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Correlation and Path Analysis for Yield and its Phenological, Physiological, Morphological and Biochemical Traits under Salinity Stress in Chickpea (*Cicer arietinum* L.)

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ABSTRACT

The investigation was carried out during *rabi* season (November–April) of 2020–2021 in the polyhouse, Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara, Punjab, India. CRD (Completely Randomize Design) were used in 3 replications with the objective to assess the performance of 20 chickpea genotypes under salinity stress conditions in order to identify genotypes that demonstrate greater tolerance to these conditions. To induce the salinity stress, NaCl salts were administer in two split doses of 120 mM during sowing and at 15 DAS. The study evaluated a range of parameters, including phenological, physiological, morphological, biochemical, and yield parameters, to examine the impact of salt stress on genotypes that exhibit varying levels of tolerance. Total proline content increment is due to increase of stress related proteins during the salinity. The yield parameters increase in non-saline conditions whereas in stress conditions, yield will get reduce. The findings revealed an increase in the total Proline content due to the production of stress-related proteins during salinity stress; however, yield parameters were negatively affected under stress conditions, with the most significant decrease observed in the 120 mM NaCl treatment group compared to the control group. ICC5439 and GNG 1581 emerged as highly tolerant chickpea genotypes under salinity stress conditions, while ICC 6050, ICC 251, ICC 252, and ICC 262 exhibited medium tolerance. In contrast, ICC253, ICC 247, and ICC 249 were found to be highly susceptible genotypes, with the remaining genotypes showing minimal tolerance and sensitivity to salinity stress.

KEYWORDS: Biochemical, morphological, NaCl, physiological, tolerant, salinity stress, susceptible

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1. INTRODUCTION

Chickpea is an important legume food, primarily cultivated in South Asia. It is the third most produced pulse globally, with a total production of about 11.6 mt, where 80% is desi and 20% is Kabuli (Merga and Haji, 2019). India is the leading producer of chickpea, accounting for 73% of global production in 2020, followed by Turkey, Myanmar, and Pakistan (Anonymous, 2022). It contributes to 27–30% of total pulse output (Dahiya et al., 1990). According to Agricultural Statistics at a Glance (2020), India has dedicated 9.55 mha for chickpea production, with a production of 9.94 mt and productivity of 806 kg ha^{-1}. The productivity of chickpea in Punjab is 700 kg ha^{-1}.

Chickpeas, along with other crops and livestock, were domesticated around 12,000 to 10,000 years ago in the Fertile Crescent (Wilford, 1997). Chickpea is divided into Kabuli and Desi, which differ in their geographic distribution, seed size, and plant type (Flowers et al., 2010, Cobos et al., 2006). Crops like wheat, barley, rye, peas, lentil, flax, and vetch, as well as livestock such as sheep, goats, pigs, and cattle, were domesticated (Harlan, 1971, Abbo et al., 2003a, Diamond, 2002). However, it is possible that chickpea domestication followed a distinct evolutionary path from other pioneer crops first domesticated in the region (Abbo et al., 2003b).

Chickpea seeds are composed of carbohydrates (50–58%), protein (15–22%), moisture (7–8%), fat (3.8–10.20%), and micronutrients (<1%) (Anonymous, 2021). With an average protein content of almost 18%, chickpeas have a higher protein content than lentils and field peas (Upadhyaya et al., 2016). Chickpeas are rich in lysine and arginine, but have low levels of sulfur-containing amino acids such as cysteine and methionine (Jukanti et al., 2012). Furthermore, according to Ibrikci et al. (2003), chickpea seeds are a valuable source of minerals. The plant is also capable of restoring and sustaining soil fertility, as well as fixing up to 140 kg N ha^{-1} $year^{-1}$ through a symbiotic relationship with Rhizobium bacteria, as reported by Rupela and Rao (1987). GRDC (2012) and Saxena (1990) also support these claims.

The self-fertilizing diploid nature of all chickpea cultivars and their wild relatives, with 2n=2x=16 chromosomes and a genome size of 740 Mbp (Varshney et al., 2013). Although there are rare reports of chickpea species with a 2n=14 chromosome number (Singh et al., 1997a,b), the chromosomes of chickpea are generally small, with an average length of 1.32–3.69 µm and mitotic metaphase chromosome length of 2.2 µm (Ahmad, 2000). The *Cicer* chromosome naming system where the longest chromosome is assigned as 1 and the shortest as 8 and a letter-based system A to H (Zatloukalova et al., 2011). Chickpeas are highly nutritious due to their high content of vitamins and minerals (Gupta et al., 2021). It also contain important amino acids along with ß-carotene, as reported by Jukanti et al. (2012) and Thudi et al. (2014).

Phenotyping for salinity tolerance in crops affected by various environmental factors and developmental stages Khan et al. (2015, 2016). Some of these studies include the works of Atieno et al. (2017), and Kotula et al. (2019). Chickpea productivity can be affected by various abiotic factors as well as biotic factors. Several studies, including those by Tripathi et al. (2015), Mishra et al. (2020), Makwana et al. (2021), Mishra et al. (2021a, 2021b), Shyam et al. (2021). The phenotypic coefficient is used to assess the influence of the environment on the genotype, while the genotypic coefficient of variation estimates the heritable variability. This research aims to contribute to the advancement of knowledge in salinity stress-related breeding programs for chickpea. However, some potential findings related to the behaviour of chickpea genotypes under salt stress conditions and their correlation with yield and various traits could include: Identification of chickpea genotypes that exhibit higher tolerance to salt stress, indicating potential candidates for breeding programs aimed at developing salt-tolerance varieties and discovery of specific phenological, morphological, biochemical, or physiological traits that are strongly associated with higher yield under salt stress conditions. Therefore, effective selection involves considering heritability, selection intensity and genetic gain. Several research studies, including those by Barfa et al. (2017), Rajpoot et al. (2020), Choudhary et al. (2021), Yadav et al. (2021), Yadav et al. (2022a), and Yadav et al. (2022b), have explored these concepts. Thus the objective of this analysis is to identify and gather essential information pertaining to the behaviour of specific chickpea genotypes under salt stress conditions with correlations and path between yield and various phenological, morphological, biochemical, and physiological traits.

2. MATERIALS AND METHODS

2.1. Experimental site

The experimental trial was conducted in a polyhouse located at the Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara, Punjab, India during the *rabi* season (November–April, 2020–2021). The experimental area had uniform topography and climate, with sandy loam soil that had low N-2 availability, medium phosphorus, and high potash. The pH value of the soil was between 7.8 to 8.5. The region has a humid subtropical climate, with cool winters from November to February and long, hot summers from April to June. The average summer temperatures range from around 25°C (77°F) to around 48°C (118°F), while winter temperatures range from highs of 19°C (66°F) to lows of -7°C (19°F). The

climate is typically dry, with an average annual rainfall of approximately 70 cm.

2.2. Experimental material

The experiment was conducted using a Completely Randomized Design (CRD) with three replications under two conditions: saline (pots without holes) and control (pots with holes). Plastic pots with a diameter of 25 cm and filled with 8 to 10 kg of properly dried sandy loam soil were used, with five seeds sown in each pot. The experimental material consisted of 20 genotypes, of which 17 were collected from ICRISAT, Hyderabad (ICC6050, ICC5003, ICC263, ICC262, ICC258, ICC5439, ICCL86111, ICC244, ICC245, ICC246, ICC247, ICC248, ICC249, ICC250, ICC251, ICC252, and ICC253), while 3 were collected from ARS, SriGanganagar (GNG1488, GNG1581 and GNG1958). The effect of NaCl salt with a concentration of 120 mM on the growth and development of the twenty chickpea genotypes was studied in pot culture.

2.3. Preparation of saline solution

Two different volumetric flasks were used to prepare solutions of sodium chloride. 1.752 g of sodium chloride was weighed and added to one flask containing about 800 ml of water. In the other flask, 3.504 g of sodium chloride was added to 800 ml of water. The flasks were gently swirled until the sodium chloride was completely dissolved. Water was then added to each flask to make the final volume to 1000 ml, resulting in solutions of 30 mM and 60 mM concentration, respectively.

2.4. Creation of salinity

Chloride-based salts, primarily sodium chloride (NaCl), were used to induce salinity stress. The plants were treated with 120 mM NaCl, split into two doses: at the time of sowing and 15 days after sowing (DAS). The control plants were irrigated with normal water.

2.5. Statistical analysis

It is stated that the data collected for all the traits were subjected to statistical analysis. The Statistical Package for Completely Randomised Design (CRD) developed at IASRI in New Delhi was used for analysing the quantitative traits.

2.6. Estimation of correlations

Correlation coefficients are used to evaluate the relationship between multiple variables. The genotypic correlation coefficient quantifies the association between different traits due to genetic factors, whereas the phenotypic correlation coefficient considers both genetic and environmental influences.

Now, genotypic and phenotypic correlation coefficients were worked out according to formula described below.

Phenotypic correlation (rp)=PCOVxy/√PVx.PVy .....(1)

Genotypic correlation (rg)=GCOVxy/√GVx.GVy.....(2)

rxy=Cov (x,y)/√V (x) x √V (y) .....(3)

Where,

r_{xy}=Correlation coefficient between character x and y,

$Cov_{x,y}$=Co-variance of character x and y,

V_x=Variance of character x

V_y=Variance of character y

rp=Phenotypic correlation

rg=Genotypic correlation.

To test the significance of phenotypic and environmental correlation coefficients, the estimated values were compared with the tabulated values of Fisher and Yates (1938) at n-2 df at two levels of probability, *viz.*, 5% and 1%.

2.7. Path coefficient analysis

Path coefficient analysis, as suggested by Wright (1921, 1935) and further explained by Dewey and Lu (1959), was employed to determine the direct and indirect contributions of various traits towards the total correlation coefficient with grain yield. This analysis involves splitting the correlation coefficient into measures of direct and indirect effects, enabling the estimation of the contribution of each independent variable on the dependent variable as well as residual effects. The resulting information aids in determining the yield and yield-contributing traits. Path coefficients were evaluated based on the scales provided by Lenka and Mishra (1973).

To estimate various direct and indirect effects, the following set of simultaneous equations were formed and solved.

$r_{1y}=P_{1y}+r_{12}P_{2y}+r_{13}P_{3y}+\ldots+r_{1I}P_{Iy}$ .....(4)

$r_{2y}=r_{2y}P_{1y}+P_{2y}+r_{23}P_{3y}+\ldots+r_{2I}P_{Iy}$ .....(5)

$r_{Iy}=r_{I1}P_{1y}+r_{I2}P_{2y}+r_{I3}P_{3y}+\ldots+P_{Iy}$ .....(6)

Where,

r_{1y} to r_{Iy}=Coefficient of correlation between causal factor 1 to I and dependent character y,

r_{12} to $r_{I-1,I}$=Coefficient of correlation among causal factors themselves, and

P_{1y} to P_{Iy}=Direct effects of characters 1 to I on character y.

Residual effect, which measures the contribution of the characters not considered in the causal scheme, was obtained as:

Residual effect

(PRY) =$\sqrt{1-R^2}$ .....(7)

Where,

$R^2=\sum_{ij} P_i^2 Y+ 2\sum_{i\neq j}^{i>j} P_{iy}P_{jy}R_{ij}$ .....(8)

2.7. Analysis of variance and covariance

The first step in analysing the data is to conduct an analysis of variance (ANOVA) to determine whether there are significant differences among the genotypes for each of the traits. The data for each trait will be analysed using appropriate methods of ANOVA and covariance, as described by Panse and Sukhatme (1967). The range, means, phenotypic and genotypic variances and covariance, standard errors, coefficients of variation, and critical differences will be calculated for all 19 traits. To determine the significance of differences among the genotypes, the calculated value of 'F' will be compared with the tabular value of 'F' at both 1 and 5% levels of probability against error degrees of freedom. The significance of differences between the genotypes for each of the traits will be tested.

3. RESULTS AND DISCUSSION

3.1. Analysis of variance

In present study, dependent character was seed yield plant^{-1} and all other remaining 18 characters were viz., days to first flowering, days to 50% flowering, days to pod initiation, days to maturity, plant height at 60 DAS, plant height at 100 DAS, biomass, total chlorophyll content at 60 DAS, total chlorophyll content at 100 DAS, relative water content at 60 DAS, relative water content at 100 DAS, lipid peroxidation at 60 DAS, lipid peroxidation at 100 DAS, Proline content at 60 DAS, Proline content at 100 DAS, total protein, number of pod plant^{-1} and seed index considered as independent characters. The results of the analysis of variance indicate a significant effect of all parameters, except for protein, which was found to be non-significant. Additionally, all 20 chickpea genotypes demonstrated genetic diversity under salinity conditions. The study monitored various parameters such as phenological, physiological, morphological, biochemical, and yield parameters to determine the effect of salt stress on genotypes exhibiting different tolerance levels as per Table 1.

Analysis of variance has shown significant affect with all the parameters except protein it has shown non-significant. All Genotypes has shown genetic diversity under salinity conditions.

The analysis of variance for the design of experiment involving 20 chickpea genotypes were evaluated in complete randomized design with three replications for the nineteen characters. The mean squares due to replications and treatments for all the characters are present in Table 2. The variation due to replications was found non - significant for all the characters and due to treatments, all the characters

Table 1: Different parameters used in analysis

Phenological parameters	Days to first flowering, 50% flowering, pod initiation and days to maturity
Morphological parameters	Plant height and biomass
Physiological parameters	Total chlorophyll content, relative water content and Lipid peroxidation
Biochemical parameters	Proline and Protein content
Yield attributing parameters	Number of pod plant^{-1}, seed index and seed yield plant^{-1}

Table 2: Analysis of variance of various characters in chickpea under 120 mM saline condition

Characters	ANOVA table for 120 mM saline condition			
	Replication		Treatment	
	MSS	f-value	MSS	f-value
Days to first flowering	4.81	1.23	48.31	12.43**
Days to 50% flowering	6.11	1.38	44.01	9.92**
Days to pod initiation	14.46	2.82	56.54	11.05**
Day to maturity	8.71	1.03	36.71	4.37**
Plant height at 60 DAS	1.74	1.41	68.09	55.30**
Plant height at 100 DAS	8.07	2.49	91.95	28.36**
Biomass	0.17	1.13	5.04	32.53**
Total chlorophyll content at 60 DAS	0.04	1.47	2.90	96.80**
Total chlorophyll content at 100 DAS	0.02	1.68	2.23	165.28**
Relative water content at 60 DAS	1.13	1.99	197.59	347.82**
Relative water content at 100 DAS	0.12	0.17	190.16	261.18**
Lipid per oxidation at 60 DAS	0.01	0.04	7.76	36.35**
Lipid per oxidation at 100 DAS	0.02	0.35	11.80	203.02**
Proline content at 60 DAS	0.02	1.58	2.42	189.26**
Proline content at 100 DAS	0.01	1.95	0.62	177.44**
Total protein	6.29	0.41	298.79	19.93**
Numbers of pod plant^{-1}	5.60	2.65	51.68	24.51**
Seed index	0.12	2.81	41.93	981.36***
Seed yield plant^{-1}	0.01	0.10	3.54	228.57**

*, **: significant at (p=0.05) and (p=0.01) probability levels respectively; df for replication and treatment- 2 and 19 respectively

were found significant under (120 mM) saline condition.

3.2. Correlation between various traits under study at 120 mM saline conditions

Correlation tells degree and direction of association traits that have significant correlation with yield may be used as indirect parameter for selecting higher yielding lines tabulated in Table 3 and Figure 1 for genotypic and Figure 2 for phenotypic respectively.

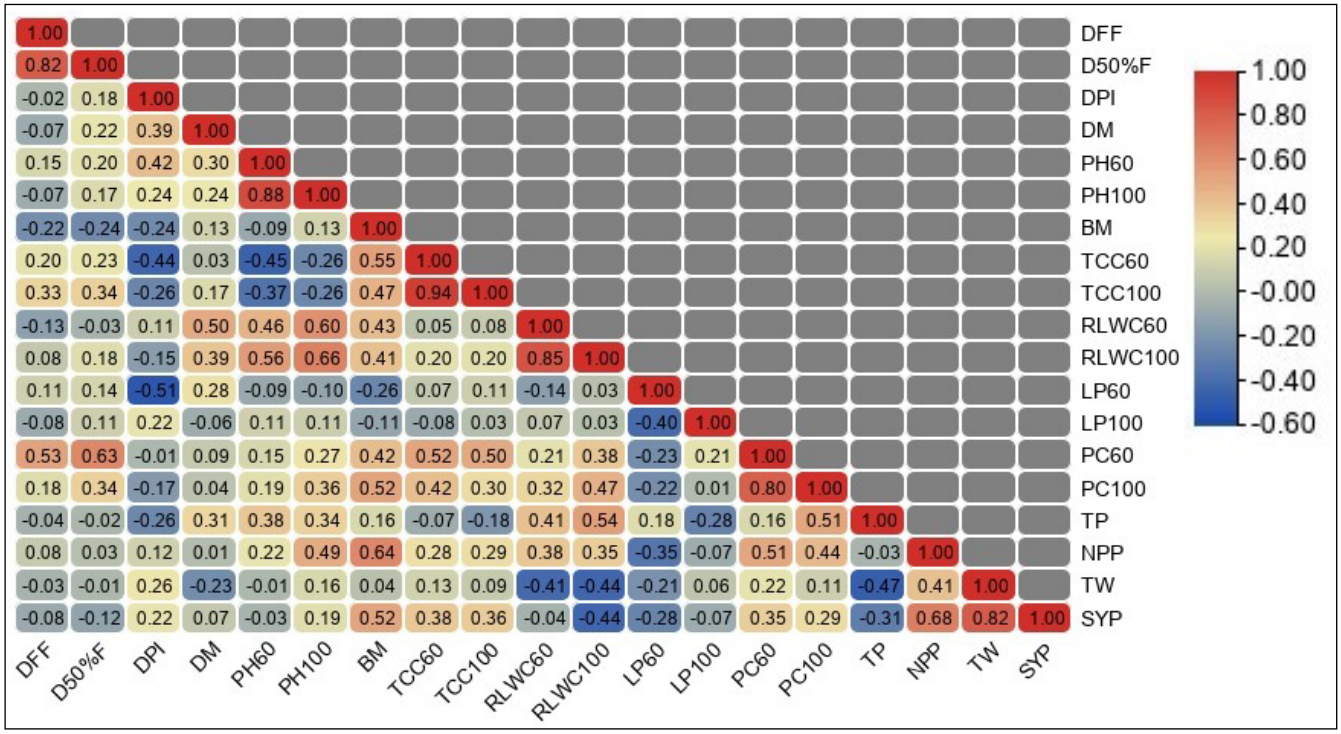

Figure 1: Correlation between various traits under study at 120 mM saline conditions at genotypic level

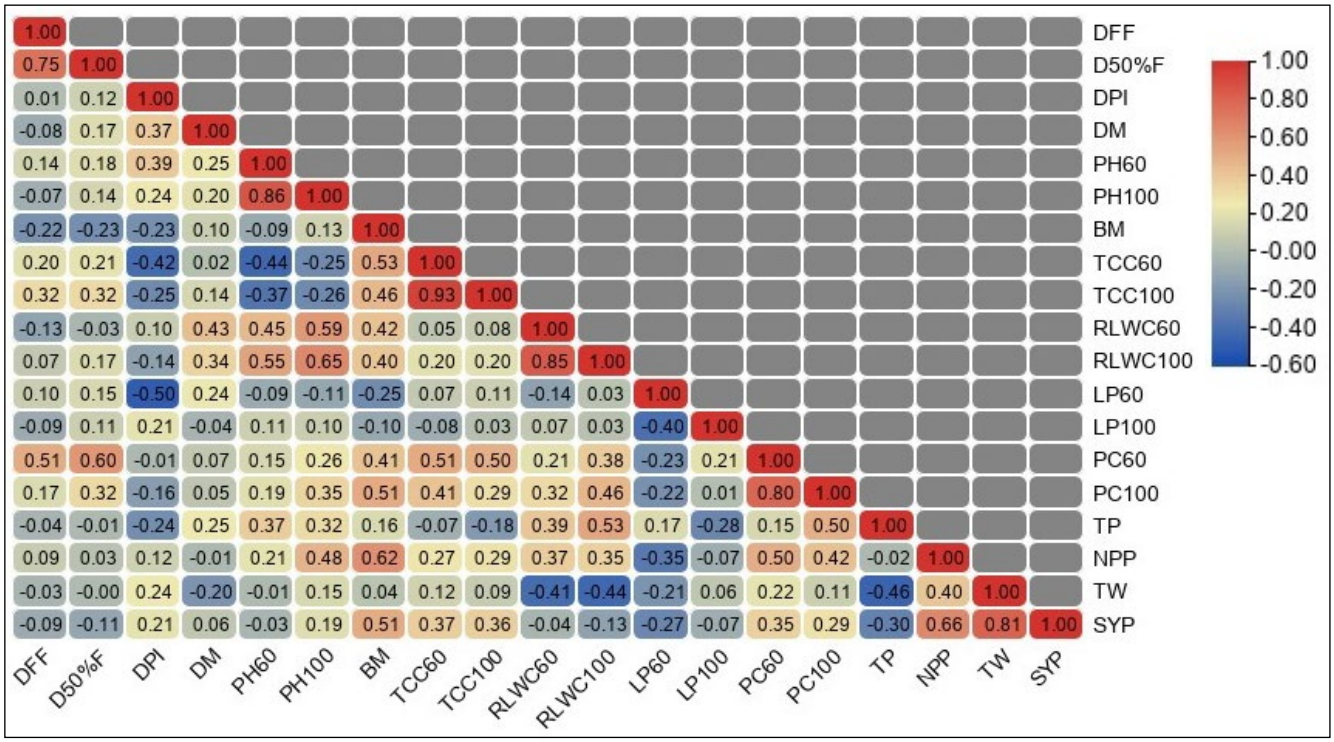

Figure 2: Correlation between various traits under study at 120 mM saline conditions at phenotypic level

Table 3: Correlation between various traits under study at 120 mM saline conditions at genotypic and phenotypic level

Characters		DFF	D50% F	DPI	DM	PH60	PH100	BM	TCC60	TCC100	RLWC60
DFF	rg	1.000									
	rp	1.000									
D50% F	rg	0.8219**	1.000								
	rp	0.7472**	1.000								
DPI	rg	-0.017	0.176	1.000							
	rp	0.007	0.119	1.000							
DM	rg	-0.072	0.219	0.3919*	1.000						
	rp	-0.082	0.173	0.374	1.000						
PH60	rg	0.151	0.198	0.4188*	0.296	1.000					
	rp	0.137	0.181	0.3888*	0.255	1.000					
PH100	rg	-0.073	0.171	0.244	0.236	0.8842**	1.000				
	rp	-0.066	0.139	0.244	0.203	0.8620**	1.000				
BM	rg	-0.225	-0.244	-0.241	0.127	-0.089	0.133	1.000			
	rp	-0.223	-0.233	-0.227	0.100	-0.092	0.126	1.000			
TCC60	rg	0.203	0.227	-0.4358*	0.034	-0.4492*	-0.255	0.5460**	1.000		
	rp	0.197	0.215	-0.4201*	0.019	-0.4418*	-0.252	0.5290**	1.000		
TCC100	rg	0.332	0.342	-0.265	0.168	-0.367	-0.258	0.4688*	0.9406**	1.000	
	rp	0.321	0.320	-0.255	0.143	-0.367	-0.256	0.4619*	0.9325**	1.000	
RLWC60	rg	-0.132	-0.031	0.106	0.4952*	0.4585*	0.603	0.4252*	0.054	0.082	1.000
	rp	-0.126	-0.029	0.098	0.4323*	0.4525*	0.5878**	0.4202*	0.055	0.083	1.000
RLWC100	rg	0.078	0.183	-0.149	0.3929*	0.5574**	0.6633**	0.4084*	0.202	0.198	0.8525**
	rp	0.073	0.171	-0.140	0.343	0.5499**	0.6532**	0.4044*	0.201	0.197	0.8495**
LP60	rg	0.114	0.142	-0.5117*	0.280	-0.089	-0.103	-0.259	0.073	0.110	-0.144
	rp	0.103	0.154	-0.5005*	0.237	-0.087	-0.108	-0.245	0.073	0.107	-0.138
LP100	rg	-0.080	0.110	0.223	-0.062	0.114	0.105	-0.106	-0.078	0.025	0.072
	rp	-0.085	0.106	0.210	-0.040	0.112	0.102	-0.102	-0.079	0.026	0.072
PC60	rg	0.5282**	0.6348**	-0.012	0.085	0.153	0.266	0.4202*	0.517	0.4996*	0.207
	rp	0.5078*	0.5987**	-0.013	0.068	0.151	0.262	0.4124*	0.5129*	0.4970*	0.207
PC100	rg	0.182	0.344	-0.166	0.045	0.195	0.356	0.5229**	0.4159*	0.295	0.320
	rp	0.172	0.323	-0.160	0.047	0.193	0.345	0.5113*	0.4120*	0.294	0.320
TP	rg	-0.043	-0.016	-0.256	0.315	0.3809*	0.335	0.157	-0.067	-0.184	0.406
	rp	-0.040	-0.011	-0.236	0.251	0.367	0.318	0.164	-0.065	-0.181	0.3942*
NPP	rg	0.084	0.032	0.123	0.015	0.219	0.4901*	0.6386**	0.285	0.292	0.3839*
	rp	0.094	0.034	0.117	-0.012	0.211	0.476	0.6239**	0.273	0.285	0.372
SI	rg	-0.034	-0.008	0.258	-0.232	-0.007	0.158	0.038	0.126	0.089	-0.4148*
	rp	-0.034	-0.005	0.244	-0.203	-0.008	0.155	0.037	0.125	0.088	-0.4139*
SYP	rg	-0.085	-0.118	0.222	0.073	-0.030	0.188	0.5186**	0.376	0.365	-0.037
	rp	-0.086	-0.112	0.211	0.060	-0.029	0.186	0.5097*	0.373	0.363	-0.036

Table 3: Continue...

Characters		RLWC100	LP60	LP100	PC60	PC100	TP	NPP	SI	SYP
RLWC100	rg	1.000								
	rp	1.000								
LP60	rg	0.033	1.000							
	rp	0.033	1.000							
LP100	rg	0.030	-0.4044*	1.000						
	rp	0.030	-0.3979*	1.000						
PC60	rg	0.3815*	-0.231	0.209	1.000					
	rp	0.3794*	-0.227	0.208	1.000					
PC100	rg	0.4673*	-0.223	0.008	0.8008**	1.000				
	rp	0.4642*	-0.220	0.010	0.7970**	1.000				
TP	rg	0.5428**	0.180	-0.282	0.160	0.5146*	1.000			
	rp	0.5313**	0.172	-0.275	0.150	0.4983*	1.000			
NPP	rg	0.355	-0.352	-0.071	0.5123*	0.4384*	-0.027	1.000		
	rp	0.351	-0.346	-0.071	0.5044*	0.4234*	-0.017	1.000		
SI	rg	-0.4382*	-0.210	0.062	0.216	0.109	-0.4704*	0.4094*	1.000	
	rp	-0.4371*	-0.206	0.062	0.215	0.109	-0.4593*	0.4014*	1.000	
SYP	rg	-0.4382*	-0.278	-0.074	0.353	0.289	-0.310	0.6752**	0.8165**	1.000
	rp	-0.132	-0.274	-0.074	0.352	0.288	-0.301	0.6567**	0.8144**	1.000

* & **: significance at (p=0.05) and (p=0.01) probability level respectively

The Proline content at 60 DAS exhibited highly significant and positive correlations both at genotypic and phenotypic levels with Days to 50% flowering (r_g=0.634, r_p=0.598), Days to First flowering (r_g=0.528) and Proline content at 60 DAS (r_g=0.800, r_p=0.797). The Proline content at 100 DAS exhibited highly significant and positive correlations both at genotypic and phenotypic levels with Proline content at 60 DAS (r_g=0.615, r_p=0.612) and Number of pod per plant (r_g=0.580, r_p=0.565). The Total protein exhibited highly significant and positive correlations both at genotypic and phenotypic levels with Relative water content at 100 DAS (r_g=0.380, r_p=0.663). Similar results was observed in mungbean investigated by Manasa (2016); Iqra et al. (2020) in resistance chickpea genotype under salinity stress in chickpea.

The Number of pod per plant exhibited highly significant and positive correlations both at genotypic and phenotypic levels with seed yield plant^{-1} (r_g=0.675, r_p=0.656), Biomass (r_g=0.638, r_p=0.623). Durga et al. (2007) also assessed positive correlation between the yield and pods plant^{-1}. The Seed index exhibited highly significant and positive correlations both at genotypic and phenotypic levels with Seed yield plant^{-1} (r_g=0.816, r_p=0.814). obtained a similar result. The seed yield plant^{-1} at 120 mM saline condition exhibited highly significant and positive correlations both at genotypic and phenotypic levels with Seed index (r_g=0.816, r_p=0.814), Biomass (r_g=0.518) and number of pod plant^{-1} (r_g=0.675, r_p=0.656). It also manifested the significant positive correlation at phenotypic level with Biomass (r_p=0.509). It also manifested the significant but negative correlation at genotypic level with Relative water content at 100 DAS (r_g=-0.438). Both genotypic and phenotypic correlations showed a high significance between the number of pods plant^{-1}, seed index, and seed yield plant^{-1} in both controlled and saline conditions. Hence, these two traits can be efficiently employed for indirect selection of higher yield. Additionally, biomass also exhibited significant correlations at both genotypic and phenotypic levels with seed yield plant^{-1} under saline conditions, making it an essential criterion for selecting high-yielding chickpea lines.

Thonta et al. (2023); Kaur et al. (2021); Nikita and Lal (2022), Tengse et al. (2022); Nasir et al. (2023); Singh et al. (2023); Ningwal et al. (2023); Jain et al. (2023); Sadji-Ait Kaci et al. (2022) and Devi et al. (2022) also reported a positive and significant correlation between seed yield and plant height, pods plant^{-1}, and seed weight. Durga et al. (2007) also found a positive correlation between yield and pods plant^{-1}. Turner et al. (2013) reported that under salinity, seed yield showed a positive correlation with total chlorophyll content, relative water content, number of filled pods, and 100-seed weight. These traits can be considered as indicators of tolerance to salinity conditions.

3.3. Path for various traits under study with seed yield plant^{-1} at 120 mM saline conditions

Correlation alone cannot determine the effectiveness of a trait for indirect selection of yield. A trait may have a significant correlation with yield, but it may not have a significant effect on yield. Therefore, it is essential to consider both correlation and the magnitude of the direct effect of the trait on yield. A trait that has a high correlation and a high direct effect on yield is a good candidate for indirect selection of yield. Genotypic and phenotypic path results tabulated in Table 4 and 5.

Under 120 mM saline condition at the genotypic level as per Table 4, seed yield plant^{-1} exhibited a very highly positive direct effect with total chlorophyll content at 60 DAS but a negative direct effect with total chlorophyll content at 100 DAS. There was a highly positive direct effect observed with days to first flowering, days to maturity, plant height at 60 DAS, biomass, lipid peroxidation at 60 and 100 DAS,

Table 4: Path coefficient analysis at genotypic level under 120 mM saline condition

	DFF	DF 50%	DPI	DM	PH 60	PH 100	BM	TC 60	TC 100	RWC 60
DFF	0.356	0.293	-0.006	-0.026	0.054	-0.026	-0.080	0.072	0.119	-0.047
DF 50%	-0.057	-0.070	-0.012	-0.015	-0.014	-0.012	0.017	-0.016	-0.024	0.002
DPI	-0.003	0.026	0.150	0.059	0.063	0.037	-0.036	-0.065	-0.040	0.016
DM	-0.027	0.082	0.148	0.377	0.112	0.089	0.048	0.013	0.063	0.187
PH 60	0.102	0.134	0.282	0.199	0.674	0.596	-0.060	-0.303	-0.247	0.309
PH 100	0.061	-0.144	-0.205	-0.198	-0.744	-0.841	-0.112	0.215	0.217	-0.507
BM	-0.078	-0.084	-0.083	0.044	-0.031	0.046	0.346	0.189	0.162	0.147
TC 60	0.311	0.348	-0.667	0.052	-0.688	-0.391	0.836	1.531	1.440	0.083
TC 100	-0.484	-0.498	0.386	-0.245	0.534	0.375	-0.683	-1.370	-1.456	-0.120
RWC 60	-0.033	-0.008	0.026	0.124	0.114	0.151	0.106	0.014	0.021	0.250
RWC 100	-0.013	-0.030	0.025	-0.065	-0.092	-0.110	-0.068	-0.034	-0.033	-0.141
LP 60	0.035	0.044	-0.157	0.086	-0.027	-0.032	-0.080	0.022	0.034	-0.044
LP 100	-0.025	0.033	0.068	-0.019	0.035	0.032	-0.032	-0.024	0.008	0.022
PC 60	-0.360	-0.433	0.008	-0.058	-0.105	-0.182	-0.287	-0.353	-0.341	-0.141
PC 100	0.090	0.170	-0.082	0.022	0.096	0.175	0.258	0.205	0.146	0.158
TP	0.015	0.005	0.090	-0.110	-0.133	-0.117	-0.055	0.023	0.064	-0.142
NPP	0.049	0.019	0.072	0.009	0.128	0.287	0.374	0.167	0.171	0.225
SI	-0.024	-0.006	0.181	-0.163	-0.005	0.111	0.026	0.088	0.062	-0.292
SYP	-0.085	-0.118	0.222	0.073	-0.030	0.188	0.519	0.376	0.365	-0.037
Partial R^2	-0.030	0.008	0.033	0.028	-0.020	-0.158	0.179	0.575	-0.531	-0.009

Table 4: Continue...

	RWC 100	LP 60	LP 100	PC 60	PC 100	TP	NPP	SI
DFF	0.028	0.041	-0.029	0.188	0.065	-0.015	0.030	-0.012
DF 50%	-0.013	-0.010	-0.008	-0.044	-0.024	0.001	-0.002	0.001
DPI	-0.022	-0.077	0.033	-0.002	-0.025	-0.038	0.018	0.039
DM	0.148	0.106	-0.023	0.032	0.017	0.119	0.006	-0.087
PH 60	0.376	-0.060	0.076	0.103	0.131	0.257	0.147	-0.005
PH 100	-0.558	0.087	-0.089	-0.224	-0.299	-0.282	-0.412	-0.133
BM	0.141	-0.090	-0.037	0.145	0.181	0.054	0.221	0.013
TC 60	0.309	0.111	-0.119	0.791	0.637	-0.102	0.436	0.193
TC 100	-0.288	-0.159	-0.036	-0.728	-0.430	0.268	-0.424	-0.129

Table 4: Continue...

	RWC 100	LP 60	LP 100	PC 60	PC 100	TP	NPP	SI
RWC 60	0.213	-0.036	0.018	0.052	0.080	0.101	0.096	-0.104
RWC 100	-0.166	-0.006	-0.005	-0.063	-0.077	-0.090	-0.059	0.073
LP 60	0.010	0.307	-0.124	-0.071	-0.068	0.055	-0.108	-0.065
LP 100	0.009	-0.123	0.305	0.064	0.003	-0.086	-0.022	0.019
PC 60	-0.260	0.157	-0.143	-0.682	-0.546	-0.109	-0.349	-0.147
PC 100	0.230	-0.110	0.004	0.395	0.493	0.254	0.216	0.054
TP	-0.190	-0.063	0.099	-0.056	-0.180	-0.350	0.009	0.165
NPP	0.208	-0.206	-0.042	0.300	0.257	-0.016	0.586	0.240
SI	-0.308	-0.147	0.044	0.152	0.077	-0.331	0.288	0.703
SYP	-0.133	-0.278	-0.074	0.353	0.289	-0.310	0.675	0.817
Partial R^2	0.022	-0.085	-0.023	-0.241	0.142	0.109	0.395	0.574

R^2=0.9676; residual effect=0.18

proline content at 100 DAS, number of pods plant^{-1}, and seed index. On the other hand, a highly negative direct effect was observed with plant height at 100 DAS, proline content at 60 DAS, and total protein. A moderately positive direct effect was observed with relative water content at 60 DAS.

Under 120 mM saline conditions, the study found that at the phenotypic level as per Table 5, seed yield plant^{-1} had a very highly positive direct effect with total chlorophyll content at 100 DAS and a highly positive direct effect with days to maturity, plant height at 100 DAS, biomass, and seed index. However, a highly negative direct effect was observed with days to 50% flowering, plant height at 60

Table 5: Path coefficient analysis at phenotypic level under 120 mM saline condition

	DFF	DF 50%	DPI	DM	PH 60	PH 100	BM	TC 60	TC 100	RWC 60
DFF	0.264	0.197	0.002	-0.022	0.036	-0.018	-0.059	0.052	0.085	-0.033
DF 50%	-0.263	-0.353	-0.042	-0.061	-0.064	-0.049	0.082	-0.076	-0.113	0.010
DPI	-0.002	-0.027	-0.227	-0.085	-0.088	-0.055	0.052	0.095	0.058	-0.022
DM	-0.026	0.054	0.116	0.309	0.079	0.063	0.031	0.006	0.044	0.134
PH 60	-0.063	-0.084	-0.179	-0.118	-0.462	-0.398	0.042	0.204	0.169	-0.209
PH 100	-0.056	0.118	0.207	0.171	0.729	0.845	0.106	-0.213	-0.217	0.497
BM	-0.073	-0.076	-0.074	0.033	-0.030	0.041	0.327	0.173	0.151	0.137
TC 60	-0.155	-0.170	0.331	-0.015	0.348	0.198	-0.417	-0.788	-0.735	-0.043
TC 100	0.323	0.322	-0.256	0.144	-0.369	-0.258	0.465	0.939	1.007	0.084
RWC 60	-0.011	-0.002	0.008	0.036	0.038	0.049	0.035	0.005	0.007	0.083
RWC 100	-0.028	-0.066	0.054	-0.133	-0.213	-0.253	-0.156	-0.078	-0.076	-0.329
LP 60	-0.039	-0.059	0.191	-0.090	0.033	0.041	0.093	-0.028	-0.041	0.053
LP 100	0.023	-0.029	-0.058	0.011	-0.031	-0.028	0.028	0.022	-0.007	-0.020
PC 60	0.090	0.106	-0.002	0.012	0.027	0.046	0.073	0.091	0.088	0.037
PC 100	-0.016	-0.029	0.014	-0.004	-0.017	-0.031	-0.046	-0.037	-0.026	-0.029
TP	-0.003	-0.001	-0.015	0.016	0.023	0.020	0.010	-0.004	-0.011	0.024
NPP	-0.028	-0.010	-0.035	0.003	-0.062	-0.141	-0.184	-0.081	-0.084	-0.110
SI	-0.024	-0.003	0.177	-0.148	-0.005	0.112	0.027	0.090	0.064	-0.300
SYP	-0.086	-0.112	0.211	0.060	-0.029	0.186	0.510	0.373	0.363	-0.036
Partial R^2	-0.023	0.039	-0.048	0.019	0.014	0.157	0.167	-0.294	0.365	-0.003

Table 5: Continue...

	RWC 100	LP 60	LP 100	PC 60	PC 100	TP	NPP	SI
DFF	0.019	0.027	-0.023	0.134	0.045	-0.011	0.025	-0.009
DF 50%	-0.060	-0.054	-0.037	-0.211	-0.114	0.004	-0.012	0.002
DPI	0.032	0.113	-0.048	0.003	0.036	0.054	-0.027	-0.055
DM	0.106	0.073	-0.012	0.021	0.015	0.078	-0.004	-0.063
PH 60	-0.254	0.040	-0.052	-0.070	-0.089	-0.169	-0.098	0.004
PH 100	0.552	-0.091	0.086	0.221	0.292	0.269	0.403	0.131
BM	0.132	-0.080	-0.033	0.135	0.167	0.054	0.204	0.012
TC 60	-0.158	-0.057	0.062	-0.404	-0.325	0.051	-0.215	-0.098
TC 100	0.198	0.108	0.026	0.501	0.296	-0.182	0.287	0.089
RWC 60	0.071	-0.012	0.006	0.017	0.027	0.033	0.031	-0.034
RWC 100	-0.387	-0.013	-0.012	-0.147	-0.180	-0.205	-0.136	0.169
LP 60	-0.013	-0.381	0.152	0.086	0.084	-0.066	0.132	0.079
LP 100	-0.008	0.109	-0.275	-0.057	-0.003	0.076	0.020	-0.017
PC 60	0.067	-0.040	0.037	0.177	0.141	0.027	0.089	0.038
PC 100	-0.042	0.020	-0.001	-0.072	-0.090	-0.045	-0.038	-0.010
TP	0.033	0.011	-0.017	0.009	0.031	0.062	-0.001	-0.028
NPP	-0.104	0.102	0.021	-0.149	-0.125	0.005	-0.295	-0.119
SI	-0.317	-0.150	0.045	0.156	0.079	-0.333	0.291	0.725
SYP	-0.132	-0.274	-0.074	0.352	0.288	-0.301	0.657	0.814
Partial R^2	0.051	0.104	0.020	0.062	-0.026	-0.019	-0.194	0.590

R^2=0.9823; residual effect=0.1332

DAS, total chlorophyll content at 60 DAS, relative water content at 100 DAS, and lipid peroxidation at 60 DAS. A moderately positive direct effect was observed with days to first flowering, while a moderately negative direct effect was observed with days to pod initiation, lipid peroxidation at 100 DAS, and number of pods plant^{-1}.

Kanouni et al. (2012) obtained similar results, where the genotypic path coefficient analysis based on seed yield plant^{-1} as a dependent variable showed that drought tolerance score, 100-seed weight, plant height, and pods plant^{-1} had high positive direct effects. Additionally, vigour, days to maturity, and 100-seed weight exhibited the highest direct influence. As a result, the research suggests that drought tolerance score and pods plant^{-1} can serve as effective selection criteria for enhancing seed yield plant^{-1} in chickpea under drought stress conditions. According to Atieno et al. (2017), path analysis conducted under non-saline conditions revealed that the number of filled pods, seed number and 100-seed weight had a moderate direct positive impact on seed yield, while the total number of pods had a moderate indirect positive effect on seed yield through the number of filled pods and seed number. Similarly, the number of filled pods had a moderate indirect positive effect on seed yield through seed number. Under saline conditions, the number of filled pods and seed number had a moderate positive direct effect on seed yield, while 100-seed weight had a weak positive direct effect on seed yield. In addition, the total number of pods had a moderate indirect positive effect on seed yield through the number of filled pods and seed number, and filled pods had a moderate indirect positive effect on seed yield through seed number.

4. CONCLUSION

The results of the correlation analysis showed that seed yield was positively and significantly correlated with the number of pods plant^{-1} and seed index at both genotypic and phenotypic levels. ICC5439 and GNG 1581 emerged as highly tolerant chickpea genotypes under salinity stress conditions, while ICC 6050, ICC 251, ICC 252, and ICC 262 exhibited medium tolerance. In contrast, ICC253, ICC 247 and ICC 249 were found to be highly susceptible genotypes, with the remaining genotypes showing minimal tolerance and sensitivity to salinity stress.

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