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GENETIC VARIABILITY STUDIES FOR YIELD AND ITS ATTRIBUTING TRAITS UNDER HEAT STRESS CONDITIONS IN CHICKPEA (*CICER ARIETINUM* L.)

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ABSTRACT

The experiment entitled "Genetic variability studies for yield and its attributing traits under heat stress conditions in Chickpea (*Cicer arietinum* L.)" was conducted at the Pulses and Castor Research Station, Navsari Agricultural University, Navsari (Gujarat). The experiment was carried out in randomized block design involving eighteen chickpea genotypes with two replications under normal (D_0: 9th Nov) and late (D_1: 4th Dec) sown condition during *rabi* 2023-24. Significant genetic variation was observed for most traits including plant height, branches per plant, dry biomass, 100-seed weight, harvest index, grain yield, chlorophyll, proline, and protein content under both environments. High GCV and PCV were recorded for chlorophyll and proline under D_0, and for protein content under D_1, indicating substantial variability and a strong genetic basis for these traits. High heritability with high genetic advance as percent of mean was observed for 100-seed weight, grain yield, chlorophyll, proline, and protein content, confirming the role of additive gene action and scope for direct selection. Grain yield per plant showed strong positive correlation with key physiological and yield traits. Path analysis revealed plant height, proline, and harvest index had major positive direct effects. Genotypes IPC-17-54, JG-14, IPC-17-292, and JG-18 exhibited superior heat tolerance and yield potential, making them valuable for future breeding programs.

***Keywords* :** Chickpea, Genetic Variability, Correlation coefficient, Path coefficient, Heat tolerance.

Introduction

Chickpea (*Cicer arietinum* L.), a diploid (2n = 2x = 16), self-pollinated leguminous crop from the family Leguminosae, is one of the most important food legumes grown in semi-arid regions of the world. It is believed to have originated in the Fertile Crescent, with Turkey being recognized as its primary center of origin (Gaur *et al.,* 2012). In India, chickpea plays a crucial role in ensuring food and nutritional security, contributing over 70% of the global production. It plays a vital role in food and nutritional security, with an area of approximately 9.46 million hectares producing 11.58 million tonnes and achieving an average productivity of 1224 kg/ha. As per the reports in Gujarat, it is grown in an area of 0.63 million hectares with production of 1.11 million tonnes and productivity of 1753 kg/ha (Anonymous, 2023-24). Despite its importance, chickpea productivity is highly vulnerable to abiotic stresses, particularly heat stress, which has become more frequent due to climate change and altered sown patterns. Terminal heat stress, especially during the reproductive phase, is one of the most damaging abiotic constraints, severely affecting physiological and reproductive functions. Temperatures exceeding 35°C during flowering and pod setting can cause flower drop, impaired pollen viability, and pod abortion, ultimately leading to significant yield loss (Krishnamurthy *et al.*, 2011; Wang *et al.*, 2006). This challenge is exacerbated by the increasing trend of late sown due to delayed harvests of preceding crops and the shifting climate patterns in major chickpea-growing regions (Gaur *et al.* 2012). In this scenario, the development and identification of heat-tolerant genotypes become imperative to sustain chickpea production under future climatic scenarios. Assessing the magnitude of genetic variability among genotypes under both normal and stress conditions provides a foundation for crop improvement. Parameters such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance are essential tools for evaluating the breeding potential of traits under selection pressure (Kumar *et al*., 2022). Furthermore, correlation and path coefficient analyses are vital in understanding the relationships among traits and their direct or indirect effects on grain yield, thereby assisting in selecting desirable genotypes with multiple favourable traits. Therefore, the present investigation was conducted to evaluate genetic variability, trait associations, and heat tolerance potential in a diverse set of chickpea genotypes under both late-sown (heat stress) and timely-sown (normal) environments, with the objective of identifying superior genotypes with enhanced yield performance and adaptability to high-temperature stress conditions.

Materials and Methods

Eighteen chickpea genotypes were sown in randomized block design along with two replications under normal and late sown condition during *rabi* 2023-24 at the Pulses and Castor Research Station, Navsari Agricultural University, Navsari (Gujarat). All genotype were accommodated in single row plots of 2.0 m length with plant to plant spacing of 45×10 cm. The genotypes were randomly allotted to each plot in each replication. All the recommended agronomic package of cultivation practices were followed timely for successful rising of crop. Observations were recorded on five randomly selected plants per replication for twelve traits *viz*., plant height, branches per plant, pods per plant, seeds per pod, dry biomass, harvest index, 100-seed weight, chlorophyll content, carotenoid content, proline content, protein content and grain yield per plant except days to 50% flowering and maturity which were recorded on plot basis. The mean values were used for calculate variance by Panse and Sukhatme (1967). The coefficient of variation was analyses by Burton, (1952). Heritability was analyses by Allard (1960) and genetic advance were calculated by following Johnson *et al.* (1955). Correlation coefficients at phenotypic and genotypic level were estimated by as per the methods suggested by Miller *et al.* (1958). Path coefficients were calculated according to Dewey and Lu (1959). Chlorophyll content was determined by 80% Acetone method given by Arnon (1949). Carotenoid content was determined by 60% KOH method given by Jensen (1978). Proline contentwas determined by Acid ninhydrin reagent method given by Bates *et al.* (1973). Protein content was estimated according to (Lowry *et al*., 1951).

Analysis of variance: The analysis of variance including Genotypic coefficient of variation, Phenotypic coefficient of variation, Heritability (Broad sense), Genotypic variance, Phenotypic variance, Genetic advance, GA as per cent of mean where estimated using INDOSTAT 8.1.

Correlation coefficients analysis: Genotypic and phenotypic correlation coefficient between various traits were estimated by using variability package in R studio 4.2.1.

Genotypic and phenotypic correlation coefficients were worked out by a method described by Panse and Sukhatme (1985).

(a) Genotypic correlation coefficient

$$rg_{xy} = \frac{COVp_{xy}}{\sigma_{gx} \times \sigma_{gy}}$$

Where,

rg_{xy}= Genotypic correlation coefficient for a pair of trait x and y, respectively,

$COVg_{xy}$= Genotypic and phenotypic covariance for a pair of characters x and y, respectively,

σ_{gx}= Genotypic standard deviation of character x,

σ_{gy}= Genotypic standard deviation of character y

(b) Phenotypic correlation coefficient

$$rp_{xy} = \frac{COVp_{xy}}{\sigma_{px} \times \sigma_{py}}$$

Where,

rp_{xy}= Phenotypic correlation coefficient for a pair of traits x and y, respectively,

$COVp_{xy}$= Phenotypic covariance for a pair of characters x and y, respectively,

σ_{px}= Phenotypic standard deviation of character x,

σ_{py}= Phenotypic standard deviation of character y

Test of significance: The significance test was carried out by referring to 'F' table value given by Fisher and Yates (1953). The differences between the variance due to genotype and that due to error was tested using 'F' test for n_1= (G-1) and n_2= (r-1) (G-1) degree of freedom both at 5 per cent and 1 per cent level of probability.

Path coefficient analysis: The direct and indirect effects were estimated using path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959) in variability package in R studio 4.2.1. The following equations were solved for estimating the various direct and indirect effects.

Residual effect was calculated using the following formula:

$$P_{Ry} = \frac{1 = P^2Ry + \sigma P_{iy}R_{iy}}{\sqrt{1-(P_{1y}r_{1y})-(P_{2y}r_{2y})\dots(P_{iy}r_{iy})}}$$

Where,

P_{Ry} is the residual effect

Results and Discussion

The estimates of various parameters *viz*., range and different parameters of genetic variability presented in Table 1 and 2 revealed that sufficient variability was present in the germplasm for all the traits. This variability can be utilized effectively to develop high yielding, heat tolerant cultivars/genotypes. The analysis of variance manifested that mean square due to the genotypes were highly significant for all characters take in present experiment justifying the choice of the experimental material. The overall analysis of ANOVA indicated wide genetic variability available in the experimental material studied can be further exploited for chickpea improvement program. The analysis of variance was performed to test the differences among genotypes for all the 14 characters and presented here. The results revealed that the mean sum of square due to genotypes were highly significant and significant for the agro-morphological characters *viz*., plant height (cm), branches per plant, dry biomass (g), pods per plant, seeds per pods, 100 seed weight (g), harvest index, chlorophyll (mg/g), carotenoid (mg/g), proline (mg/g), protein (%) except days to 50% flowering and days to maturity under normal (D_0) sown condition, while in late (D_1) sown condition such agro-morphological characters *viz*., plant height (cm), days to 50% flowering, days to maturity, branches per, dry biomass (g), 100 seed weight (g), harvest index (%), chlorophyll (mg/g), carotenoid (mg/g), proline (mg/g), protein (%) except pods per plant and seeds per pods were highly significant and significant which indicated that presence of considerable amount of variability among genotypes for various characters. As traits *viz*., days to 50% flowering and days to maturity under normal sown condition, while pods per plant and seeds per pod under late sown condition found non-significant, it is not used for further analysis. Similar results for normal sown condition were also reported by Babar *et al.* (2012), Dar *et al.* (2012), Sewak *et al.* (2012), Jivani *et al.* (2013), while Kuldeep *et al.* (2014), Devasirvatham *et al.* (2015), Jha *et al.* (2015), Agrawal *et al.* (2018), and Kushwah *et al.* (2021) were also reported similar results for late sown condition.

To better understand the variation among genotypes, the use of statistical measures such as the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (in broad sense), and genetic advance as a percentage of the mean (GAM) becomes essential. The range values of characters offer a preliminary idea of variability, but being dependent on units and extremes, they are less precise compared to coefficients of variation, which are dimensionless and allow for better trait comparison. A higher magnitude of GCV reflects a greater potential for selection and improvement, especially when accompanied by high heritability and substantial genetic advance. Typically, PCV values exceed the corresponding GCV values, which suggests that the environment has a modest influence on trait expression. In cases where the difference between PCV and GCV is small, it implies that the character is largely governed by genetic factors, and thus, selection based on phenotype can be effective. The values of PCV were observed slightly higher than GCV for all the fourteen characters under normal and late sown condition indicating minor influence of environmental factors. Additionally, the differences between values of GCV and PCV for all the traits were very low indicating the influence of environment to be the minimum. Therefore, these traits could be easily exploited through selection.

The results revealed GCV values were close to PCV for the traits chlorophyll (mg/g), carotenoid (mg/g), proline (mg/g) and protein (%) under normal sown condition, while 100 seed weight (g), chlorophyll (mg/g), proline (mg/g) and protein (%) under late sown condition indicating the trait is governed mainly by genetic factors with minimal environmental influence, and hence, selection based on phenotype will be effective. Chlorophyll and proline showed higher value of GCV and PCV under normal sown condition indicating the greater scope of improving this character by applying theselection in an appropriate direction, while protein (%) under late sown condition has highest GCV and PCV value.Under normal sown condition the traits *viz.,* branches per plant, dry biomass (g), pods per plant, seed per pods, 100 seed weight (g), harvest index (%), grain yield per plant (g) and protein (%) showed moderate value of GCV and PCV indicating the greater scope of improving this character by applying selection in an appropriate direction. Similar trend was observed for genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for almost all the traits by Bala *et al.* (2015), Chopdar *et al.* (2017) and dehal *et al.* (2016). In late sown condition the traits *viz.,* days to maturity, branches per plant, dry biomass (g), 100 seed weight (g), grain yield per plant (g), chlorophyll (mg/g) and proline (mg/g) showed moderate value of GCV and PCV indicating the greater scope of improving this character by applying selection in an appropriate direction. Similar trend was observed for genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for almost all the traits by Kuldeep *et al.* (2014), Devasirvatham *et al.* (2015) and Jha *et al.* (2015). Under normal sown condition, low GCV and PCV values were obtained in the carotenoid trait only. While in late sown condition, days to 50% flowering, pods per plant and seed per pods have low GCV and low PCV indicating a narrow range of variability for these traits and restricting the scope of selection for these traits. Low GCV and moderate PCV values were obtained in the traits plant height, days to 50% flowering and days to maturity under normal sown condition, while for late sown plant height and carotenoid were having low GCV and moderate PCV which indicates the presence of limited genetic variability coupled with a noticeable environmental influence on their expression. This suggests that the phenotypic variation is largely due to non-heritable environmental factors. Therefore, direct selection for these traits may not be highly effective.

The heritability estimates help the breeders in selection based on the phenotypic performance. Higher heritability coupled with high genetic advance as percent mean is observed for six different traits *viz.*, pods per plant, 100 seed weight (g), grain yield per plant (g), chlorophyll (mg/g), proline (mg/g) and protein (%) in both the sown condition. Similar results were also reported by Kuldeep *et al.* (2014), Singh *et al.* (2021), Kumar *et al.* (2019), Kushwah *et al.* (2021). This confirmed higher additive gene action; thus, improvement could be brought by direct phenotypic selection over the genotypes. Moderate heritability with medium genetic advance as per cent is observed in plant height (cm), branches per plant, dry biomass (g) and seed per pods under normal sown condition while, only plant height (cm) for late sown condition indicating the effect of non-additive gene action. Moderate heritability with low genetic advance as per cent mean was observed for days to 50% flowering, days to maturity and carotenoid under normal sown condition while, pods per plant and seed per pods for late sown condition. High heritability with moderate genetic advance as per cent mean was observed for harvest index under normal sown condition while, days to 50% flowering, days to maturity, harvest index and carotenoid under late sown condition. Similar results for normal sown condition were also reported by Raju *et al.* (2021) and Roy *et al.* (2016), while Kuldeep *et al.* (2014) were also reported similar results for late sown condition.

The yield is a complex character and the multiplicative end product of many quantitative traits. Understanding the interrelationships among yield and its contributing traits is essential for effective crop improvement. Yield is a complex trait influenced by multiple morphological and physiological characters, many of which are interrelated. Therefore, analysing the degree of association between grain yield and its components provides valuable insight for the identification and selection of superior genotypes in breeding programs. While phenotypic correlations can offer preliminary information, they are often confounded by environmental influences, potentially leading to inaccurate conclusions. In contrast, genotypic correlations offer a more reliable measure by isolating the genetic contribution, thus enabling more precise selection decisions. A comprehensive understanding of these genetic relationships is crucial for enhancing selection efficiency and accelerating genetic gains in chickpea improvement under both optimal and stress conditions (Table 3 and 4).

In the investigation, grain yield per plant exhibited highest significant positive association with chlorophyll, harvest index, pods per plant, plant height, branches per plant, 100 seed weight, days to 50% flowering, seeds per pods and proline under normal sown condition, while under late sown condition seeds per pods, protein, 100 seed weight, pods per plant, chlorophyll, plant height, branches per plant, days to maturity, harvest index and proline exhibited positive and highly significant correlation with grain yield per plant. Thus, these characters turned out to be the major components of grain yield. Such positive interrelationships between grain yield and these attributes have also been reported in chickpea by Ali and Ahsan (2012), Chopdar *et al.* (2017), Hama *et al.* (2019), Agrawal *et al.* (2018), Kumar *et al.* (2019) and Mishra *et al.* (2014).Since early maturity is considered as a desirable criterion, the relationship of days to maturity with grain yield per plant was found in desirable direction. Such negative associations were also reported by Malik *et al.* (2010), Ali and Ahsan (2012).

Among the yield contributing characters, days to 50% flowering showed highly significant positive correlation with chlorophyll, branches per plant, harvest index, proline, 100 seed weight and protein under normal sown condition while under late sown condition showed highly significant positive correlation with 100 seed weight and pods per plant. Plant height exhibited highly significant positive correlation with days to 50% flowering, chlorophyll, proline, branches per plant and 100 seed weight under normal sown condition while under late sown condition showed highly significant positive correlation with seeds per pods, branches per plant, 100 seed weight, carotenoid, proline, pods per plant, protein and days to maturity. Branches per plant showed highly significant positive correlation with seeds per pods, chlorophyll, pods per plant, proline, 100 seed weight and protein under normal sown condition while under late sown condition showed highly significant positive correlation with seeds per pods, pods per plant, 100 seed weight, proline, protein and chlorophyll. Dry biomass exhibited highly significant positive correlation with proline under normal sown condition while under late sown condition showed highly significant positive correlation with pods per plant. Pods per plant showed highly significant positive correlation with 100 seed weight, chlorophyll and proline under normal sown condition while under late sown condition showed significant positive correlation with seeds per pods, 100 seed weight, protein, proline and carotenoid. 100 seed weight showed highly significant positive correlation with chlorophyll and proline under normal sown condition while under late sown condition showed significant positive correlation with proline, protein, chlorophyll and carotenoid.

In order to further elucidate the association of yield components as a function of their relative influence on the complex dependent character yield, path analysis was performed (Table 5 and 6). Path coefficient analysis indicates higher positive direct effect on grain yield per plant by dry biomass (g) followed by harvest index (%) for both the sown condition. Thus, these characters turned out to be the major components of grain yield. Selection of these traits may be rewarded in other words these traits should give importance, while practicing selection aimed at improvement of grain yield in chickpea. Similar results have also been reported by Mishra *et al.* (2014) and Parhe *et al.* (2014), Kumar *et al.* (2017) and Hamza *et al.* (2023). Normal sown condition shows positive direct effect on grain yield by plant height (cm), days to 50% flowering, days to maturity, branches per plant, seed per pods and chlorophyll (mg/g) while, under late sown condition for the characters days to 50% flowering, pods per plant, seed per pods, carotenoid (mg/g) and proline (mg/g) exhibited positive direct effect on grain yield. Similar results have also been reported by Ali and Arhan *et al.* (2012), Hagos *et al.* (2018), Hama *et al.* (2019), Usman *et al.* (2012) and Roy *et al.* (2016), Jha *et al.* (2015), Kumar *et al.* (2019), Kushwah *et al.* (2021). Thus, these characters turned out to be the major components of grain yield per plant (g) and revealed a true relationship between these characters and grain yield. Therefore, direct selection of these characters could be effective for improving grain yield in chickpea. pods per plant, carotenoid (mg/g), proline (mg/g) and protein (%) exhibited negative direct effect on grain yield per plant (g) for normal sown. For late sown negative direct effect on grain yield shown by plant height (cm), days to maturity, branches per plant, chlorophyll (mg/g) and protein (%).Path coefficient analysis for grain yield per plant revealed residual of 0.011 and 0.019 for normal and late sown condition, respectively.

The present study on chickpea genotypes under normal and heat stress (late sown) conditions revealed significant genetic variability for most of the yield and stress-associated traits, underscoring the potential for genetic improvement through selection. The significant mean sum of squares observed for the majority of traits indicates the presence of ample genetic variation, which is a prerequisite for any successful crop improvement program. Notably, a wider range of variation under heat stress conditions for several traits suggests that environmental stress may enhance phenotypic expression, enabling the identification of heat-resilient genotypes. The observed closeness between genotypic (GCV) and phenotypic coefficients of variation (PCV) across traits reflects a relatively low environmental influence, reinforcing the reliability of phenotype-based selection. High heritability estimates, coupled with high genetic advance as percent of mean, particularly for traits like grain yield per plant, proline content, protein content, chlorophyll content, dry biomass, harvest index, and 100-seed weight, suggest additive gene action. These traits are thus amenable to improvement through direct phenotypic selection. Conversely, traits exhibiting high heritability but low genetic advance, such as days to 50% flowering and carotenoid content, may be governed by non-additive gene effects and environmental interactions, indicating the need for advanced breeding strategies like recurrent selection, hybridization with diverse germplasm, or marker-assisted selection.

Correlation and path coefficient analyses provided further insights into the relationships among traits. Grain yield per plant exhibited strong positive genotypic and phenotypic correlations with important yield components, including plant height, branches, pods per plant, 100-seed weight, harvest index, chlorophyll, proline, and protein content, indicating that these traits contribute directly or indirectly to yield and can be prioritized in selection programs. The negative association of days to maturity with yield under normal conditions highlights the importance of early maturing genotypes in escaping terminal heat stress and maintaining yield stability. Path analysis revealed that dry biomass and harvest index had the most substantial direct effects on grain yield in both environments, validating them as reliable selection criteria. Interestingly, proline content showed a positive direct effect under heat stress but a negative one under normal conditions, emphasizing its role as a physiological indicator of stress adaptation. These findings highlight the complex interplay between yield components and environmental stress, emphasizing the need for multi-trait and environment-specific selection approaches.

In conclusion, this investigation identifies key traits that are genetically controlled, heritable, and positively associated with grain yield under both normal and stress conditions. These include grain yield per plant, harvest index, 100-seed weight, dry biomass, protein content, chlorophyll content, and proline content, which serve as valuable selection indices for breeding heat-tolerant chickpea cultivars. Future breeding efforts should emphasize the use of genetically diverse and stress-resilient genotypes, focus on additive gene-driven traits, and integrate physiological and biochemical markers for enhanced selection efficiency. Additionally, the incorporation of early maturing genotypes will be vital in mitigating yield losses under terminal heat stress. Overall, the findings provide a solid foundation for designing targeted, environment-responsive breeding strategies aimed at developing high-yielding and climate-resilient chickpea varieties to ensure food security in the context of changing climatic scenarios.

Table 1: Result of measures of variability parameters of agro-morphological characters studied under normal sown condition.

Characters	Range		σ_g^2	σ_p^2	GCV (%)	PCV(%)	h_{bs}^2(%)	GA	GAM (%)
	MIN.	MAX.							
PH	44.22	66.83	21.08	38.27	8.87	11.95	55.00	7.02	13.56
DFF	47.56	66.23	14.27	38.00	6.38	10.41	38.00	4.77	8.06
DM	84.89	110.95	47.27	123.78	6.79	10.99	38.00	8.75	8.65
BP	4.48	7.07	0.35	0.89	10.26	16.43	39.00	0.76	13.20
DB	10.11	17.72	3.08	5.66	12.90	17.49	54.00	2.67	19.60
PP	38.50	70.40	47.23	67.42	13.13	15.68	70.00	11.85	22.63
SPP	1.10	1.63	0.03	0.06	12.47	17.49	51.00	0.26	18.31
HSW	18.45	29.70	13.05	16.57	15.69	17.68	79.00	6.61	28.69
HI	46.03	69.20	34.11	53.69	10.87	13.64	64.00	9.59	17.85
GYPP	11.91	20.95	5.42	8.98	14.68	18.89	60.00	3.73	23.51
CHLOROPYLL	0.81	1.97	0.09	0.11	25.36	26.69	90.00	0.60	49.64
CAROTENOID	0.03	0.04	5.8×10^{-6}	9.9×10^{-6}	6.05	7.89	58.00	0.004	9.54
PROLINE	1.10	2.48	0.15	0.16	24.81	25.24	96.00	0.79	50.22
PROTEIN	12.01	23.86	11.83	12.98	17.14	17.96	91.00	6.76	33.72

Table 2: Result of measures of variability parameters of agro-morphological characters studied under late sown condition.

Characters	Range		σ_g^2	σ_p^2	GCV (%)	PCV (%)	h_{bs}^2(%)	GA	GAM (%)
	MIN.	MAX.							
PH	40.66	59.74	14.44	24.56	7.72	10.07	59.00	6.00	12.20
DFF	42.39	62.57	17.12	27.68	7.65	9.73	62.00	6.70	12.39
DM	77.43	110.87	96.19	138.91	10.00	12.02	69.00	16.81	17.14
BP	4.33	7.69	0.71	0.90	14.48	16.36	78.00	1.54	26.41
DB	7.45	18.42	4.67	5.87	17.96	20.14	80.00	3.97	33.00
PP	43.60	57.63	9.72	17.62	6.38	8.59	55.00	4.77	9.76
SPP	1.00	1.50	0.01	0.01	6.50	9.55	46.00	0.12	9.12
HSW	14.91	28.17	8.28	10.29	15.06	16.79	81.00	5.32	27.84
HI	45.43	66.03	24.47	35.20	8.99	10.78	70.00	8.50	15.44
GYPP	8.03	19.86	6.72	7.90	17.54	19.02	85.00	4.93	33.33
CHLOROPYLL	0.04	2.06	0.07	0.08	16.81	17.35	94.00	0.53	33.56

CAROTENOID	0.03	2.17	1.3×10^{-5}	1.6×10^{-5}	9.96	10.61	88.00	0.01	19.23
PROLINE	1.53	2.88	0.14	0.15	17.28	17.71	95.00	0.75	34.72
PROTEIN	8.84	22.03	24.55	24.91	30.41	30.63	99.00	10.13	62.19

*PH= Plant height (cm), DFF= Days to 50% flowering, DM= Days to maturity, BP= Branches per plant, DB= Dry biomass (g), PP= Pods per plant, SPP= Seeds per pods, HSW= 100-Seed weight (g). HI= Harvest index (%), GYPP= Grain yield per plant (g), CHLO= Chlorophyll (mg/g), CARO= Carotenoid (mg/g), GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, h^2_{bs} (%) =Heritability (Broad sense), σ^2_g = Genotypic variance, σ^2_p Phenotypic variance, GA= Genetic advance, GAM (%)= GA as per cent of mean

Table 3: Genotypic and Phenotypic correlation coefficients of grain yield per plant with other characters in eighteen Genotypes in chickpea under normal sown condition

Traits		PH	DFF	DM	BP	DB	PP	SPP	HSW	HI	CHLO	CARO	PRL	PRN	GYP
PH	G	1**													
PH	P	1**													
DFF	G	0.992**	1**												
DFF	P	0.335*	1**												
DM	G	-0.855**	-0.534*	1**											
DM	P	-0.225	-0.102	1**											
BP	G	0.827**	1.012**	-0.923**	1**										
BP	P	0.339*	0.259	-0.383*	1**										
DB	G	0.106	-0.577*	-0.013	0.339	1**									
DB	P	0.057	-0.047	-0.188	0.173	1**									
PP	G	0.550*	0.455	-0.768**	0.902**	0.231	1**								
PP	P	0.590**	0.253	-0.407*	0.508**	0.279	1**								
SPP	G	0.379	0.455	-0.903**	1.066**	-0.206	0.429	1**							
SPP	P	0.182	0.530**	-0.285	0.502**	0.015	0.338*	1**							
HSW	G	0.738**	0.718**	-0.595**	0.623**	0.134	0.791**	0.473*	1**						
HSW	P	0.441**	0.369*	-0.361*	0.426**	0.018	0.548**	0.344*	1**						
HI	G	0.451	0.862**	-0.575*	0.260	-0.695**	0.411	0.581*	0.364	1**					
HI	P	0.295	0.223	-0.133	0.184	-0.747**	0.253	0.260	0.386	1**					
CHLO	G	0.879**	1.015**	-0.669**	0.939**	-0.047	0.720**	0.649**	0.756**	0.628**	1**				
CHLO	P	0.632**	0.507**	-0.468**	0.472**	-0.015	0.554**	0.404*	0.684**	0.409*	1**				
CARO	G	-0.075	0.170	0.388	-0.028	-0.195	-0.087	0.056	-0.072	0.174	0.096	1**			
CARO	P	-0.078	-0.086	0.078	-0.110	-0.152	-0.071	-0.006	-0.109	0.155	0.055	1**			
PRL	G	0.842**	0.744**	-0.670**	0.753**	0.536*	0.645**	0.467	0.717**	0.123	0.792**	-0.124	1**		
PRL	P	0.643**	0.409*	-0.432**	0.458**	0.381*	0.558**	0.314	0.591**	0.102	0.723**	-0.017	1**		
PRN	G	0.308	0.670**	-0.210	0.610**	-0.342	0.421	0.658**	0.555*	0.538*	0.609**	0.157	0.268	1**	
PRN	P	0.239	0.443**	-0.125	0.358*	-0.275	0.372*	0.419*	0.463*	0.426**	0.517**	0.027	0.239*	1**	
GYPP	G	0.744**	0.671**	-0.874**	0.713**	-0.105	0.787**	0.629**	0.678**	0.791**	0.860**	0.099	0.655**	0.458	1**
GYPP	P	0.515**	0.299	-0.387*	0.431**	-0.156	0.658**	0.402	0.583**	0.766**	0.582**	0.084	0.520**	0.384*	1**

*, ** significant at 5% and 1% levels, respectively.

PH= Plant height (cm), DFF= Days to 50% flowering, DM= Days to Maturity, BP= Branches per plant, DB= Dry biomass (g), PP= Pods per plant, SPP= Seeds per pods, HSW= 100 seed weight (g), HI= Harvest index (%), CHLO= Chlorophyll (mg/g), CARO= Carotenoid (mg/g), PRL= Proline (mg/g), PRN= Protein (%), GYPP= Grain yield per plant (g), G= Genotypic correlation coefficient, P= Phenotypic correlation coefficient

Table 4: Genotypic and Phenotypic correlation coefficients of grain yield per plant with other characters in eighteen Genotypes in chickpea under late sown condition

Traits		PH	DFF	DM	BP	DB	PP	SPP	HSW	HI	CHLO	CARO	PRL	PRN	GYP
PH	G	1**													
PH	P	1**													
DFF	G	0.182	1**												
DFF	P	0.025	1**												
DM	G	0.622**	-0.323	1**											
DM	P	0.369*	-0.330*	1**											
BP	G	0.957**	0.104	0.544*	1**										
BP	P	0.556**	0.004	0.299	1**										
DB	G	0.495*	-0.319	0.604**	0.383	1**									
DB	P	0.336*	-0.144	0.327	0.178	1**									
PP	G	0.769**	-0.490*	0.621**	1.083**	0.598**	1**								
PP	P	0.650**	-0.077	0.382	0.646**	0.222	1**								

SPP	G	1.323**	0.246	0.692**	1.355**	0.359	1.561**	1**							
SPP	P	0.404*	0.077	0.118	0.408*	0.177	0.381*	1**							
HSW	G	0.934**	-0.588*	0.718**	0.891**	0.221	1.160**	1.00**	1**						
HSW	P	0.480**	-0.082	0.311	0.636**	0.105	0.635**	0.460**	1**						
HI	G	0.068	-0.201	0.061	0.145	-0.493	0.129	0.450	0.495*	1**					
HI	P	0.026	-0.099	0.117	0.226	-0.612**	0.232	0.001	0.458**	1**					
CHLO	G	0.267	-0.240	0.402	0.656**	0.030	0.546*	0.827**	0.672**	0.697**	1**				
CHLO	P	0.261	-0.093	0.213	0.451**	0.027	0.317	0.405*	0.540**	0.495**	1**				
CARO	G	0.835**	-0.342	0.555*	0.148	0.199	0.674**	-0.048	0.609**	0.176	0.023	1**			
CARO	P	0.379*	-0.371*	0.308	0.162	0.092	0.209	0.04	0.387*	0.150	0.036	1**			
PRL	G	0.785**	-0.015	0.237	0.849**	0.213	0.687**	0.659**	0.892**	0.311	0.613**	0.416	1**		
PRL	P	0.462**	-0.091	0.263	0.705**	0.171	0.377*	0.313	0.652**	0.231	0.552**	0.385*	1**		
PRN	G	0.728**	-0.321	0.657**	0.767**	0.489*	0.927**	0.926**	0.778**	0.343	0.490*	0.215	0.519*	1**	
PRN	P	0.421*	-0.207	0.506**	0.620**	0.338	0.557**	0.456**	0.626**	0.304	0.452**	0.196	0.494**	1**	
GYPP	G	0.721**	-0.457	0.613**	0.664**	0.361	0.803**	0.979**	0.822**	0.611**	0.777**	0.430	0.606**	0.840**	1**
GYPP	P	0.454**	-0.237	0.483**	0.530**	0.164	0.591**	0.290	0.735**	0.660**	0.644**	0.310	0.518**	0.734**	1**

*, ** significant at 5% and 1% levels, respectively.

PH= Plant height (cm), DFF= Days to 50% flowering, DM= Days to Maturity, BP= Branches per plant, DB= Dry biomass (g), PP= Pods per plant, SPP= Seeds per pods, HSW= 100 seed weight (g), HI= Harvest index (%), CHLO= Chlorophyll (mg/g), CARO= Carotenoid (mg/g), PRL= Proline (mg/g), PRN= Protein (%), GYPP= Grain yield per plant (g), G= Genotypic correlation coefficient, P= Phenotypic correlation coefficient

Table 5: Genotypic path coefficients of grain yield per plant with other characters eighteen genotypes in chickpea Under normal sown condition

Traits	PH	DFF	DM	BP	DB	PP	SPP	HSW	HI	CHLO	CARO	PRL	PRN	GYPP
PH	**0.106**	0.036	-0.107	0.056	0.113	-0.058	0.054	0.184	0.671	0.040	0.001	-0.301	-0.051	0.744**
DFF	0.106	**0.036**	-0.067	0.069	-0.620	-0.048	0.064	0.179	1.284	0.046	-0.002	-0.266	-0.110	0.670**
DM	-0.091	-0.019	**0.125**	-0.063	-0.014	0.081	-0.128	-0.148	-0.857	-0.030	-0.004	0.240	0.035	-0.873**
BP	0.088	0.036	-0.115	**0.068**	0.365	-0.095	0.151	0.155	0.387	0.043	0.0003	-0.270	-0.101	0.712**
DB	0.011	-0.021	-0.002	0.023	**1.074**	-0.024	-0.029	0.033	-1.035	-0.002	0.002	-0.192	0.056	-0.105
PP	0.059	0.016	-0.096	0.061	0.249	**-0.106**	0.061	0.197	0.613	0.033	0.001	-0.231	-0.069	0.787**
SPP	0.040	0.016	-0.113	0.073	-0.221	-0.045	**0.141**	0.118	0.866	0.029	-0.0005	-0.167	-0.108	0.628**
HSW	0.079	0.026	-0.074	0.042	0.144	-0.083	0.067	**0.249**	0.542	0.034	0.001	-0.257	-0.091	0.678**
HI	0.048	0.031	-0.072	0.018	-0.747	-0.043	0.082	0.091	**1.490**	0.029	-0.002	-0.044	-0.089	0.791**
CHLO	0.093	0.036	-0.084	0.064	-0.050	-0.076	0.092	0.188	0.935	**0.045**	-0.001	-0.283	-0.100	0.860**
CARO	-0.006	0.005	0.038	-0.001	-0.163	0.007	0.005	-0.014	0.201	0.003	**-0.013**	0.035	-0.020	0.098
PRL	0.090	0.027	-0.084	0.051	0.576	-0.068	0.066	0.178	0.184	0.036	0.001	**-0.358**	-0.044	0.655**
PRN	0.033	0.024	-0.026	0.042	-0.368	-0.044	0.093	0.138	0.801	0.028	-0.002	-0.096	**-0.165**	0.457

*, ** Significant at 5 and 1 % levels, respectively. Residual effect = 0.011 (Genotypic)

Table 6: Genotypic path coefficients of grain yield per plant with other characters eighteen genotypes in chickpea under late sown condition

Traits	PH	DFF	DM	BP	DB	PP	SPP	HSW	HI	CHLO	CARO	PRL	PRN	GYPP
PH	**-0.188**	0.038	-0.023	-0.028	0.430	0.244	0.098	0.009	0.073	-0.022	0.125	0.020	-0.055	0.721**
DFF	-0.034	**0.210**	0.012	-0.003	-0.277	-0.156	0.018	-0.006	-0.215	0.020	-0.051	-0.0004	0.024	-0.457
DM	-0.117	-0.068	**-0.037**	-0.016	0.524	0.197	0.051	0.007	0.065	-0.033	0.083	0.006	-0.050	0.613**
BP	-0.180	0.022	-0.020	**-0.030**	0.332	0.344	0.101	0.009	0.155	-0.054	0.022	0.022	-0.058	0.664**
DB	-0.093	-0.067	-0.022	-0.011	**0.868**	0.190	0.027	0.002	-0.527	-0.002	0.030	0.005	-0.037	0.361
PP	-0.145	-0.103	-0.023	-0.032	0.519	**0.317**	0.116	0.011	0.138	-0.045	0.101	0.018	-0.070	0.803**
SPP	-0.249	0.052	-0.026	-0.040	0.312	0.495	**0.074**	0.010	0.482	-0.069	-0.010	0.017	-0.070	0.979**
HSW	-0.176	-0.124	-0.027	-0.027	0.192	0.368	0.075	**0.010**	0.530	-0.056	0.091	0.023	-0.059	0.822**
HI	-0.013	-0.042	-0.002	-0.004	-0.428	0.041	0.033	0.005	**1.070**	-0.058	0.026	0.008	-0.026	0.611**
CHLO	-0.050	-0.050	-0.015	-0.020	0.026	0.173	0.061	0.006	0.746	**-0.083**	0.003	0.016	-0.037	0.777**
CARO	-0.179	-0.082	-0.024	-0.005	0.197	0.244	-0.006	0.007	0.215	-0.002	**0.132**	0.012	-0.019	0.43
PRL	-0.148	-0.003	-0.009	-0.025	0.185	0.218	0.049	0.009	0.332	-0.051	0.062	**0.026**	-0.039	0.606**
PRN	-0.137	-0.067	-0.024	-0.023	0.425	0.294	0.069	0.007	0.367	-0.041	0.032	0.013	**-0.076**	0.840**

*, ** Significant at 5 and 1 % levels, respectively. Residual effect = 0.019 (Genotypic)

PH= Plant height (cm), DFF= Days to 50% flowering, DM= Days to Maturity, BP= Branches per plant, DB= Dry biomass (g), PP= Pods per plant, SPP= Seeds per pods, HSW= 100 seed weight (g), HI= Harvest index (%), CHLO= Chlorophyll (mg/g), CARO= Carotenoid (mg/g), PRL= Proline (mg/g), PRN= Protein (%),GYPP= Grain yield per plant (g)

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