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Correlation and Path Coefficient Analysis for Yield and its Phenological, Physiological, Morphological and Biochemical Traits under 60 mM 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 to assess the performance of chickpea genotypes under salinity stress conditions. 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). Twenty genotypes were collected out of which seventeen from ICRISAT, Hyderabad and three from ARS, SriGanganagar. The salinity stress was created using salts NaCl, which were administered in split doses of 60 mM at the time of sowing and 15 DAS. 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. The results showed that the total proline content increased due to the production of stress-related proteins during salinity stress. However, the yield parameters were reduced under stress conditions, with the highest decrease observed in the 60 mM NaCl treatment group compared to the control group. Based on the results of the study, ICC5439 and GNG 1581 are highly tolerant chickpea genotypes under salinity stress conditions. ICC 6050, ICC 251, ICC 252, and ICC 262 are medium tolerant genotypes, while ICC253, ICC 247, and ICC 249 are highly susceptible genotypes. Remaining are minimum tolerant and sensitive genotypes.

KEYWORDS: Biochemical, morphological, physiological, susceptible and tolerant

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1. INTRODUCTION

Chickpea is a significant legume food primarily grown in South Asia. It ranks as the third most produced pulse worldwide, with an overall output of approximately 11.6 million tons, where 80% is desi and 20% is Kabuli (Merga and Haji, 2019). In 2020, India led global chickpea production, contributing 73% of the total, followed by Turkey, Myanmar, and Pakistan (Anonymous, 2022). It represents 27–30% of the total pulse production (Dahiya et al., 1990). According to Agricultural Statistics at a Glance (2020), India has allocated 9.55 mha for chickpea cultivation, yielding 9.94 mt with a productivity rate of 806 kg ha^{-1}. In Punjab, the productivity of chickpea is 700 kg ha^{-1}.

Chickpeas, along with other crops and livestock, were domesticated approximately 12,000 to 10,000 years ago in the Fertile Crescent (Wilford, 1997). The chickpea is categorized into Kabuli and Desi varieties, which differ in geographic distribution, seed size, and plant characteristics (Flowers et al., 2010; Cobos et al., 2007). Other domesticated crops include wheat, barley, rye, peas, lentils, flax, and vetch, along with livestock such as sheep, goats, pigs, and cattle (Harlan, 1971; Abbo et al., 2003a; Diamond, 2002). It is suggested that chickpea domestication may have followed a unique evolutionary trajectory compared to other early domesticated crops in the region (Abbo et al., 2003b).

Chickpea seeds contain carbohydrates (50–58%), protein (15–22%), moisture (7–8%), fat (3.8–10.20%), and micronutrients (<1%) (Anonymous, 2021). With an average protein level nearing 18%, chickpeas boast a higher protein content than lentils and field peas. They are particularly rich in lysine and arginine but have lower amounts of sulfur-containing amino acids, such as cysteine and methionine (Jukanti et al., 2012). Additionally, chickpea seeds are recognized as a valuable source of minerals (Ibrikci et al., 2003). The plant is capable of enhancing and maintaining soil fertility, fixing as much as 140 kg of nitrogen per hectare annually through a symbiotic relationship with Rhizobium bacteria, as noted by Rupela and Rao (1987).

All chickpea cultivars and their wild relatives are self-fertilizing diploids, characterized by 2n=2x=16 chromosomes and a genome size of 740 Mbp (Varshney et al., 2013). While there are rare instances of chickpea species with a chromosome count of 2n=14 (Singh et al., 1997), the chromosomes are generally small, averaging 1.32-3.69 μm in length, with a mitotic metaphase chromosome length of 2.2 μm (Ahmad, 2000). The Cicer chromosome naming system designates the longest chromosome as 1 and the shortest as 8, along with a letter-based classification from A to H (Zatloukalova et al., 2011). Chickpeas are highly nutritious, containing significant amounts of vitamins and minerals (Gupta et al., 2021), as well as essential amino acids and ß-carotene, as identified by Thudi et al. (2014).

Phenotyping for salinity tolerance in crops is influenced by various environmental factors and developmental stages (Khan et al., 2015). Notable studies in this field include those by Kotula et al. (2019). Chickpea productivity is susceptible to both abiotic and biotic factors, with several studies documenting these influences, including works by Mishra et al. (2021), Makwana et al. (2021) and Mishra et al. (2022), among others. The phenotypic coefficient assesses environmental impact on the genotype, while the genotypic coefficient of variation estimates heritable variability. Effective selection will require consideration of heritability, selection intensity, and genetic gain. Multiple research studies, including those by Rajpoot et al. (2020), Choudhary et al. (2021) and Yadav et al. (2022) have explored these themes. This analysis aims to gather vital information regarding the behavior of specific chickpea genotypes under salt stress, including correlations and pathways between yield and various phenological, morphological, biochemical, and physiological traits. The research aspires to enhance understanding for salinity stress-related breeding programs for chickpea.

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 60 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 60 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)×√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)=√(1-R^2)..... ……(7)

Where,

$R^2=\sum_{ij}P_i^2\ Y+2\sum_{\substack{i\#j\\ i>j}}P_{iy}\ P_{jy}\ R_{ij}$ .....……(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

The present study utilized seed yield plant^{-1} as the dependent variable, with the remaining 18 variables serving as independent variables. These independent variables included 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 pods plant^{-1}, and seed index. 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.

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	No. of pod plant^{-1}, seed index and seed yield plant^{-1}

In the experiment, 20 chickpea genotypes were evaluated using a completely randomized design with three replications for 19 different parameters. The mean squares for both the replications and treatments for all parameters can be found in Table 2. The analysis revealed that the variation due to replications was non-significant for all the characters. However, the variation due to treatments was significant for all the characters under saline condition, specifically at 60 mM.

Table 2: ANOVA for various characters in chickpea under 60mM saline condition

Characters	Replication		Treatment	
	MSS	f-value	MSS	f-value
Days to first flowering	2.81	0.68	38.72	9.41**
Days to 50% flowering	1.26	0.25	35.41	7.20**
Days to pod initiation	2.46	0.43	42.76	7.58**
Day to maturity	31.85	2.96	20.42	1.90*
Plant height at 60 DAS	0.32	0.19	82.09	49.04**
Plant height at 100 DAS	9.03	2.65	67.24	19.75**
Biomass	0.18	1.19	5.24	33.41**
Total chlorophyll content at 60 DAS	0.07	1.44	2.68	54.31**
Total chlorophyll content at 100 DAS	0.01	0.20	2.31	63.79**
Relative water content at 60 DAS	1.46	0.85	171.98	100.37**
Relative water content at 100 DAS	1.09	1.15	169.94	179.32**
Lipid per oxidation at 60 DAS	0.07	0.62	5.25	46.94**
Lipid per oxidation at 100 DAS	0.03	0.68	4.12	81.72**
Proline content at 60 DAS	0.01	0.67	2.02	260.44**
Proline content at 100 DAS	0.01	2.51	0.43	187.80**
Total protein	1.21	0.08	282.83	20.58**
No. of pod plant^{-1}	4.86	2.79	40.95	23.48**
Seed index	0.08	0.93	53.29	556.72**
Seed yield plant^{-1}	0.01	0.69	3.57	218.24**

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

3.2. Correlation between various traits under study at 60 mM conditions

The current study aimed to determine the extent of association among 19 different characters by estimating both genotypic and phenotypic correlation coefficients. The estimates for these correlation coefficients under 60 mM conditions presented in Table 3 and Figure 1. Correlation coefficients provide information on the degree and direction of association between different traits. Traits that demonstrate significant correlation with yield can be considered as indirect parameters for selecting higher yielding lines.

The seed yield plant^{-1} at 60 mM saline condition exhibited

Table 3: Correlation between various traits under study at 60 mM saline conditions at genotypic and phenotypic level

Characters		DFF	D50% F	DPI	DM	PH60	PH100	BM	TCC60	TCC100
DFF	rg	1.000								
	rp	1.000								
D50%F	rg	0.9264**	1.000							
	rp	0.8493**	1.000							
DPI	rg	0.4432*	0.378	1.000						
	rp	0.367	0.317	1.000						
DM	rg	0.5827**	0.272	0.8804**	1.000					
	rp	0.364	0.138	0.6853**	1.000					
PH60	rg	-0.110	-0.321	-0.003	0.123	1.000				
	rp	-0.110	-0.291	-0.008	0.089	1.000				
PH100	rg	0.357	-0.5558**	-0.201	-0.066	0.9037**	1.000			
	rp	-0.340	-0.5020*	-0.182	-0.065	0.8753**	1.000			
BM	rg	-0.140	-0.031	-0.262	-0.185	0.033	0.080	1.000		
	rp	-0.116	-0.012	-0.248	-0.106	0.033	0.083	1.000		
TCC60	rg	0.212	0.4129*	0.020	-0.007	-0.5568**	-0.5447**	0.5078*	1.000	
	rp	0.199	0.3808*	0.017	-0.016	-0.5466**	-0.5266**	0.4980*	1.000	
TCC100	rg	0.274	0.4198*	0.126	0.205	-0.5102*	-0.5593**	0.5467**	0.9489**	1.000
	rp	0.263	0.3836*	0.115	0.137	-0.5042*	-0.5436**	0.5353**	0.9412**	1.000
RLWC60	rg	-0.238	-0.303	-0.288	-0.022	0.4435*	0.6216**	0.371	-0.092	-0.149
	rp	-0.226	-0.282	-0.257	0.005	0.4393*	0.6066**	0.368	-0.093	-0.147
RLWC100	rg	-0.071	-0.174	-0.230	-0.090	0.4923*	0.6227**	0.3567*	0.035	-0.038
	rp	-0.075	-0.169	-0.211	-0.060	0.4841*	0.6010**	0.349	0.034	-0.039
LP60	rg	-0.007	0.037	-0.023	-0.122	-0.104	-0.143	0.034	0.371	0.304
	rp	0.002	0.033	-0.022	-0.103	-0.095	-0.136	0.037	0.363	0.296
LP100	rg	-0.107	0.068	0.019	-0.342	0.048	0.182	0.056	-0.070	-0.085
	rp	-0.102	0.050	0.031	-0.229	0.048	0.179	0.057	-0.070	-0.086
PC60	rg	0.335	0.373	0.108	0.454	0.295	0.220	0.328	0.173	0.247
	rp	0.316	0.346	0.105	0.320	0.291	0.213	0.323	0.169	0.245
PC100	rg	0.032	0.057	-0.049	0.179	0.235	0.344	0.4895*	0.184	0.217
	rp	0.033	0.058	-0.050	0.114	0.232	0.335	0.4821*	0.184	0.216
TP	rg	-0.3788*	-0.3884*	-0.421	-0.342	0.5075*	0.5462**	0.213	-0.219	-0.275
	rp	-0.353	-0.359	-0.3968*	-0.195	0.4940*	0.5132*	0.201	-0.216	-0.269
NPP	rg	0.218	0.210	-0.040	0.109	0.286	0.350	0.7932**	0.198	0.274
	rp	0.193	0.180	-0.050	0.068	0.278	0.326	0.7567**	0.198	0.269
SI	rg	0.012	0.064	0.289	0.256	0.4317*	0.340	0.388	0.070	0.129
	rp	0.008	0.057	0.270	0.180	0.4273*	0.331	0.3821*	0.069	0.128
SYP	rg	-0.029	0.061	0.272	0.362	0.076	0.037	0.552	0.347	0.4356*
	rp	-0.030	0.052	0.253	0.253	0.077	0.035	0.5420**	0.344	0.4326*

Characters		RLWC60	RLWC100	LP60	LP100	PC60	PC100	TP	NPP	SI	SYP
RLWC60	rp	1.000									
	rg	1.000									
RLWC100	rp	0.8324**	1.000								
	rg	0.8268**	1.000								
LP60	rp	0.002	0.249	1.000							
	rg	0.001	0.244	1.000							
LP100	rp	0.062	0.037	-0.317	1.000						
	rg	0.065	0.038	-0.307	1.000						
PC60	rp	0.241	0.221	-0.089	0.375	1.000					
	rg	0.239	0.220	-0.087	0.372	1.000					
PC100	rp	0.348	0.4428*	-0.002	0.177	0.6155**	1.000				
	rg	0.344	0.4391*	-0.002	0.174	0.6121**	1.000				
TP	rp	0.6194**	0.6802**	0.4745*	-0.054	0.169	0.313	1.000			
	rg	0.6007**	0.6634**	0.4601*	-0.047	0.166	0.302	1.000			
NPP	rp	0.3934*	0.3809*	-0.232	-0.014	0.4044*	0.5805**	0.073	1.000		
	rg	0.3794*	0.373	-0.227	-0.012	0.3932*	0.5652**	0.072	1.000		
SI	rp	-0.061	-0.129	-0.225	0.017	0.352	0.243	-0.188	0.5871**	1.000	
	rg	-0.061	-0.128	-0.222	0.017	0.351	0.242	-0.183	0.5723**	1.000	
SYP	rp	-0.090	-0.224	-0.153	-0.119	0.218	0.252	-0.298	0.6151**	0.8757**	1.000
		-0.090	-0.222	-0.151	-0.118	0.216	0.251	-0.287	0.6046**	0.8737**	1.000

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

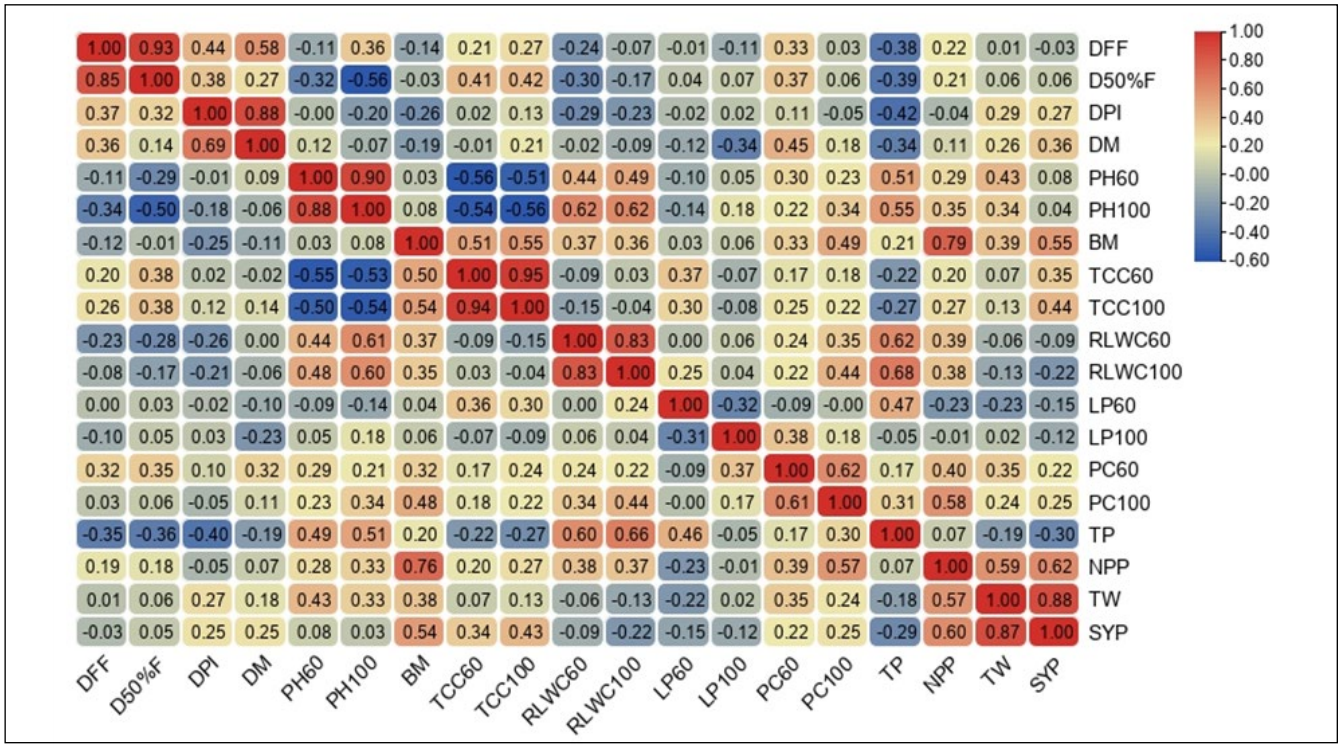

Figure 1: Correlation between various traits at genotypic and phenotypic level heat map

highly significant and positive correlations both at genotypic and phenotypic levels with seed index (r_g=0.875, r_p=0.873), Biomass (r_p=0.542), and number of pod plant^{-1} (r_g=0.615, r_p=0.604). It also manifested the significant positive correlation at both genotypic and phenotypic level with Total chlorophyll content at 100 DAS (r_g=0.435, r_p=0.432). The analysis indicated that the number of pods per plant and seed index demonstrated a highly significant correlation, both genotypically and phenotypically, with seed yield plant^{-1} under controlled and saline conditions. These two traits can be effectively used for indirect selection of higher yield. Additionally, biomass showed significant genotypic and phenotypic correlation with seed yield plant^{-1} under saline conditions, indicating that it can be considered an important parameter for selecting high yielding lines.

Arshad et al. (2003) observed a positive and significant correlation between seed yield and plant height, pods plant^{-1}, and seed weight. Durga et al. (2007) also reported a positive correlation between yield and pods plant^{-1}. Turner et al. (2013) and Tutlani et al. (2023) found that under salinity conditions, seed yield showed a positive correlation with total chlorophyll, relative water content, filled pods, and 100 seed weight, indicating that these traits are considered to be tolerant under salinity conditions. However, correlation alone is not sufficient to represent indirect parameters for selecting higher yield, as a trait with significant correlation must have a higher effect on yield. Therefore, traits that have both a high correlation and a high effect can be used for indirect selection of yield.

3.3. Path coefficient analysis at genotypic level under 60 mM saline condition

Under 60 mM saline condition, the genotypic level analysis revealed presented in Table 4 revealed that seed yield plant^{-1} had a highly positive direct effect on days to first flowering, days to pod initiation, plant height at 100 DAS, total chlorophyll content at 60 DAS, total protein content, and number of pods plant^{-1}. On the other hand, there was a highly negative direct effect with days to 50% flowering and relative water content at 100 DAS. Additionally, a moderately positive direct effect was observed with relative water content at 60 DAS and seed index.

The phenotypic analysis presented in Table 5 revealed that plant height at 100 DAS had a very highly negative direct effect on seed yield plant^{-1}, while days to maturity, plant height at 60 DAS, relative water content at 60 DAS, lipid

Table 4: Path coefficient analysis at genotypic level under 60 mM saline condition

	DFF	DF 50%	DPI	DM	PH 60	PH 100	BM	TC 60	TC 100	RWC 60	RWC 100
DFF	0.320	0.296	0.142	0.186	-0.035	-0.114	-0.045	0.068	0.088	-0.076	-0.023
DF 50%	-0.430	-0.465	-0.175	-0.126	0.149	0.258	0.014	-0.192	-0.195	0.141	0.081
DPI	0.182	0.155	0.411	0.362	-0.001	-0.083	-0.108	0.008	0.052	-0.118	-0.095
DM	-0.056	-0.026	-0.084	-0.095	-0.012	0.006	0.018	0.001	-0.020	0.002	0.009
PH 60	-0.001	-0.004	0.000	0.001	0.011	0.010	0.000	-0.006	-0.006	0.005	0.006
PH 100	-0.193	-0.300	-0.108	-0.035	0.487	0.539	0.043	-0.294	-0.302	0.335	0.336
BM	0.016	0.003	0.029	0.021	-0.004	-0.009	-0.111	-0.057	-0.061	-0.041	-0.040
TC 60	0.185	0.360	0.018	-0.006	-0.486	-0.475	0.443	0.872	0.828	-0.080	0.030
TC 100	0.019	0.028	0.009	0.014	-0.034	-0.038	0.037	0.064	0.068	-0.010	-0.003
RWC 60	-0.071	-0.091	-0.086	-0.007	0.132	0.186	0.111	-0.028	-0.044	0.299	0.249
RWC 100	0.084	0.205	0.271	0.106	-0.580	-0.734	-0.421	-0.041	0.045	-0.981	-1.179
LP 60	0.001	-0.006	0.004	0.020	0.017	0.023	-0.005	-0.060	-0.049	0.000	-0.040
LP 100	0.006	-0.004	-0.001	0.020	-0.003	-0.011	-0.003	0.004	0.005	-0.004	-0.002
PC 60	-0.052	-0.058	-0.017	-0.071	-0.046	-0.034	-0.051	-0.027	-0.039	-0.038	-0.035
PC 100	0.000	0.000	0.000	0.000	0.001	0.001	0.001	0.000	0.001	0.001	0.001
TP	-0.164	-0.168	-0.182	-0.148	0.220	0.236	0.092	-0.095	-0.119	0.268	0.294
NPP	0.123	0.119	-0.023	0.062	0.162	0.198	0.449	0.112	0.155	0.223	0.216
SI	0.003	0.015	0.066	0.058	0.098	0.077	0.088	0.016	0.029	-0.014	-0.029
SYP	-0.029	0.061	0.272	0.362	0.076	0.037	0.552	0.347	0.436	-0.090	-0.224
Partial R^2	-0.009	-0.028	0.112	-0.035	0.001	0.020	-0.062	0.302	0.029	-0.027	0.264

Table 4: Continue...

	LP 60	LP 100	PC 60	PC 100	TP	NPP	SI
DFF	-0.002	-0.034	0.107	0.010	-0.121	0.070	0.004
DF 50%	-0.017	-0.032	-0.173	-0.027	0.180	-0.097	-0.030
DPI	-0.009	0.008	0.044	-0.020	-0.173	-0.017	0.119
DM	0.012	0.033	-0.043	-0.017	0.033	-0.010	-0.024
PH 60	-0.001	0.001	0.003	0.003	0.006	0.003	0.005
PH 100	-0.077	0.098	0.119	0.186	0.295	0.189	0.184
BM	-0.004	-0.006	-0.037	-0.055	-0.024	-0.088	-0.043
TC 60	0.324	-0.061	0.151	0.160	-0.191	0.172	0.061
TC 100	0.021	-0.006	0.017	0.015	-0.019	0.019	0.009
RWC 60	0.001	0.019	0.072	0.104	0.185	0.118	-0.018
RWC 100	-0.294	-0.043	-0.261	-0.522	-0.802	-0.449	0.152
LP 60	-0.161	0.051	0.014	0.000	-0.076	0.037	0.036
LP 100	0.019	-0.060	-0.022	-0.011	0.003	0.001	-0.001
PC 60	0.014	-0.058	-0.156	-0.096	-0.026	-0.063	-0.055
PC 100	0.000	0.000	0.001	0.002	0.001	0.001	0.001
TP	0.205	-0.023	0.073	0.135	0.433	0.032	-0.081
NPP	-0.131	-0.008	0.229	0.328	0.041	0.566	0.332
SI	-0.051	0.004	0.080	0.055	-0.043	0.134	0.227
SYP	-0.153	-0.119	0.218	0.252	-0.298	0.615	0.876
Partial R^2	0.025	0.007	-0.034	0.001	-0.129	0.348	0.199

R Square = 0.9847; Residual effect=0.1235

Table 5: Path coefficient analysis at phenotypic level under 60 mM saline condition

	DFF	DF 50%	DPI	DM	PH 60	PH 100	BM	TC 60	TC 100	RWC 60	RWC 100
DFF	-0.226	-0.192	-0.083	-0.082	0.025	0.077	0.026	-0.045	-0.059	0.051	0.017
DF 50%	-0.219	-0.257	-0.082	-0.036	0.075	0.129	0.003	-0.098	-0.099	0.073	0.044
DPI	-0.128	-0.111	-0.349	-0.239	0.003	0.064	0.087	-0.006	-0.040	0.090	0.074
DM	0.125	0.047	0.235	0.342	0.031	-0.022	-0.036	-0.006	0.047	0.002	-0.020
PH 60	-0.042	-0.111	-0.003	0.034	0.383	0.335	0.013	-0.209	-0.193	0.168	0.185
PH 100	0.357	0.527	0.191	0.068	-0.918	-1.049	-0.088	0.553	0.570	-0.636	-0.631
BM	0.055	0.006	0.118	0.051	-0.016	-0.040	-0.478	-0.238	-0.256	-0.176	-0.166
TC 60	-0.002	-0.003	0.000	0.000	0.004	0.004	-0.004	-0.008	-0.008	0.001	0.000
TC 100	0.031	0.045	0.014	0.016	-0.059	-0.064	0.063	0.110	0.117	-0.017	-0.005
RWC 60	-0.087	-0.108	-0.099	0.002	0.169	0.233	0.141	-0.036	-0.057	0.384	0.317
RWC 100	0.009	0.020	0.025	0.007	-0.057	-0.071	-0.041	-0.004	0.005	-0.098	-0.119
LP 60	0.001	0.011	-0.007	-0.034	-0.032	-0.045	0.012	0.121	0.099	0.000	0.081
LP 100	-0.031	0.015	0.010	-0.070	0.015	0.055	0.018	-0.021	-0.026	0.020	0.012
PC 60	-0.093	-0.101	-0.031	-0.094	-0.085	-0.062	-0.095	-0.050	-0.072	-0.070	-0.065
PC 100	0.006	0.011	-0.010	0.022	0.044	0.064	0.092	0.035	0.041	0.066	0.084
TP	0.078	0.080	0.088	0.043	-0.110	-0.114	-0.045	0.048	0.060	-0.133	-0.147

Table 5: Continue...

	DFF	DF 50%	DPI	DM	PH 60	PH 100	BM	TC 60	TC 100	RWC 60	RWC 100
NPP	0.126	0.118	-0.033	0.045	0.182	0.213	0.494	0.130	0.176	0.248	0.244
SI	0.008	0.057	0.269	0.179	0.425	0.329	0.380	0.068	0.127	-0.061	-0.128
SYP	-0.030	0.052	0.253	0.253	0.077	0.035	0.542	0.344	0.433	-0.090	-0.222
Partial R^2	0.007	-0.014	-0.089	0.087	0.030	-0.036	-0.259	-0.003	0.051	-0.035	0.026

Table 5: Continue...

	LP 60	LP 100	PC 60	PC 100	TP	NPP	SI
DFF	-0.001	0.023	-0.071	-0.008	0.080	-0.043	-0.002
DF 50%	-0.008	-0.013	-0.089	-0.015	0.092	-0.046	-0.015
DPI	0.008	-0.011	-0.037	0.018	0.139	0.017	-0.095
DM	-0.035	-0.078	0.110	0.039	-0.067	0.023	0.062
PH 60	-0.036	0.018	0.111	0.089	0.189	0.107	0.164
PH 100	0.142	-0.188	-0.224	-0.352	-0.539	-0.342	-0.347
BM	-0.018	-0.027	-0.154	-0.230	-0.096	-0.361	-0.183
TC 60	-0.003	0.001	-0.001	-0.002	0.002	-0.002	-0.001
TC 100	0.035	-0.010	0.029	0.025	-0.032	0.031	0.015
RWC 60	0.000	0.025	0.092	0.132	0.231	0.146	-0.024
RWC 100	-0.029	-0.005	-0.026	-0.052	-0.079	-0.044	0.015
LP 60	0.334	-0.102	-0.029	-0.001	0.154	-0.076	-0.074
LP 100	-0.094	0.305	0.114	0.053	-0.014	-0.004	0.005
PC 60	0.025	-0.109	-0.293	-0.179	-0.049	-0.115	-0.103
PC 100	0.000	0.033	0.117	0.191	0.058	0.108	0.046
TP	-0.102	0.011	-0.037	-0.067	-0.222	-0.016	0.041
NPP	-0.148	-0.008	0.257	0.369	0.047	0.653	0.374
SI	-0.221	0.017	0.349	0.240	-0.182	0.569	0.994
SYP	-0.151	-0.118	0.217	0.251	-0.287	0.605	0.874
Partial R^2	-0.050	-0.036	-0.063	0.048	0.064	0.395	0.869

R Square=0.9847; Residual effect=0.1235

peroxidation at 60 and 100 DAS, number of pods plant^{-1}, and seed index had highly positive direct effects on seed yield plant^{-1}. Days to pod initiation and biomass had highly negative direct effects, while days to first flowering, days to 50% flowering, proline content at 60 DAS, and total protein had moderately negative direct effects on seed yield plant^{-1}. Relative water content at 60 DAS, number of pods plant^{-1}, and seed index showed direct positive phenotypic effects on yield, indicating that an increase in these traits under moderate salinity conditions could lead to an increase in seed yield.

According to Kanouni et al. (2012), their study revealed that the genotypic path coefficient analysis based on seed yield plant^{-1} demonstrated significant positive direct effects, with vigour, days to maturity, and 100–seed weight exhibiting the most significant direct influence. Based on these findings, the research proposes that drought tolerance score and pod plant^{-1} could serve as effective selection criteria for enhancing seed yield plant^{-1} in drought-stressed chickpea environments. Atieno et al. (2017) conducted path analysis and found that under non-saline conditions, 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 impact on seed yield through the number of filled pods and seed number. Additionally, the number of filled pods had a moderate indirect positive impact on seed yield through seed number. Under salinity conditions, the number of filled pods and seed number had a moderate positive direct impact on seed yield, whereas 100–seed weight had a weak positive direct impact on seed yield. Similarly, the total number of pods had a moderate indirect positive impact on seed yield

through the number of filled pods and seed number, and the number of filled pods had a moderate indirect positive impact on seed yield through seed number.

4. CONCLUSION

Proline content, relative water content, number of pods per plant, and seed index showed higher positive direct genotypic effect, suggesting that indirect selection for these traits could lead to an increase in yield at high salinity levels.

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