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Genotypic Variability and Character Associations of Kabuli Chickpea (*Cicer artietinum* L.) Genotypes for Yield and Yield Related Traits at Arsi-Robe, Southeastern Ethiopia

Gizachew Yilma Kebede[1], **Bulti Tesso**[2] and **Tesfahun Alemu**[3]

[1]Ethiopian Institute of Agricultural Research (EIAR), Kulumsa Agricultural Research Center, Asella, Ethiopia
[2]School of Plant Science, Haramaya University, Dire Dawa, Ethiopia
[3]Ethiopian Institute of Agricultural Research (EIAR), Holleta Agricultural Research Center, Holleta, Ethiopia

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Corresponding gizachewy8@gmail.com

0009-0001-5665-5618

ABSTRACT

The study was conducted at Arsi-robe, Southeast Ethiopia during August–December, 2020 to understand the extent of genetic variability and association for yield and yield related traits among Kabuli chickpea genotypes. Forty-nine Kabuli chickpea genotypes were evaluated for 11 traits at Arsi-robe using 7×7 simple lattice designs. The analysis of variance showed significant differences among genotypes. The phenotypic variances of the traits were higher than the genotypic variances, implying the influence of environment on the expression of the traits. Genotypic coefficient of variation (GCV) ranged from 1.28 for days to maturity to 41.74% for grain yield and phenotypic coefficient of variation (PCV) ranged from 1.47 to 44.06% for days to maturity and grain yield, respectively. High heritability was recorded from grain yield. High broad-sense heritability coupled with high genetic advance was observed for grain yield, number of secondary branches and hundred seed weight. Grain yield showed highly significant and positive genotypic correlations with grain filling period, number of seed plant^{-1} and plant height. Genotypic path coefficient analysis showed that days to maturity, number of pods plant^{-1}, number of seed plant^{-1}, plant height and hundred seed weight had positive direct effects on grain yield. Number of pods plant^{-1} exhibited a maximum positive direct effect on grain yield. The observed variations indicate the possibility for further improvement of grain yield and associated traits by utilizing selected parental genotypes and targeted crossing schemes in breeding programs.

KEYWORDS: Chickpea, path analysis, genotypes, correlation, variability, heritability

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1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) belongs to the family leguminosae. It is one of the most important food grain legumes in the world after common bean (*Phaseolus vulgaris L.*) and field pea (*Pisum sativum* L.) (Muehlbauer and Sarker, 2017). Chickpea is annual, self-pollinated and diploid species with 2n=2x=16 chromosomes (Van der Maesen, 1987). In Ethiopia, chickpea covers 242,703 ha, which is 15.2% of the pulse area, with 499,426 tons of grain production (16.8% of pulses) (Anonymous, 2019). Ethiopia is the largest producer, consumer, and exporter of chickpea in Africa and shares 4.5% of global and more than 60% of Africa's global chickpea market (Anonymous, 2018). Kabuli type chickpea is one of the major pulses grown in Ethiopia, mainly by subsistence farmers usually under rain fed conditions.

In Ethiopia, the production of the chickpea is constrained by many factors including the use of low productive farmers' varieties, unimproved traditional practices, biotic and abiotic factors (Upadhyaya et al., 2002). The crop is planted at the end of the rainy season and grows on residual soil moisture because of high disease pressure, especially root rot diseases, during the peak rainy season. This late planting predisposes the crop to moisture stress during critical reproductive stages, leading to low productivity.

Efforts have been made to develop improved varieties by the regional and national research centers and different varieties have been released. However, the major challenge of chickpea improvement program in Ethiopia has been lack of genotypes that consistently perform well across different chickpea growing environments and resistant to biotic factors. Therefore, developing high yielding and disease resistant genotypes remains very important for farmers to sustain their production and to ensure the sustainability of food and nutritional security.

Genetic improvement of polygenically inherited complex traits such as yield is difficult and requires much time and effort due to high environmental influence and, thus low heritability of the traits. Heritability explains whether the differences observed among individuals arose because of differences in genetic makeup or due to environmental factors. Genetic advance gives an idea of possible improvement of a new population through selection, when compared to the original population. The amount of genetic variability present in the base population of a crop is important for its genetic improvement (Dutta et al., 2013, Holme et al., 2019). Therefore, understanding the extent of existing genetic variability in the germplasm of a crop and the heritability of the target traits is imperative in order to design appropriate breeding schemes and genetic improvement of the crop for the desired traits. The variability available in the population can be partitioned into heritable and non-heritable components (Begna, 2021).

Yield improvement cannot be solely achieved through direct selection because yield depends on various yield-contributing characters (Kumar et al., 2019). The concept of correlation among yield and yield related traits is essential in studying the magnitude and direction of association of one character with another (Rathi and Dhaka, 2007, Kalapchieva et al., 2021). Correlation coefficient and path analysis deals a means for determining the importance of traits affecting the dependent variables. Moreover, these complex traits are highly influenced by environment, which reduces the progress to be achieved through direct selection. In such cases, there is another option which is known as indirect selection for yield, which selection of elite genotypes based on yield related traits rather than the yield (Dewey and Lu, 1959). In view of this, the present investigation was aimed at studying genetic variability and character associations among yield and yield related traits of chickpea genotypes.

2. MATERIALS AND METHODS

2.1. *Description of the study area*

The experiment was conducted under field condition at Arsi-robe, southeast Ethiopia, with an altitude of 2420 masl, latitude of 07°53'02"N and longitude of 39°37'40"E, during the 2019/20 main cropping season (August–December 2020). The average rainfall at the research center was 890 mm per annum having peaks in July and August. The mean maximum and minimum temperatures were 22.1°C and 6°C, respectively. The soil type is classified as heavy clay with pH value of 6.0.

2.2. *Experimental materials*

A total of 49 Kabuli chickpea genotypes listed in Table 1 were used for the study. The genotypes status was advanced breeding lines developed through hybridization and introduction material by ICARDA.

2.3. *Experimental design and trial management*

The experiment was carried out using 7×7 simple lattice designs. The plot size was 4 m long and 1.2 m wide, i.e. 4.8 m^2 areas with spacing of 0.3 m and 0.1 m between rows and plants, respectively as per the existing recommendation. Each plot had four rows and the spacing between incomplete blocks was 1 m, and 0.6 m spacing was kept between plots within incomplete blocks. Planting was done at the end of August on randomly allocated plots within each replication by hand drilling. 100 kg ha^{-1} of NPS fertilizer was applied and all other agronomic practices were done throughout the growing season.

Table 1: List of experimental materials

Genotype code	Genotype name	Source	Genotype code	Genotype name	Source
G-1	DZ-2012-CK-0310	Hybridization	G-26	DZ-2012-CK-0295	Hybridization
G-2	DZ-2012-CK-0303	Hybridization	G-27	Flip-03-101C	ICARDA
G-3	ICCMABCB-8	ICARDA	G-28	ICCV-07313	ICARDA
G-4	Flip-08-254C	ICARDA	G-29	ICCV-09315	ICARDA
G-5	Flip-07-6C	ICARDA	G-30	DZ-2012-CK-0271	Hybridization
G-6	Flip-09-155C	ICARDA	G-31	DZ-2012-CK-0267	Hybridization
G-7	DZ-2012-CK-0309	Hybridization	G-32	DZ-2012-CK-0242	Hybridization
G-8	Flip-84-92C	ICARDA	G-33	ICCV-09304	ICARDA
G-9	Flip-09-188C	ICARDA	G-34	Flip-09-184C	ICARDA
G-10	ICCMABCB-3	ICARDA	G-35	DZ-2012-CK-0062	Hybridization
G-11	Flip-11-34C	ICARDA	G-36	DZ-2012-CK-0281	Hybridization
G-12	DZ-2012-CK-0300	Hybridization	G-37	Flip-09-181C	ICARDA
G-13	Flip-93-93C	Hybridization	G-38	DZ-2012-CK-0286	Hybridization
G-14	DZ-2012-CK-0269	Hybridization	G-39	DZ-2012-CK-0066	Hybridization
G-15	ICCMABCB-5	ICARDA	G-40	DZ-2012-CK-0290	Hybridization
G-16	ICCMABCC-2	ICARDA	G-41	ICCV-10311	ICARDA
G-17	Flip-03-128C	ICARDA	G-42	DZ-2012-CK-0274	Hybridization
G-18	Flip-88-93C	ICARDA	G-43	Flip-09-377C	ICARDA
G-19	DZ-2012-CK-0276	Hybridization	G-44	DZ-2012-CK-0214	Hybridization
G-20	DZ-2012-CK-0287	Hybridization	G-45	Flip-06-14C	ICARDA
G-21	ICCU-09311	ICARDA	G-46	DZ-2012-CK-0266	Hybridization
G-22	ICC-8261	ICARDA	G-47	Flip-09-197C	ICARDA
G-23	Flip-05-63C	ICARDA	G-48	DZ-2012-CK-0305	Hybridization
G-24	Flip-06-135C	ICARDA	G-49	Flip-09-120C	ICARDA
G-25	DZ-2012-CK-0294	Hybridization			

G: Genotype

2.4. Data collected

Data on days to 50% flowering (DF), grain filling period (GFP), days to maturity (DM), stand count (SC), hundred seed weight (HSW), and grain yield ha^{-1} (GYH) were collected on plot basis. Data for plant height (HGT), number of primary branches (NPB), number of secondary branches (NSB), number of pods plant^{-1} (NPP), and number of seeds plant^{-1} (NSPP) were collected from five randomly taken sample plants on the two middle rows of each plot. The data were analyzed using R-software (R version 3.6.1).

3. RESULTS AND DISCUSSION

3.1. Analysis of variance

The ANOVA results for 11 traits are presented in Table 2. The result showed highly significant ($p \leq 0.01$) variation for days to 50% flowering, days to maturity, grain filling period, number of secondary branches, hundred seed weight, number of pods plant^{-1} and grain yield ha^{-1}, and significant ($p \leq 0.05$) differences among genotypes for number of seeds plant^{-1} and plant height. These highly significant differences indicate the existence of wide genetic variability among genotypes. The same result were reported by Getachew et al. (2015) for all traits. Significantly different ($p \leq 0.05$) results were previously reported for days to 50% flowering, days to maturity, number of pods plant^{-1}, plant height, hundred seed weight, and grain yield (Getachew et al., 2015) in a different set of genotypes. The presence of significant differences among Kabuli chickpea genotypes for yield and yield components was also reported by Biru et al. (2017). Fasil (2020) also reported highly significant variation among genotypes for days to 50% flowering,

Table 2: Mean square values from analysis of variance for 11 traits in chickpea genotypes

Traits	Rep (df= 1)	Genotype (df= 48)	Block/ Rep (df= 12)	Intra block error (df= 36)	CV (%)
FD	21.59	53.33**	20.87	9.94	4.64
MD	0.50	7.57**	2.29	1.9	1.03
GFP	15.52	36.78**	17.02	10.7	4.41
SC	19.76	82.23^{ns}	65.00	51.76	23.98
PBR	0.50	0.47^{ns}	0.12	0.29	17.97
SBR	82.63	8.54**	5.05	2.49	19.72
PPP	58.94	197.53**	68.31	72.45	20.27
SPPL	0.01	247.86*	134.08	122.46	24.06
HGT (cm)	50.00	72.37*	55.79	38.9	10.57
HSW (g)	26.54	25.81**	5.01	5.69	7.95
GYH (kg ha^{-1})	451929	596102**	289454	69005	19.98

Df: Degrees of freedom; FD: Days to 50% flowering; MD: days to maturity; GFP: Grain filling period; SC: Stand count at harvest; PBR: Number of primary branches; SBR: Number of secondary branches; PPP: Number of pods plant^{-1}; SPPL: Number of seeds plant^{-1}; HGT: Plant height; HSW: Hundred seed weight; GYH: Grain yield ha^{-1}; CV: Coefficient of variation; **: Significant at (p=0.01) level of significance; *: Significant at (p=0.05) level of significance; ns: Non-significant

days to maturity, number of secondary branches, hundred seed weight, number of pods plant^{-1}, and grain yield ha^{-1}. Thus, assembling the genetically variable germplasm and utilizing in a breeding program is possible for improving the economically desirable traits of the crop.

3.2. Estimation of genetic parameters

3.2.1. Phenotypic and genotypic coefficients of variation

In this study, the phenotypic variances were higher than the corresponding genotypic variance for all traits, but the differences range from small (e.g., for MD and SBR) to high (e.g., for PPP, SPPL, HGT, and GYH), indicating the differential environmental influences on the expression of the traits (Table 3).

Relatively high genotypic variances were found for number of pods plant^{-1}, number of seeds plant^{-1} and grain yield while low genotypic variance were found for number of secondary branches and days to maturity. Hussain et al. (2016) reported higher genotypic variance for plant height, hundred seed weight and number of pods plant^{-1}. The same authors also reported lower value of genotypic variance for number of primary and secondary branches. Banik et al. (2018) also reported higher genotypic variance for number of pods per plant and days to 50% flowering for chickpea.

In this study, the phenotypic coefficient of variation ranged from 1.47–44.06%, while the genotypic coefficient of variation varied from 1.28–41.74%. Phenotypic and genotypic coefficients of variation values more than 20% are considered to be high, between 10 and 20% as moderate and less than 10% as low (Deshmukh et al., 1986). Accordingly to this bench mark, high phenotypic and genotypic coefficients of variation were observed for grain yield, number of secondary branches plant^{-1} and

Table 3: Estimates of genetic parameters of 9 traits

Traits	Mean	GV	PV	GCV (%)	PCV (%)	H (%)	GA	GAM (%)
FD	68	24.79	29.76	7.32	8.02	0.833	9.37	13.79
MD	139	3.16	4.18	1.28	1.47	0.756	3.19	2.29
GFP	71	15.42	20.32	6.66	7.64	0.759	7.06	11.96
SBR	8	3.45	4.70	23.22	27.10	0.734	3.28	41.04
PPP	44	71.47	107.69	20.13	24.98	0.664	14.06	33.48
SPPL	46	71.66	132.89	18.40	25.06	0.539	12.82	27.88
HGT (cm)	59	19.12	38.57	7.41	10.53	0.496	6.35	10.76
HSW (g)	30	11.50	14.34	11.30	12.62	0.802	6.27	20.88
GYH (kg ha^{-1})	1315	301198.3	335700.7	41.74	44.06	0.897	1072.5	81.55

FD: Days to 50% flowering; MD: Days to maturity; GFP: Grain filling period; SBR: Number of secondary branches; PPP: Number of pods plant^{-1}; SPPL: Number of seeds plant^{-1}; HGT: Plant height; HSW: Hundred seed weight; GYH: Grain yield ha^{-1}; GAM: Genetic advance as percent of mean; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; H: Broad sense heritability; GA: Genetic advance; GV: Genotypic variance; PV: Phenotypic variance number of pods plant^{-1}. Awol et al. (2019) reported high genotypic coefficient of variation for grain yield, number of seeds plant^{-1} and number of pods plant^{-1}. Similar results were reported for grain yield and number of pods plant^{-1} by Banik et al. (2018) and Raju et al. (2017). Hussain et al. (2016) also reported higher genotypic coefficient of variation for grain yield. The high genotypic coefficient of variation reported in our study showed the existence of high genetic variability that can be exploited to improve grain yield in this chickpea population.

Moderate genotypic coefficients of variation were recorded for hundred seed weight and number of seed plant^{-1}. Awol et al. (2019) also reported moderate genotypic coefficients of variation for hundred seed weight. While lowest genotypic and phenotypic coefficient of variation was recorded for days to maturity, days to 50% flowering and grain filling period. Awol et al. (2019) reported lowest genotypic and phenotypic coefficient of variation for days to maturity. Fasil (2020) reported lowest genotypic and phenotypic coefficient of variation for days to 50% flowering, days to maturity and plant height. This indicates the presence of narrow genotypic variation of these traits and improvement of the traits through simple selection may not be possible.

3.2.2. Estimation of heritability and genetic advance

Heritability values ranged from 49.6%–89.7% for plant height and grain yield respectively. Heritability estimates in broad sense is categorized as high (>70%), moderate (50–70%) and low (<50%) as suggested by Robinson (1966). Accordingly, high estimates of heritability were found for days to 50% flowering, days to maturity, grain filling period, number of secondary branches, hundred seed weight and grain yield ha^{-1}. The higher heritability value of such traits indicates that direct selection can be employed at phenotypic level to improve the traits as the environmental influence on the expression of the phenotype is low.

Similar findings were reported by Awol et al. (2019), Hussain et al. (2016), Raju et al. (2017) and Tesfamichael et al. (2014) for grain yield and hundred seed weight. Arpita and Police (2011), Shengu et al. (2018) and Banik et al. (2018) reported high estimate of heritability for grain yield, days to 50% flowering, days to maturity and hundred seed weight. Banik et al. (2018), Muhammad et al. (2008), Khan et al. (2006) and Atta et al. (2008) also reported high heritability estimates for grain yield, days to 50% flowering and maturity date. Ali and Ahsan (2012), Getachew et al. (2015) and Fasil (2020) reported high heritability for 100 seed weight, number of pods plant^{-1}, plant height and days to 50% flowering.

Moderate heritability was observed for number of pods plant^{-1} and number of seeds plant^{-1}. The observed results are in agreements with Avinash et al. (2013) who reported moderate broad sense heritability for number of pods plant^{-1}. The lowest estimate of heritability was observed for plant height; which indicates that this trait is highly influenced by the environment. Traits with low heritability estimates are highly controlled by the non-additive gene actions and selection of these traits based on phenotypic performance may not give better population improvement (Lush, 1943).

Genetic advance as percent of mean ranged from a 2.29%–81.55%. Johansen et al. (1955) classified genetic advances as a percentage of the mean (GAM) as high (>20%), moderate (10–20%) and low (<10%). According to this benchmark, high genetic advance as percent of mean were recorded for number of secondary branches, numbers of pods plant^{-1}, numbers of seeds plant^{-1}, hundred seed weight, and grain yield ha^{-1}. This indicates it is possible to select the genotypes with better performance for these traits. Similar to this result, high GAM was reported for grain yield, number of secondary branches and number of pods plant^{-1} (Raju et al., 2017). Muhammad et al. (2008) and Awol et al. (2019) also reported high GAM for grain yield. Awol et al. (2019) and Banik et al. (2018) reported the same result for number of pod plant^{-1}.

Moderate genetic advance as percent of mean were observed for days to 50% flowering, grain filling period and plant height. In accordance with this finding, Banik et al. (2018) and Raju et al. (2017) reported moderate GAM for hundred seed weight and days to 50% flowering. Lowest GAM values found from days to maturity; implies that selection will not make any improvement for these traits in the chickpea genotypes. Awol et al. (2019) reported low genetic advance as percentage of mean for days to maturity.

High heritability coupled with high genetic advance as percent of mean is very essential to improve traits of interest (Johnson et al., 1955). In this study, grain yield, number of secondary branches and hundred seed weight showed high heritability coupled with high genetic advance as present of mean; implying that maximum improvements can be made for these traits. High heritability along with high genetic advance was previously reported for grain yield by Awol et al. (2019) and Hussain et al. (2016). High heritability and moderate genetic advance were observed for grain filling period and days to 50% flowering, while high heritability and low genetic advance as present of mean was observed for days to maturity. High broad sense heritability coupled with low genetic advance may result from high dominance gene action and low additive gene action (Alard, 1999).

3.4. Association of characters

3.4.1. Genotypic correlation coefficients

The results of genotypic correlation showed that grain yield ha^{-1} showed highly significant and positive correlations with grain filling period, number of pod plant^{-1}, number of seeds' plant^{-1} and plant height. This also indicates these traits genetically correlated with grain yield and the improvement of one trait can result the similar effect on the other trait. So to improve grain yield more emphasis should be given to these characters during selection since yield is the product of different traits. In agreement with this finding Getachew et al. (2015) and Farshadfar and Farshadfar (2008) reported positive and significant association of grain yield ha^{-1} with plant height. Similarly the positive association reported among number of seeds' plant^{-1}, hundred seed weight and number of pods plant^{-1} with grain yield ha^{-1} by Arpita and Police (2011), Farshadfar and Farshadfar (2008).

Highly significant and negative correlations were observed between grain yield with traits of days to 50% flowering, days to maturity and hundred seed weight. This negative correlation of traits with grain yield indicated that the increase in days to maturity, days to 50% flowering and hundred seed weight could result in the decrease of grain yield. Hundred seed weight showed highly significant and negatively correlated with plant height, number of seed per plant, number of pod plant^{-1} and number of secondary branches but non-significantly and positive correlation with days to 50% flowering and days to maturity. Getachew et al. (2015) reported highly significant and negative correlation of hundred seed weight with number of pods plant^{-1} and days to maturity (Table 4).

Plant height showed positive and highly significant genotypic correlation with number of pod plant^{-1}, number of seeds plant^{-1}, grain yield ha^{-1} and grain filling period.

Table 4: Estimates of correlation coefficients (r) at genotypic level (below diagonal) and at phenotypic level (above diagonal) among 9 traits

Trait	FD	MD	GFP	SBR	PPP	SPPL	HGT (cm)	HSW (g)	G Y H (kg ha^{-1})
FD	1	0.708^{**}	-0.286	0.212	-0.074	-0.209^{**}	0.089^{*}	0.039	-0.337^{*}
MD	0.611^{**}	1	-0.933^{**}	-0.053	-0.465	-0.374^{**}	-0.109	0.185	-0.62^{**}
GFP	-0.948^{**}	-0.445^{**}	1	0.161	0.529	0.358^{*}	0.172	-0.206	0.600^{**}
SBR	-0.057 ns	0.192^{ns}	0.159^{ns}	1	0.644^{**}	0.452^{**}	0.132	-0.334^{**}	0.137
PPP	-0.611^{**}	-0.232^{ns}	0.738^{**}	0.684^{**}	1	0.766^{**}	0.317^{*}	-0.467	0.551^{**}
SPPL	-0.547^{**}	-0.401^{**}	0.512^{**}	0.449^{**}	0.807^{**}	1	0.369^{**}	-0.370^{**}	0.617^{**}
HGT(cm)	-0.193 ns	0.295^{*}	0.379^{**}	0.037^{ns}	0.375^{**}	0.716^{**}	1	-0.145	0.351^{*}
HSW(g)	0.251^{ns}	0.106^{ns}	-0.271^{ns}	-0.445^{**}	-0.643^{**}	-0.58^{**}	-0.339^{*}	1	-0.315^{*}
GYH (kg ha^{-1})	-0.697^{**}	-0.395^{**}	0.706^{**}	0.093^{ns}	0.668^{**}	0.824^{**}	0.413^{**}	-0.317^{*}	1

FD: Days to 50% flowering; MD: Days to maturity; GFP: Grain filling period; SC: Stand count at harvest; PBR: Number of primary branches; SBR: Number of secondary branches; PPP: Number of pods plant^{-1}; SPPL: Number of seeds plant^{-1}; HGT: Plant height; HSW: Hundred seed weight in gram; GYH (kg ha^{-1}): Grain yield ha^{-1}; CV: Coefficient of variation; **: Significant at (p=0.01) level of significance; *: Significant at (p=0.05) level of significance; ns: Non-significant

In accordance with this finding, Farshadfar and Farshadfa (2008) reported positive and significant association of plant height with number of pods plant^{-1}. Getachew et al. (2015) reported highly significant and positive association of plant height with grain yield. Number of secondary branch showed positive and non-significant association with grain yield; implies that this character is independent of other traits and they could be selected independently to improve grain yield. Number of secondary branches showed positive and non-significant association with number of pods plant^{-1} and number of seed plant^{-1}. Fasil (2019) reported highly significant and positive association of number of secondary branches with number of seed plant^{-1} and number of pods plant^{-1}.

Number of pods plant^{-1} also showed a positive and highly significant correlation with number of seed plant^{-1}, number of secondary branches and grain filling period, while highly significantly and negatively correlated with day to 50% flowering and hundred seed weight. Usman et al. (2012) reported positive and highly significant association of number of pod plant^{-1} with number of secondary branches. Grain filling period showed a highly significant and negatively correlation with days to 50% flowering and days to maturity but highly significant and positively correlated with number of pods plant^{-1}, number of seed plant^{-1}, plant height and grain yield. Days to 50% flowering also showed a positive and highly significant correlation with days to maturity.

3.5. Path coefficient analysis

3.5.1. Genotypic direct and indirect effects

In the present study, only characters that had significant relationship with grain yield were included in the path analysis (Dewy and Lu, 1959). Path coefficient analysis showed that number of pods plant^{-1} (0.385) exhibited a maximum positive direct effect on grain yield while a maximum negative direct effect was recorded by days to 50% flowering (-0.366). Number of pods plant^{-1}, number of seeds plant^{-1}, days to maturity, plant height and hundred seed weight had a positive direct effect on grain yield. The positive direct effect of these traits implies that direct selection of such traits would improve the grain yield if the correlation with grain yield is positive and significant (Table 5).

Tibebu et al. (2017) reported a positive direct effect of number of pods plant^{-1} on grain yield. Fasil (2020) reported positive direct effect of days to maturity, number of pods per plant and hundred seed weight on grain yield. Shafique et al. (2016) reported positive direct effect of plant height, number of pods plant^{-1} and number of seed plant^{-1} on grain yield. Pandey et al. (2013) reported positive direct effect of hundred seed weight and number of pods plant^{-1} on grain yield. Avinash et al. (2013) reported positive direct effect of number of pods plant^{-1} and hundred seed weight on grain yield. Muhammad et al. (2012) reported a positive direct effect of days to maturity, plant height, number of seed plant^{-1} and hundred seed weight.

In present study, number of pods plant^{-1}, number of seeds plant^{-1} and plant height has positive association with grain yield and have positive direct effect on grain yield. Thus, these traits used as effective selection parameters for obtaining maximum yield in breeding program for yield improvement. Avinash et al. (2013) reported a significant positive correlation of number of pod per plant with grain yield and exerted high direct positive effect on grain yield. Days to 50% flowering exhibited negative direct effect on grain yield. The negative selection for these traits can help to improve grain yield in chickpea population (Table 6).

Table 5: Genotypic direct (diagonal) and indirect effects of seven traits on grain yield

Traits	FD	MD	PPP	SPPL	HGT (cm)	HSW (g)	rgGYH (kg ha^{-1})
FD	-0.366	0.025	-0.235	-0.127	-0.013	0.041	-0.697**
MD	-0.259	0.036	-0.089	-0.093	0.020	0.017	-0.395**
PPP	0.223	-0.008	0.385	0.218	0.028	-0.103	0.668**
SPPL	0.200	-0.014	0.362	0.232	0.048	-0.094	0.824**
HGT (cm)	0.071	0.011	0.159	0.166	0.067	-0.055	0.413**
HSW (g)	-0.092	0.004	-0.244	-0.134	-0.023	0.162	-0.317*

Residual effect=0.4166. R-squared=0.8264; *: Significant at (p=0.05) level of significance; ns: Non-significant

Number of seed plant^{-1} had positive indirect effect on grain yield through number of pods plant^{-1} and plant height. Days to 50% flowering had a negative direct effect on grain yield; however, they have positive indirect effect on grain yield via days to maturity and hundred seed weight. Muhammad et al. (2012) reported a positive indirect effect of days to 50% flowering on grain yield via days to maturity and hundred seed weight. Plant height had a positive direct effect on grain yield but had a negative indirect effect through hundred seed weight. The direct effect of number of pod plant^{-1} on grain yield was positive and also they had positive indirect effect on grain yield via plant height and plant height. The significant and positive correlation of traits with grain yield might be due to considerable positive indirect effects of yield

Table 6: Phenotypic direct (diagonal) and indirect effects of seven traits on grain yield

Traits	FD	MD	PPP	SPPL	HGT (cm)	HSW (g)	rpGYH
FD	-0.444	0.039	-0.135	-0.115	-0.015	0.013	-0.622**
MD	-0.302	0.057	-0.049	-0.079	0.020	0.005	-0.337*
PPP	0.247	-0.012	0.243	0.219	0.034	-0.032	0.551**
SPPL	0.216	-0.019	0.225	0.236	0.053	-0.028	0.617**
HGT	0.072	0.013	0.091	0.137	0.091	-0.015	0.351*
HSW	-0.103	0.005	-0.140	-0.120	-0.024	0.056	-0.315*

Residual effect=0.4897, R-squared=0.7602; *: Significant at (p=0.05) level of significance; ns: Non-significant related traits on grain yield.

The residual effect of (0.4166) indicates that characters which are included in the genotypic path analysis explained 58.34% of the total variation in grain yield. The remaining 41.66% was the contribution of other factors.

4. CONCLUSION

The phenotypic variances were higher than genotypic variance; indicated influence of environments. Higher genotypic coefficients of variation were recorded for grain yield, number of secondary branches and number of pods plant^{-1}. Most traits recorded higher heritability and significant positive correlations with grain yield. In this study the amounts of genetic variability were determined among grain yield and yield related traits.

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6. REFFERENCES

Allard, R.W., 1999. Principles of plant breeding. John Wiley, New York. 663p.

Anonymous, 2019. Annual Report 2018, Healthy food systems: The foundation for a better World. Hyderabad, India, ICRISAT. 24 pp. Available from https://www.icrisat.org/wp-content/uploads/2019/11/ICRISAT_Annual_Report_2018.pdf.

Anonymous, 2019. Agricultural sample survey, 2018/19 Volume I: Report on area and production of major crops (Private peasant holdings, Meher season). Statistical Bulletin 589, Addis Ababa, 54 p. 2019. Available from http://www.sciepub.com/reference/339908.

Awol, M., Bulti, T., Chris Ojiewo, S.A., 2019. Assessment of genetic variability and heritability of agronomic traits in Ethiopian chickpea (*Cicer arietinum* L.) landraces. BS Publishers 2(1), 10–15.

Banik, M., Deore, G.N., Mandal, A.K., Mhase, L.B., 2018. Genetic variability and heritability studies in chickpea (*Cicer arietinum L.*). Current Journal of Applied Science and Technology 31(1), 1–6.

Begna, T., 2021. Role and economic importance of crop genetic diversity in food security. International Journal of Agricultural Science and Food Technology 7(1), 164–169.

Bekele, S., Hailemariam, T., 2007. Structure and functioning of chickpea markets in Ethiopia: Evidence based on analyses of value chains linking smallholders and markets. Improving Productivity and Market Success (IPMS) of Ethiopian Farmers Project Working Paper 6. ILRI (International Livestock Research Institute), Nairobi, Kenya. 63 pp

Biru, A., Kassahun, T., Teklehaimanot, H., Dagnachew, L., 2017. Broad sense heritability and genetic advance for grain yield and yield components of chickpea (*Cicer arietinum* L.) genotypes in western Ethiopia. International Journal of Genetics and Molecular Biology 9(4), 21–25.

Deshmukh, S.N., Basu, M.S., Reddy, P.S., 1986. Genetic variability, character association and path coefficients of quantitative traits in virginia bunch varieties of groundnut. Indian Journal of Agricultural Sciences 56(12), 816–821.

Deway, D.R., Lu, K.H., 1959. A correlation and path coefficient analysis of components of crested wheat grasses kernel production. Agronomy Journal 51, 515–518.

Dutta, P., Borua, P.K., 2013. Morphological traits as selection indices in rice: a statistical view. Universal Journal of Agricultural Research 1(3), 85–96.

Falak, N., Muhammad, A., Abdul, G., 2003. Path analysis and relationship among quantitative traits in chickpea (*Ciser arietinum* L.). Pakistan Journal of Biological Sciences 6(6), 551–555.

Farshadfar, E., Farshadfar, F., 2008. Genetic variability and path analysis of chickpea (*Cicer arientinum* L.) landraces and lines. Journal of Applied Science 8(21), 3951–3956.

Fasil, H., 2020. Genetic variability, heritability and genetic advance of kabuli chickpea (*Cicer arietinum* L.) for agronomic traits at central Ethiopia. International Journal of Plant Breeding and Crop Science 7(1), 710–714.

Gaur, M.P., Aravind, K.J., Rajeev, K.V., 2012. A review of impact of Genomic technologies on chickpea breeding strategies. Agronomy 2, 200–203.

Getachew, T., Ferew, M., Asnake, F., 2015. Current research in agricultural sciences genetic divergence and character association of kabuli type chickpea (*Cicer arietium* L.) genotype under rainfed conditions in Ethiopia. Current Research in Agricultural Sciences 2(4), 123–131.

Holme, I.B., Gregersen, P.L., Brinch-Pedersen, H., 2019. Induced genetic variation in crop plants by random or targeted mutagenesis: Convergence and differences. Frontiers in Plant Science 10, 1468. DOI 10.3389/fpls.2019.01468.

Hussain, N., Ghaffar, A., Aslam, M., Hussain, K., 2016. Assessment of genetic variation and mode of inheritance of some quantitative traits in chickpea (C*icer arietinum* L.). The Journal of Animal & Plant Sciences 26(5), 1334–1338.

Johnson, H.W., Robinson, H.F., Comstock, R.E., 1955. Estimates of genetic and environmental variability in soybeans. Agronomy Journal 47, 314–318.

Kalapchieva, S., Kosev, V., Vasileva, V., 2021. Correlation dependences of quantitative traits in garden pea (*Pisum sativum* L.). The Annals of Oradea University, Biology Fascicle 28(1), 85–90.

Kumar, M., Jeberson, M.S., Singh, N.B., Sharma, R., Patel, R.S., 2019. Analysis of trait association and principal component of variability in field pea (*Pisum sativum* L.) genotypes. The Pharma Innovation 7(8), 437–441.

Khan, F.A., Ali, S., Shakeel, A., Saeed, A., Abbas, G., 2005. Genetic variability and genetic advance analysis for some morphological traits in (*Brassica napus* L.). Journal of Agricultural Research 44(2), 83–88.

Muehlbauer, F.J., Sarker, A., 2017. Economic importance of chickpea: production, value, and world trade. In The Chickpea Genome, pp. 5–12. Springer, Cham.

Muhammad, A.A., Nausherwan, N.N., Ghulam, R., Muhmmad, S., 2008. Estimates of variability and correlations for quantitative traits in cicer arietinum. Journal of Agriculture and Social Sciences 4, 177–79.

Muhammad, S.S., Muhammad, A., Zafar, M., Muhammad, A., Awais, S., Muhammad, I.A., 2016. Genetic variability and interrelationship of various agronomic traits using correlation and path analysis in chickpea (*Cicer arietinum* L.). Academia Journal of Agricultural Research 4(2), 082–085.

Naveed, M.T., Ali, Q., Ahsan, M., Hussain, B., 2012. Correlation and path coefficient analysis for various quantitative traits in chickpea (*Cicer arietinum* L.). International Journal for Agro Veretnary and Medical Sciences 6(2), 97–106.

Pandey, A., Kumar, A., Thongbam, P., Pattanayak, A. 2013. Genetic divergence , path coefficient and cluster analysis of chickpea (*Cicer arietinum* L.) cultivars, in the mid-altitudes of Meghalaya. Indian Journal of Agricultural Sciences 83(13), 1300–1304.

Raju, T., Sadhukhan, R., Sathish, V., 2017. Genetic variability studies in chickpea (*Cicer arietinum* L.) for yield and yield related traits. Bulletin of Environment, Pharmacology and life Sciences 6, 177–183.

Rathi, R.S., Dhaka, R.P.S., 2007. Genetic variability, correlation and path analysis in pea (*Pisum sativum* L.). Indian Journal of Plant Genetic Resources 20(2), 126–129.

Shafique, M.S., Muhammad, A., Zafar, M., Muhammad, A., Awais, S., Ahmad, M.I., 2016. Genetic variability and interrelationship of various agronomic traits using correlation and path analysis in chickpea (*Cicer arietinum* L.). Academia Journal of Agricultural Research 4(2), 82–85.

Sharifi, P., Astereki, H., Pouresmael, M., 2018. Evaluation of variations in chickpea (*Cicer arietinum* L.) yield and yield components by multivariate technique. Annals of Agrarian Science 16, 136–142.

Shengu, M.K., Hirpa, D., Wolde, Z., 2018. Genetic variability of some chickpea (*Cicer arietinum* L.) genotypes and correlation among yield and related traits in humid tropics of southern Ethiopia. Journal of Plant Breeding and Crop Science 10(October), 298–303.

Tesfamichael, S.M., Githiri, S.M., Nyende, A.B., Rao, N.V.P.R.G., 2015. Variation for agro morphological traits among kabuli chickpea (*Cicer arietinum* L.) genotypes. Journal of Agricultural Science 7(7), 75–92.

Tibebu, B., Firew, M., Million, E., 2017. Assessment of genetic improvement in grain yield potential and related traits of kabuli type chickpea (*Cicer arietinum* L.) varieties in Ethiopia. Advances in Crop Science and Technology 5(3), 1–10.

Upadhyaya, H.D., Ortiz, R., Bramel, P.J., Singh, S., 2002. Phenotypic diversity for morphological and agronomic traits in chickpea core collection. Euphytica 123, 333–342.

Van der Maesen, L.J.G., 1987. Origin, history and taxonomy of chickpea. In: Saxena, M.C., Singh, K.B. (Eds.), The Chickpea, pp11, CAB International, Wallingford, The international Center for Agricultural Research in the Dry Areas.

Wood, J.A., Grusak, M.A., 2007. Nutritional value of chickpea. In: Yadav, S.S., Redden, R., Chen, W., Sharma, B. (Eds.), Chickpea breeding and management. CAB, Wallingford, UK, 101–142.