer Arietinum* L.) at Bule Hora, Southern Ethiopia

Taera Itana^{1,*} , Wassu Mohammed², Seltene Abady²

¹Yabello Pastoral and Dryland Agriculture Research Centre, Oromia Agricultural Research Institute, Yabello, Ethiopia

²Department of Plant Science, Haramaya University, Haramaya, Ethiopia

Abstract

Chickpea is one of most important pulse crops in Ethiopia. Despite its significance, the national average chickpea yield is low due to many constraints of which the unavailability of improved varieties for each growing and potential area. This research was conducted to evaluate genetic variability, heritability, and expected genetic advance of yield and yield related traits in chickpea genotypes. It was conducted at Bule Hora during 2022/23 cropping season that 36 Desi type of chickpea genotypes were evaluated using a 6 x 6 simple lattice design. The results of the analysis of variance showed the presence of significant variations among genotypes for nine characteristics. In this study, the phenotypic variance was higher than the genotypic variance for all the traits studied. However, the difference between phenotypic and genotypic variances was low, ranging from 0.05 to 5.46 for four traits, and the difference between phenotypic and genotypic coefficients of variation was <5% (1.89 to 4.32%) for six of nine traits. Furthermore, Phenotypic (PCV) and genotypic (GCV) coefficient of variations ranged from 5.32 to 41.77% and 3.43 to 37.45%, respectively. Heritability (H^2) in broad sense and genetic advance as percent of mean (GAM) ranged from 23.91 to 80.40 and 5.89 to 69.18%, respectively. The estimates of GCV and PCV, H^2 and GAM were high for number of pods per plant, seeds per plant in gram, and grain yield.

Keywords

Genotypic Coefficient of Variation, Genetic Advance as Percent of Mean Heritability, Phenotypic Coefficient of Variation

1. Introduction

Pulse crops play a driver in the home of agriculture for economic growth and food security. It accounts for about 13% of cultivated land and 10% of agricultural value-added [3]. They also contribute significantly to smallholder income creation, as they are a higher-value crop than cereals and a

cost-effective source of protein, accounting for roughly 15% of total protein consumption [29]. Pulses, including chickpea (*Cicer arietinum* L.), are an important source of human diet in the world [14]. Chickpeas are grown in two different varieties around the world, viz., Desi and Kabuli. The Desi-type

*Corresponding author: taeraitanakenea430@gmail.com (Taera Itana)

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has shared 80–85% of the world's chickpea land [21]. In Ethiopia, the traditional production of Desi chickpea had a larger share of cultivated land at about 177,546.76 hectares than Kabuli type, which was cultivated on 43,172.44 hectares of land during the 2020–21 Meher season [5].

Ethiopia is Africa's biggest producer, consumer, and exporter of chickpeas [16]. The country is the world's seventh-greatest producer, contributing approximately 2% of total chickpea production. Ethiopia is the largest producer of chickpeas in sub-Saharan Africa, accounting for over 90% of chickpea production in the region and being ranked sixth globally [18]. Chickpea is the third important food legume, both in area and production, after common beans and faba beans in Ethiopia.

The number of smallholder farmers growing chickpeas and their production have increased in Ethiopia. The total production increased by 41.66% within 10 years, viz., from 322838.827 tons in 2010–11 [7] to 457319.37 tons during the 2020–21 Meher season [7]. The national average yield was 1.549 t/ha in 2010/11, whereas it was 2.107 t/ha in 2020/21, which was increased by 41.66%, but the cultivated land increased only by 5.92% from 208,388.62 ha in 2010/11 [7] to 220719.2 ha during the 2020/21 Meher season [7]. The considerable efforts made by the national chickpea improvement program to develop and release 32 varieties (18 Desi and 14 Kabuli types) [28] and management technologies coupled with their dissemination to farmers are expected to increase the productivity of the crop. Oromia Regional State is the largest producer of chickpeas, accounting for 53.9 and 57.67% of the land cultivated and total production of the country, respectively. The average yield of chickpea was 2.254 t/ha, which was higher by 6.98% than the national average yield [7]. The major producing zones are southwest Shewa (76501.294 tons), east Shewa (33320.89 tons), and north Shewa (28349.43 tons), which account for about 56.428% of the total area and production in the regional state. In spite of its immense use, chickpea production is not well known in the potential areas of Guji Zones, and the cultivated land and production data are not available. The variety adaptation research activities have started recently, realizing that the lack of improved chickpea varieties that adapt to the prevailing environment is due to production constraints [11].

Testing the adaptability of improved chickpea varieties in West Guji zone is one of the options to the improvement of the production of the crop. The varieties were developed for major pulse crop production areas and might not be adapted the environment of the West Guji zone area. For instance,

nine improved chickpea varieties released from 2004 to 2016 were evaluated for two consecutive years in 2017 and 2018 at Bule hora, West Guji zone and produced 0.5717 to 1.0875 t/ha [11] while the national and Oromia Regional State average yield was 1.969 and 2.234 t/ha, respectively, during 2016/17 Meher season [6]. Thus, assessing genetic variability of chickpea genotypes is vital and it is the first step to develop varieties to the area. The success of breeding program is largely determined by the genetic variability contained in the breeding materials [24]. Thus, a breeder's understanding of genetic diversity, heritability, and genetic progress is critical to selecting genotypes with desirable traits and effectively utilizing them for crop improvement [15]. However, the majority of studies on chickpea variability were undertaken outside the Guji zone (southern Ethiopia), where chickpea is the most widely cultivated pulse crop. Hence the present study was undertaken to estimate the extent of genetic variability, heritability and genetic advance in chickpea genotypes for yield and yield related traits.

2. Materials and Methods

The experiment was conducted at Bule Hora during the 2022–23 cropping season. Bule Hora is located at 465 km along the Addis Ababa-Moyale main road in southern Ethiopia. The site is situated at 05° 75' 87" N latitude and 038° 02' 84.8" E longitude, with an elevation of 2371 meters above sea level (m.a.s.l.). The area has bimodal rainfall patterns, and there are two separate crop-growing seasons locally called Gana and Hagaya. The main season, Gana, extends from mid-March to July, and Hagaya from September to October. The area receives a minimum of 748.7mm and a maximum 1353.5mm of annual rainfall, with annual mean maximum and minimum temperatures of 10.70 °C and 25.3 °C, respectively. The soils are predominantly sandy loam [8].

2.1. Experimental Materials

A total of 36 Desi chickpea genotypes were obtained, of which three improved varieties were obtained from the Debre Zeit Agriculture Research Centre (DZARC) and evaluated for yield and yield-related traits. The varieties Natoli, Tekataye, and Dimtu were released in 2007, 2013, and 2016, respectively, by the Debre Zeit Agriculture Research Centre (DZARC) for areas at altitudes of 1800–2800 meters above sea level.

Table 1. List of chickpea genotypes.

No	Genotype	Origin	No	Genotype	Origin
1	ICCV-10	ICRISAT	19	ICCXE7-1700-29AB-1-3	ICARDA
2	Dz-2012-CK-2015-3-0043	ICRISAT	20	MABC-14	ICARDA

No	Genotype	Origin	No	Genotype	Origin
3	ICCMABCD-18	ICARDA	21	Dz-2012-CK-2015-2-00-42	ICARDA
4	ICCXE7-1600-13 ABF-2-1	ICRISAT	22	Dz-2012-CK-0034	ICARDA
5	Dz-2012-CK-0039	ICRISAT	23	<i>Dimtu</i>	DZARC
6	Dz-2012-CK-0034-1	ICARDA	24	XO-15-TR-55-3	ICARDA
7	CK-COM-ICC-MABCD-336	ICRISAT	25	Dz-2012-CK-00-30	ICARDA
8	CCMABCD-21	ICRISAT	26	MABC-13	ICARDA
9	ICCXE7-160011ABF-7-2	ICARDA	27	<i>Natoli</i>	DZARC
10	ICCMABCD-19	ICARDA	28	ICCXE7-1700 10AB-2-6-2	ICARDA
11	<i>Tekataye</i>	DZARC	29	ICCV-13-62-3	ICARDA
12	ICCMABCD-14	ICRISAT	30	ICCXE7-1700-29AB-1-8-2	ICARDA
13	ICCXE7-16001FABF-1-4	ICRISAT	31	Dz-2012-CK-2015-2-00-29	ICARDA
14	ICCB-14106	ICARDA	32	ICCE7-1070029-AB-1-5-4	ICARDA
15	ICCV-16107	ICARDA	33	ICCXE7-16009ABF-4-3	ICARDA
16	ECD 17 1081	ICRISAT	34	ICCMABCA-30	ICARDA
17	ICCMABCD-5	ICRISAT	35	ICCX060039-F3-P85-BP	ICARDA
18	ICCXE7-1700-10-AB-2-6-1	ICRISAT	36	MABC-2	ICARDA

Source: Debre Ziet Agriculture Research Center

2.1.1. Experimental Design and Management

The experiment was laid out in a simple 6 x 6 lattice design. Each entry was planted in a plot with 4 rows of 1.4 m in length. The plants in two rows were harvested, and two border rows were left to exclude the border effect. The row and plant spacing were kept at 40 and 10 cm, respectively. Individual plot sizes were 1.6 m × 1.4 m = 2.24 m² and 1.5 and 1 m between replications and subblocks, respectively. The recommended 100 kg ha⁻¹ NPS fertilizer was applied. All the recommended crop management practices were applied based on the recommendations.

2.1.2. Data Collection

Data Collected on Plot Basis

Days to 50% flowering: number of days from the date of emergence to the date on which about 50% of the plants in each plot produce flower was taken.

Days to maturity: the number of days from planting to the date when the morphological observation of the plant turned to yellow straw color were determined.

Grain yield (t/ha): grain yield obtained from each plot were used to estimate grain yield (tons) per hectare.

Thousand seed weight (g): 1000 seeds were randomly taken from the yield obtained at each experimental plot and weighted by using sensitive balance.

Data Collected on Plant Basis

Plant height at harvest (cm): height of 10 randomly taken plants during harvest period from each experimental unit were measured in centimeter from the ground to top of the plant and the average height was recorded.

Number of primary branches: number of productive branches extending from the main stem were recorded from five randomly selected plants.

Number of pods per plant: this was recorded as average total number of pods of ten randomly selected plants from each experimental plot at harvest.

Number of seeds per pod: this was recorded as average total number of seed of ten randomly selected plants from each experimental plot divided by total number of pods of the same plants at harvest.

Seed yield per plant (g): the average weight in grams of seeds adjusted to 14% moisture content was recorded from ten randomly selected plants on each plot.

2.2. Data Analysis

2.2.1. Analysis of Variance

The SAS GLM (General Linear Model) procedure (SAS Institute Inc. 2002) was employed for the analysis of variance. Duncan Multiple Range Tests (DMRT) at the 5% level of significance were used for mean comparisons whenever genotype differences were significant.

Model of simple lattice design:

$$Y_{ijl} = \mu + r_j + g_i + Pl(j) + \varepsilon_{ijl}$$

Where: Y_{ij} is observed value of the trait of the Y for the i th genotype in j th replication

μ = the general mean of trait Y

r_j = the effect of j th replication

g_i = the effect of i th genotypes and

$Pl(j)$ = block within replicate effect

ε_{ijl} = the experimental error associated with the trait y for the i th genotype in l th block with in replication and j th replication

Where, r: Number of replications, k2: Number of treatments, k: Number of treatments in a block

Table 2. Analysis of variance for simple lattice design.

Source of variation	DF	SS	Mean square	F value
Replication	r-1	SSr	MSr	MSr/Mse
Treatments	t-1	SSt	MSt	MSt/Mse
Block within replication (b)	r (b-1)	SSb	MSb	MSb/Mse
Intra block error	(b-1) (rb-b-1)	SSe	Mse	
Total	TSS			

r = number of replications, t = number of treatments, df = degree of freedom, b = block SS = Sum of squares, MS = mean squares, SSr and MSr are sums of squares and mean of replication, respectively; SSt and MSt are sums of squares and mean of treatments respectively; SSb and MSb are sums of squares and mean of blocks within replication respectively, SSe and MSe are sums of squares and mean of intra-block error, respectively and SST is sum of squares of the total.

2.2.2. Variability Components Analysis

Phenotypic and genotypic variability

The genotypic and phenotypic variance components and coefficient of phenotypic and genotypic variability were estimated according to statistical procedure by using the formula adopted by Sharma and Sigh [26, 25], considering the incomplete blocks as a source of variation.

$$\text{Genotypic variance } (\sigma^2_g) = (K + 1/kr) (MS_g - Mse)$$

Where: MS_g = mean square due to genotypes

Mse = error mean square, r = the number of replications, K = Block size

Environmental variance (σ^2_e) = error mean square = MS_e

Phenotypic variance (σ^2_p) = (σ^2_g) + (σ^2_e)

Coefficient of variation at phenotypic, genotypic and environmental levels was estimated using the following formulae.

$$\text{Phenotypic coefficient of variation (PCV)} = (\sqrt{\sigma^2_p} / \bar{X}) * 100$$

$$\text{Genotypic Coefficient of variation (GCV)} = GCV = (\sqrt{\sigma^2_g} / \bar{X}) * 100$$

Where: \bar{x} = grand mean of character

Estimate of heritability

Heritability in broad sense for all traits was computed by adopting the formulae presented by Allard [2].

$$\text{Heritability } (Hb^2) = (\sigma^2_g / \sigma^2_p) * 100$$

Where: Hb^2 = Heritability in broad sense

σ^2_p = Phenotypic variance, σ^2_g = Genotypic variance

Estimation of expected genetic advance

The genetic advance for selection intensity (k) at 5% was estimated by the following formula [16, 2]

$$EGA = k * \sigma_{ph} * h^2 b$$

Where,

EGA represents the expected genetic advance under selection; σ_{ph} is the phenotypic standard deviation; $h^2 b$ is heritability in broad sense and k is selection differential (k=2.06 at 5% selection intensity). The genetic advance as percent of population mean could be also estimated following the procedure of Johnson [16].

$$\text{Genetic advance per population means} = (EGA / \text{grand mean}) * 100.$$

3. Results and Discussion

3.1. Analysis of Variance

The analysis of variance was carried out for nine phenotypic traits, and the results revealed the existence of highly significant ($P < 0.01$) differences among the test genotypes for

all the traits (Table 3). These highly significant differences showed the existence of considerable variability among genotypes, which can be exploited through selection for developing high-yielding chickpea varieties with desirable agronomic traits. [4, 12] reported significant differences among

chickpea genotypes for phenology parameters and yield and yield components, respectively. A significant blocking effect was observed for the number of primary branches, seed yield per plant, and grain yield, implying that blocking was efficient to single out the heterogeneity of the experimental field.

Table 3. Mean squares from the analysis of variance for nine traits of 36 Desi chickpea genotypes evaluated at Bule hora during 2022/23 rainy season.

Trait	Replication (DF=1)	Block (Replication) (DF =10)	Genotype (DF=35)	Error (DF=25)	CV (%)
Days to flowering	1.38	66.67	94.83***	24.35	7.6
Days to maturity	0.88	70.72	117.57***	20.07	3.8
Plant height (cm)	39.01	8.17	59.9***	8.71	7.8
Number of primary branches	0.016	0.10**	0.16***	0.043	9.18
Number of pods per plant	499.28	155.5	900.99**	203.55	25.3
Number of seeds per pod	0.12	0.01**	0.104***	0.007	5.29
Seeds per plant(g)	6.51	1.21	18.82***	2.04	20.85
Hundred seed weight (g)	1.33	2.31	34.15***	5.98	12.9
Grain yield (kg/ha)	6779	117151.4*	1249973.2**	48295.5	17.78

*, ** and *** significant, highly significant and very highly significant at $P < 0.05$, $P < 0.01$ and $P < 0.001$, respectively. DF = Degree of freedom and CV (%) = percentage coefficient of variation.

3.2. Estimates of Variance Components

3.2.1. Phenotypic and Genotypic Coefficients of Variation

The estimates of phenotypic variances (σ^2_p), genotypic variance (σ^2_g), phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV) are presented in Table 4. In this study, the phenotypic variance was higher than the genotypic variance for all the traits studied. However, the difference between phenotypic and genotypic variances was low, ranging from 0.05 to 5.46 for four traits, and the difference between phenotypic and genotypic coefficients of variation was $< 5\%$ (1.89 to 4.32%) for six of nine traits. The relatively narrow gap between the phenotypic variance and genotypic variance values indicated the smaller contribution of the environmental effects on the expression of most of the traits.

According to Deshmukh [9], PCV and GCV values greater than 20 percent are considered to be high, values between 10 and 20 percent as moderate, and values less than 10 percent as low. High GCV and PCV values were estimated for grain yield, seed per plant (g), and number of pods per plant, and moderate GCV and PCV values were calculated for hundred seed weight. This showed the correspondence between genotypic and pheno-

typic expression in these traits due to the low influence of environmental factors, which suggested selection-based phenotypic expression of genotypes is rewarding to improve for these traits. Many authors suggested that the high phenotypic and genotypic coefficients of variation are an indication of the less influence of environmental factors in the expression of traits and the higher chance to improve the traits through selection breeding [19, 20, 22]. On the other hand, moderate PCV and low GCV values were estimated for plant height, number of primary branches, and number of seeds per pod, while low PCV and GCV values were calculated for days to flowering and maturity. This showed that the improvement of these traits through selection is hardly possible due to the limited variability of the genotypes for these particular traits. The success of any selection program depends largely upon the magnitude of genetic variability present in the population [28].

The results of this study were in agreement with [12], who reported high GCV and PCV for grain yield, number of pods per plant, and number of seeds per plant. Dev [10] also reported low PCV and GCV for days to maturity. Amar [4] reported low GCV and PCV values for seed per pod and the number of primary branches. Gizaw [13] reported moderate GCV and PCV values for day to flowering, plant height, number of secondary branches per plant, and seed weight.

Table 4. Estimates of variance, genotypic and phenotypic coefficients of variability, broad sense heritability, and genetic advance as a mean for nine traits of *Desi* type chickpea genotypes based on analysis of variance.

Trait	Means	σ^2_e	σ^2_g	σ^2_p	ECV%	GCV%	PCV%	H ² %	GA%	GAM%
DF	64.39	21.54	14.53	36.07	7.21	5.94	9.33	40.28	4.98	7.74
DM	116	22.34	15.79	38.12	4.07	3.43	5.32	41.41	5.27	4.54
PH	37.55	10.22	9.07	19.29	8.51	8.02	11.69	47.01	4.25	11.33
NPB	2.25	0.06	0.02	0.07	10.44	5.85	11.97	23.91	0.13	5.89
NPP	56.23	201.44	147.66	349.10	25.24	21.61	33.23	42.30	16.28	28.95
NSPP	1.68	0.01	0.02	0.03	6.58	7.89	10.27	59.06	0.21	12.49
SPPT	6.87	2.01	3.33	5.34	20.66	26.57	33.66	62.33	2.97	43.22
HSW	18.9	5.46	5.07	10.53	12.36	11.91	17.17	48.15	3.22	17.03
GY	1278.7	55904.70	229334.35	285239.05	18.49	37.45	41.77	80.40	884.57	69.18

σ^2_g = genotypic variance, σ^2_p = phenotypic variance, GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, H² = broad sense heritability, GA = genetic advance, GAM = genetic advance as percent of mean, DF = days to flowering, DM = days to maturity, PH = plant height, NPB = number of primary branches, NPP = number of pods per plant, NSPP = number of seed per pod, SPPT = Seed per plant, HSW = Hundred seed weight, GY = grain yi

3.2.2. Broad Sense Heritability

The broad-sense heritability values of the traits based on the analyses of variance at the test location were estimated and ranged from 23.91% for the number of primary branches to 80.40% for grain yield (Table 4). As suggested by [16], heritability estimates are high (>60%), moderate (30–60%), and low (<30%). Accordingly, high broad-sense heritability estimates were found for traits such as grain yield and seed per plant per gram. A high estimate of broad sense heritability and genetic advance as a percentage of the mean was recorded for grain yield, which implies that if the character is governed by additive gene action, both heritability and genetic advance would be high [10]. Characters that had high broad sense heritability indicate that selection based on the phenotypic expression of individual genotypes might be easy due to the relatively small contribution of the environment to the phenotype. Johnson and Barad [17, 5] reported high heritability for thousand seed weight, number of primary branches, number of pods per plant, seed yield per plant, and grain yield.

Moderate heritability values were observed for days to flowering, days to maturity, plant height, number of pods per plant, and hundred seed weight, and low broad sense heritability was estimated for the number of primary branches. Fasil [12] reported a moderate heritability value for biological yield and the number of seeds per pod. However, selecting superior individuals based on heritability estimates alone may not be evidence for genetic improvement. According to Johnson [16], heritability estimates along with genetic advances would be more useful in predicting the effectiveness of selecting the best individuals.

3.2.3. Genetic Advance

Genetic advance as a percent of the mean ranged from 4.54% for days to maturity to 69.18% for grain yield (Table 4). According to [16], genetic advances as a percentage of the mean (GAM) are classified as high (>20%), moderate (10–20%), and low (<10%). Considering these categories, high genetic advance estimates as percent of the mean were recorded for the number of pods per plant (28.95%), seed per plant (g) (43.22%), and grain yield (69.18%). A high estimate of these traits indicates that whenever we select the best 5% genotypes for a given trait, the genotypic value of the new population for the trait will be highly improved. Amare [4] reported a high value of genetic advance as a percentage of the mean for grain yield and the number of pods per plant. Yilma [30] reported a high value of genetic advance as a percentage of the mean for numbers of pods per plant, numbers of seeds per plant, and grain yield per hectare. Ali and Ahsan [1] reported similar results of high genetic advance as a percent of the mean for the number of seeds per plant and the number of pods per plant.

Moderate genetic advance values as a percent of the mean were (11.13%) plant height, (12.49%) number of seeds per pod, and (17.3%) hundred seed weight. In contrast, low genetic advance as a percent of the mean was obtained for days to flowering (7.74%), (5.89%) number of primary branches, and (4.54%) days to maturity. These indicate that selection of genotypes based on those traits as parents might result in a low response in a new population. Fasil [12] reported low genetic advance as a percentage of the mean for the grain filling period and days to maturity. Amare [4] also reported low genetic advance as a percentage of the mean

harvest index, followed by the number of seeds per pod and the and the number of primary branches. In addition to these, high heritability and high genetic advance were very essential to improving traits of interest [16]. Accordingly, in the present study, relatively high heritability along with high genetic advance estimates were obtained for grain yield and seed yield per plant (g). As a result, grain yield and seed yield per plant (g) are governed by additive gene action, and selection will be beneficial for such traits. Therefore, these traits are significant for the genetic improvement of the desi chickpea. [12] reported high heritability along with a high genetic advance for the number of pods per plant, the number of seeds per plant, and grain yield. Hussain [14] reported similar results with the present study regarding high heritability coupled with high genetic advance as a percent of the mean for the number of pods per plant and grain yield.

4. Summary and Conclusion

High genotypic (GCV) and phenotypic (PCV) coefficient of variation values were estimated for grain yield, seed per plant (g), number of pods per plant, and moderate GCV and PCV values were calculated for hundred seed weight. Moderate PCV and low GCV values were estimated for plant height, number of primary branches, and number of seeds per pod, while low PCV and low GCV values were calculated for days to flowering and maturity. High broad sense heritability (H₂) was estimated for grain yield and seed per plant in grams; moderate heritability values were estimated for days to flowering, days to maturity, plant height, number of pods per plant, and hundred seed weight; and low broad sense heritability was estimated for the number of primary branches. High genetic advances as percent of mean (GAM) were recorded for the number of pods per plant, seed per plant, and grain yield. Moderate GAM is estimated for plant height, number of seeds per pod, and seed weight. Moreover, high values of GCV, PCV, H₂, and GAM are estimated for grain yield and seed per plant; high values of GCV, PCV, GAM, and moderate H₂ are estimated for the number of pods per plant; and moderate values for all parameters are estimated for the hundred seed weight. This showed high heritability of these traits; the correspondence of genotypic and phenotypic expression in these traits is due to the low influence of environmental factors, and the selection of high-performing genotypes is rewarding to improve for the traits.

Conflicts of Interest

The authors declare no conflicts of interest.

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