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Research Paper

Genetic studies through generation mean analysis in chickpea under timely and delayed planting

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ABSTRACT

Afield experiment was conducted to study gene effects by using 6 generations (P_1, P_2, F_1, F_2, B_1 and B_2) of each of four crosses (RSG-973 × HC-5, RSG-963 × RSG-973, CSJD-884 × Avrodhi and RSG-974 × CSJ-515). The G × E interaction was found significant in each cross for all characters. The mean performance was greater for every character in every generation of every cross under timely sowing compared to late sowing conditions. The environment and the genetic constitution of parents used in the crosses affected the magnitude as well asthe direction of the various components of the gene (d, h, i, j, and l) in the majority of cases. Duplicate epistasis was more prevalent than complementary epistasis. The magnitude of dominance effects and epistasis effects were observed higher than additive and main effects, respectively. Under both conditions, mostly crosses for various traits showed the prevalence of non-additive type of gene effects (h, j, and l).

Key words**:** Chickpea, gene interaction, duplicate epistasis, complementary epistasis

INTRODUCTION

Legumes have a pivotal part in human nutrition; they not only supplement the diet with nutrients but also enhance the flavor and texture of staple foods (Varol *et al.* 2020). The Leguminosae family, which includes legumes, comprises 20,000 species and up to 750 genera (Graham and Vance 2003). Chickpea (Bengal gram) stands third in popularity globally, following dry beans and peas (Yegrem 2021). *Desi* and *Kabuli* are two commercial types of chickpea, which are separated based on the size of the seeds and their place of origin. *Desi* type shares 85 % of the total chickpea production and Indian origin. Chickpea yield declines have been mostly attributed to global climate instability and future food security in underdeveloped nations may be seriously threatened by this climatic shift (Jameel *et al*. 2021, Prasanthi *et al*. 2023). The present areas under the cultivation of chickpeas are in danger due to rising temperatures, according to research on climate change and production patterns (Berger *et al.* 2011, Devasirvatham and Tan 2018). Over the past thirty years, India's chickpea farming scenarios have seen major changes, moving from the heated, regions having shorter seasonsinthe middle and south of India to the colder, long-season habitats of northern India (Gaur *et al.* 2008, Gowda *et al.* 2009). It is commonly known that during blooming and podding, chickpeas are particularly sensitive to environmental changes. Plants exposed to high temperatures when the post-flowering period showed a substantial reduction in seed yield (Khetarpal *et al.* 2009, Devasirvatham *et al.* 2012, Mohapatra *et al.* 2020).

The nature of the gene effect may be used to predict the efficacy of selection for any traits in populations. A plant breeder may create a more successful breeding program by having a clear understanding of types of gene effects, their magnitude, and genetic variations. Information on gene effect and the proportion of its genetic components (additive and dominant) has been estimated through the use of line-tester and differential analysis. However, it does not offer an idea of non-allelic gene effects functioning in the inheritance process, in contrast to generation mean analysis, there is limited information on the dynamics of water and heat balance for chickpea during reproductive stages on these aspects. It is, therefore, imperative to analyze the factors involved in better plant water status influencing yield in chickpea.

MATERIALS AND METHODS

In the present study, seven genetically different genotypes (HC-5, RSC-973, RSG-963, CSJD-884, Avrodhi, CSG-515 and RSG-974) of chickpea were obtained from RARI, Durgapura, Jaipur based on the broad genetic variability for the main components of yield. To generate F_1s, the parental genotypes were crossed following a specific method in the *Rabi* season of 2019–20. The parental genotypes and their corresponding F_1s were then planted during the *Rabi* season of 2020-21, resulting F_1, F_2, B_1, and B_2 generations generated. The material included 4 single crosses: RSG-973 × HC-5 (C1), RSG-963 × RSG-973 (C2), CSJD-884 × Avrodhi (C3) and RSG-974 × CSJ-515 (C4). During Rabi 2021–2022, a total of 24 treatments (4 crosses and their 6 generations each) were raised in a compact family block design in three replications at the RARI in Jaipur, Rajasthan, India. Different planting dates-first in November and the second in December of 2021, respectively created two environments. The number of rows in the plots for the various generations varied, with two rows for each parent and F_1, four rows for each backcross (B_1 and B_2), and six rows for the F_2 generations. The observations were recorded onprimary branches per plant, secondary branches per plant, pods per plant, 100 seed weight (g), biological yield per plant (g), and seed yield per plant (g). The Hayman and Mather (1955) individual scaling tests (A, B, C, and D) were employed to evaluate the suitability of the additive-dominant model. According to Jinks and Jones (1958), the estimates and magnitudes of main gene effects were determined for crosses in which the additive-dominance model was appropriate. In cases when the additive-dominance model proved to be insufficient, Hayman's (1958), six-parameter model was employed to assess different types of gene effects.

RESULTS AND DISCUSSION

The effects of environments on character expression were shown by the pooled ANOVA over environments, which indicated significant variations between environments in all crosses for allstudied traits (Table 1). For every character in every cross, the interaction between generation and environment was equally significant. Allard and Bradshaw (1964) agreed with the general belief that the genotype × environment interaction is common in crop plant species. In comparison to delayed planting (E2), the mean value was found greater for all traits in various generations in all crosses under timely sowed (E1) conditions (Figs. 1 and 2). The considerable reduction under late sown conditions was also noticed by Prasad *et al.* (2018) and Thombre *et al.* (2019) in chickpea. In almost all of the crosses for every character under both timely (E1) and delayed planting (E2), the mean values of F_1s were seen to be typically greater than the means of the parents, whilst the mean values of F_2s were found to be generally lower value than F_1s.

To estimate the genetic components of variation, the three-parameter model/additive-dominance model was employed, as the lack of significance of all individual scaling tests advocated the absence of interaction effects. The parameter model was used to evaluate the impacts of different genes when the additive-dominance model proved to be inadequate as demonstrated by any significant individual scaling test results. A significant number of crosses for every character under both conditions showed at least one of the four scaling (A, B, C, and D), with the exception of the following: primary branches per plant in RSG-973 × RSG-973 (E1) and RSG 974 × CSJ-515 (E2), secondary branches per plant in CSJD-884 × Avrodhi (E1), pods per plant in RSG-973 × HC-5 (E2), and biological yield per plant in RSG-974 × CSJ-515 (E1).

All of the characters under study in each cross had a significant value for the "m" component of the gene effect, indicating that the generations under study differed statistically from one another and that there was enough variability between them (Tables 3 and 4). The duplicate type of epistasis indicated by significant estimates of dominance effect (h) and dominance × dominance effect (l) components were observed for secondary branches per plant in RSG-973 × HC-5 and RSG-963 × RSG-973 under E1 and CSJD-884 × Avrodhi under E2; for 100-seed weight in RSG-973 × HC-5 under both conditions; for seed yield per plant in CSJD-884 × Avrodhi under E2; for biological yield per plant in RSG 963 × RSG-973 under E1. The results corroborated the findings in several chickpea crosses (Kumhar *et al.* 2013, Deshmukh and Gawande 2016, Samad *et al.* 2016). Because duplicate types of epistasis can impede progress and make it challenging to fix genotypes at substantial levels of manifestation, it may result in inaccurate selection in the early generations of segregation. However, by inter-mating the chosen segregants and postponing selection for further generations, such gene effects can be taken advantage of (Sundaram *et al.* 2018).

Heritable-fixable is the additive effect (d) and additive ×additive effect (i) (Mather 1949). For each

Table 1. Pooled analysis of variance (mean squares) for seed yield and its attributing traits in four crosses of chickpea

Crosses	Source of variations/d.f.				
	Env. (1)	Rep. × Env. (2)	Gen. (5)	Gen. × Env. (5)	Error (20)
Primary branches per plant					
RSG-973 × HC-5 (C1)	1.138*	0.010	0.454*	0.084*	0.026
RSG-963 × RSG-973 (C2)	0.810*	0.006	0.478*	0.093*	0.034
CSJD-884 × Avrodhi (C3)	3.868**	0.054	0.826*	0.104**	0.020
RSG-974 × CSJ-515 (C4)	2.525*	0.041	0.215	0.209*	0.051
Secondary branches per plant					
RSG-973 × HC-5 (C1)	8.999**	0.215	2.693*	0.461*	0.150
RSG-963 × RSG-973 (C2)	16.741**	0.425	5.964*	0.717*	0.258
CSJD-884 × Avrodhi (C3)	15.800**	0.105	8.958*	0.839*	0.301
RSG-974 × CSJ-515 (C4)	10.671**	0.149	1.778	0.559**	0.115
Pods per plant					
RSG-973 × HC-5 (C1)	158.340**	1.005	19.357	6.972**	1.158
RSG-963 × RSG-973 (C2)	95.556**	1.520	26.766	5.635**	1.051
CSJD-884 × Avrodhi (C3)	471.613**	2.624	320.723**	14.686**	2.580
RSG-974 × CSJ-515 (C4)	361.957**	1.788	185.825**	11.054**	2.163
100-seed-weight (g)					
RSG-973 × HC-5 (C1)	23.424**	0.192	4.652**	0.424*	0.155
RSG-963 × RSG-973 (C2)	19.784**	0.117	7.749*	0.740**	0.145
CSJD-884 × Avrodhi (C3)	22.477**	0.171	4.471**	0.351*	0.117
RSG-974 × CSJ-515 (C4)	22.457**	0.266	3.973*	0.695*	0.181
Seed yield per plant (g)					
RSG-973 × HC-5 (C1)	9.508**	0.112	0.558	0.305**	0.058
RSG-963 × RSG-973 (C2)	6.176**	0.134	2.089*	0.256*	0.078
CSJD-884 × Avrodhi (C3)	9.481**	0.140	3.550*	0.468*	0.157
RSG-974 × CSJ-515 (C4)	6.041**	0.038	3.983**	0.360*	0.088
Biological yield per plant (g)					
RSG-973 × HC-5 (C1)	111.392*	0.209	4.645	7.582**	0.593
RSG-963 × RSG-973 (C2)	44.301*	1.368	7.443	4.852**	0.890
CSJD-884 × Avrodhi (C3)	21.692**	0.292	4.637*	0.904*	0.244
RSG-974 × CSJ-515 (C4)	13.953*	0.444	5.834	1.381*	0.347

*,** Significant at 5 per cent and 1 per cent, respectively

plant's secondary branches, additive effect (d) and additive × additive effect (i)were more prevalent under E2 in RSG-973 × HC-5. It was predicted that early segregating generations of these crosses would respond very well to the direct selection of secondary branches per plant. Samad *et al.* (2016) and Nehra *et al.* (2020) also noted that distinct morphological traits in chickpea showed a majority of additive effect (d) and/or additive × additive effect (i).

Non-additive (h and/or j and/or l) gene effects predominated, accompanied by the presence of additive effect (d) and/or additive × additive effect (i), as evident in various crossbreeds and environmental conditions. Specifically, these impacts were noted for primary branches/plant in RSG-973 × HC-5 and RSG-974 × CSJ-515 under E1, as well as RSG-963 × RSG-973 under E2. Additionally, they were noted for secondary branches per plant in RSG-973 × HC-5 and RSG-974 × CSJ-515 under E1, and CSJD-884 × Avrodhi under E2. Furthermore, pods per plant exhibited similar patterns in various crosses and conditions, such as RSG-973 × HC-5 under E1, RSG-963 × RSG-973 under E2, and CSJD-884 × Avrodhi, as well as RSG-974 × CSJ-515 under both E1 and E2. For 100-seed weight, the presence of a non-additive effect was observed in CSJD-884 × Avrodhi and RSG-974 × CSJ-515 under E2, and RSG-973 × HC-5. Similar trends were noted for seed yield per plant in most crosses under both E1 and E2, and for biological yield per plant in RSG-973 × HC-5 under E1, RSG-974 × CSJ-515 under E2, and RSG-963 × RSG-973 under both E1 and E2 (Table 3 and Table 4). The present results concur with the verdict of Mujjassim *et al.* (2018), Najan and Kadam (2018), Nehra *et al.* (2020) and Ghasemi *et*

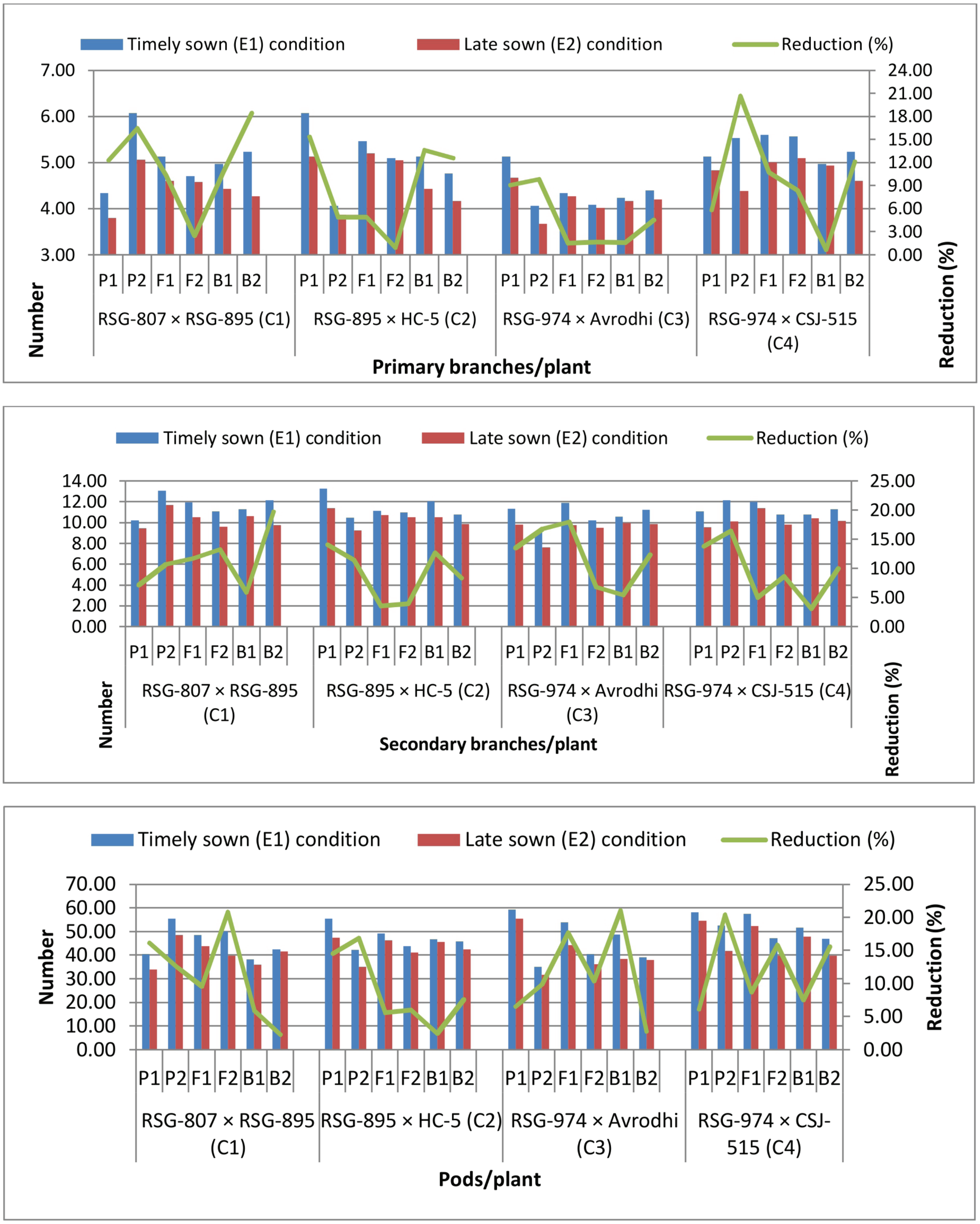

Fig. 1. Mean performance of all six generations of all four crosses of primary branches per plant, secondary branches per plant and pods per plant under timely (E1) and delayed planting (E2) and reduction percent (C1-RSG-973 × HC-5, C2-RSG-963 × RSG-973, C3-CSJD-884 × Avrodhi, C4-RSG-974 × CSJ-515)

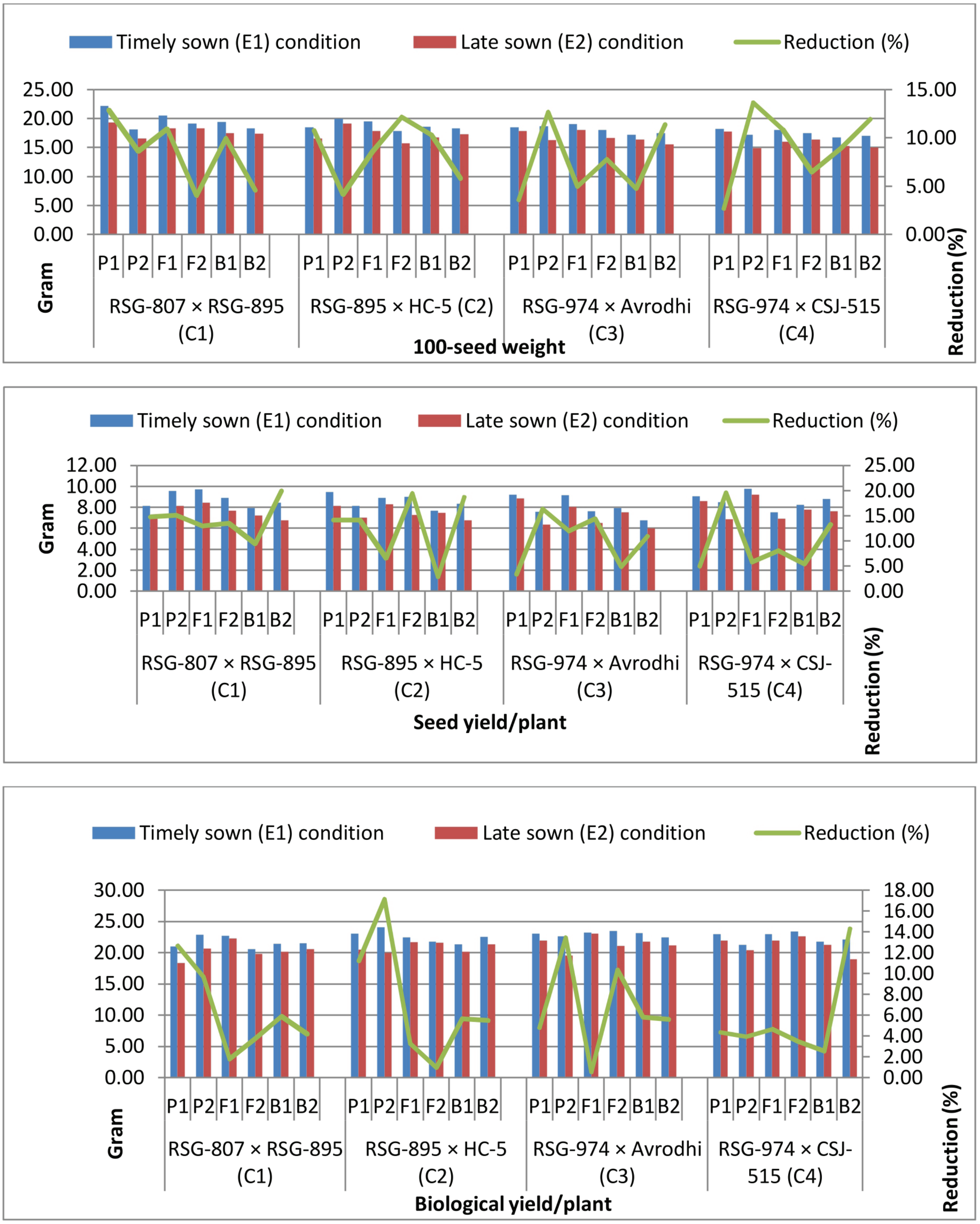

Fig. 2. Mean performance of all six generations of all four crosses of 100-seed weight, seed yield per plant and biological yield per plant under timely (E1) and delayed planting (E2) and reduction percent (C1-RSG-973 × HC-5, C2-RSG-963 × RSG-973, C3-CSJD-884 × Avrodhi, C4-RSG-974 × CSJ-515)

Table 2. Estimates of individual scaling tests of four crosses for all studied traits under timely (E1) and delayed planting (E2)

	RSG-973 × HC-5 (C1)		RSG-963 × RSG-973 (C2)		CSJD-884 × Avrodhi (C3)		RSG-974 × CSJ-515 (C4)	
	E1	E2	E1	E2	E1	E2	E1	E2
Primary branches per plant								
A	-0.66 ± 0.59	-0.33 ± 0.46	-0.93 ± 0.54	-1.73** ± 0.44	-1.46* ± 0.55	-1.40** ± 0.47	-0.80 ± 0.53	-0.19 ± 0.47
B	-0.60 ± 0.56	0.06 ± 0.46	-0.73 ± 0.56	-0.53 ± 0.48	-0.93 ± 0.54	-0.40 ± 0.41	-0.66 ± 0.52	-0.33 ± 0.46
C	0.60 ± 0.94	1.20 ± 0.81	-1.46 ± 1.07	-0.73 ± 0.74	-2.20** ± 0.83	-3.00** ± 0.78	0.39 ± 0.83	0.80 ± 0.90
D	0.93* ± 0.37	0.73* ± 0.33	0.09 ± 0.48	0.76* ± 0.34	0.09 ± 0.37	-0.59 ± 0.35	0.93* ± 0.41	0.66 ± 0.40
Secondary branches per plant								
A	2.46** ± 0.92	0.01 ± 0.8	0.93 ± 0.91	1.40 ± 1.11	-1.40 ± 0.99	1.00 ± 0.91	-1.53 ± 0.96	-0.06 ± 0.79
B	1.40 ± 1.02	1.86* ± 0.92	2.46* ± 1.12	1.53 ± 0.89	0.40 ± 1.04	0.59 ± 0.99	-1.53 ± 1.11	-1.20 ± 0.75
C	0.73 ± 1.55	1.26 ± 1.27	1.33 ± 1.59	4.26* ± 1.64	-3.00 ± 1.57	-3.26* ± 1.40	-4.20* ± 1.69	-3.19* ± 1.39
D	-1.56* ± 0.64	-0.29 ± 0.65	-1.03 ± 0.77	0.66 ± 0.82	-0.99 ± 0.68	-2.43** ± 0.70	-0.56 ± 0.72	-0.96 ± 0.63
Pods per plant								
A	-1.06 ± 2.51	3.86 ± 2.88	-3.13 ± 3.38	-5.86 ± 3.16	-15.86** ±3.52	-1.59 ± 3.70	-12.33** ± 2.91	-11.53** ± 3.57
B	3.46 ± 3.22	-0.73 ± 3.19	-6.93* ± 3.40	-4.00 ± 3.33	-15.13** ±3.77	-13.93** ± 3.31	-15.93** ± 2.76	-14.86** ± 4.29
C	-6.13 ± 4.80	2.33 ± 5.35	-13.06* ± 5.29	-19.86** ± 5.67	-32.20** ±5.49	-26.73** ± 6.37	-36.60** ± 4.36	-42.20** ± 6.35
D	-4.26* ± 1.95	-0.39 ± 2.01	-1.50 ± 2.11	-5.00* ± 2.38	-0.60 ± 2.84	-5.60 ± 3.28	-4.16* ± 2.03	-7.89* ± 3.11
100-seed weight								
A	-0.95 ± 0.58	1.04 ± 0.63	4.28** ± 0.94	1.42* ± 0.69	-1.81* ± 0.7	-4.07** ±0.63	-2.82** ±0.92	-3.33** ±0.88
B	2.04* ± 0.81	2.03* ± 0.80	0.06 ± 1.38	-1.74 ± 1.13	-1.74* ± 0.71	-1.89** ±0.65	-1.20 ± 0.97	-0.96 ± 0.92
C	-3.72** ±0.95	-4.89** ±1.19	1.56 ± 1.37	-0.85 ± 1.33	-4.03**±1.22	-7.02** ±0.94	-1.55 ± 1.46	0.68 ± 1.40
D	-2.40** ±0.49	-3.98** ±0.61	-1.39 ± 0.97	-0.26 ± 0.77	-0.23 ± 0.47	-0.52 ± 0.42	1.23 ± 0.71	2.49** ±0.66
Seed yield per plant								
A	0.22 ± 0.52	0.31 ± 0.44	-0.98 ± 0.75	-1.97** ± 0.61	-4.66**±0.59	-2.18** ±0.68	-2.33** ±0.62	-2.20** ±0.45
B	-0.19 ± 0.53	-2.13** ±0.48	-2.14** ±0.69	-3.16** ± 0.62	-2.98**±0.67	-2.30** ±0.62	-0.65 ± 0.65	-0.75 ± 0.63
C	-2.02* ± 0.84	-0.36 ± 0.71	-3.82** ±1.02	-4.46** ± 0.96	-5.01**±0.98	-0.55 ± 0.80	-7.02** ±0.76	-6.18** ±0.65
D	-1.02* ± 0.43	0.72 ± 0.38	-0.34 ± 0.51	0.33 ± 0.45	1.31** ±0.47	1.96** ± 0.47	-2.02** ±0.47	-1.60** ±0.42
Biological yield per plant								
A	-5.45** ±1.22	4.21** ± 1.26	2.70* ± 1.21	1.86 ± 1.54	1.38 ± 1.62	0.19 ± 1.33	-2.35 ± 1.2	-1.40 ± 1.34
B	-1.06 ± 1.14	2.96* ± 1.17	-1.27 ± 1.40	-1.54 ± 1.45	-3.94* ±1.77	-3.12* ± 1.36	0.01 ± 1.54	-4.40** ±1.46
C	-13.33*±1.87	3.80 ± 2.23	-9.90** ±1.99	-6.86** ± 1.98	-1.11 ± 2.74	0.61 ± 2.34	3.45 ± 2.82	4.17 ± 3.01
D	-3.40** ±0.96	-1.68 ± 0.94	-5.66** ±1.0	-3.59** ± 1.01	0.72 ± 1.22	1.77 ± 0.92	2.89 ± 1.50	4.99** ± 1.60

Table 3. Estimates of gene effects using six generations of four crosses for primary branches per plant, secondary branches per plant and pods per plant

	RSG-973 × HC-5 (C1)		RSG-963 × RSG-973 (C2)		CSJD-884 × Avrodhi (C3)		RSG-974 × CSJ-515 (C4)	
	E1	E2	E1	E2	E1	E2	E1	E2
Gene effects (Three or six parameter model) and type of epistasis								
Primary branches per plant								
m	4.70** ± 0.13	4.36** ± 0.12	5.20** ± 0.98	4.43** ± 0.12	4.38** ± 0.12	3.55** ± 0.13	5.56** ± 0.15	6.00** ± 0.83
d	0.40 ± 0.25	0.01 ± 0.21	0.06 ± 0.18	-0.29 ± 0.24	0.13 ± 0.28	-0.23 ± 0.21	-0.26 ± 0.28	0.26 ± 0.16
h	-1.50 ± 0.84	-1.33 ± 0.73	-2.33 ± 2.35	-1.43 ± 0.73	-0.19 ± 0.82	1.66* ± 0.75	-1.60 ± 0.88	-2.73 ± 0.20
i	-1.86* ± 0.74	-1.46* ± 0.66	-	-1.53* ± 0.68	-0.19 ± 0.74	1.20 ± 0.70	-1.86* ± 0.83	-
j	-0.03 ± 0.35	-0.20 ± 0.26	-	-0.59* ± 0.28	-0.26 ± 0.33	-0.50 ± 0.27	-0.06 ± 0.34	-
l	3.13* ± 1.37	1.73 ± 1.17	-	3.80** ± 1.22	2.60 ± 1.40	0.60 ± 1.17	3.33* ± 1.40	-
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Secondary branches per plant								
m	10.38** ± 0.22	9.71** ± 0.21	11.45** ±0.27	10.66** ± 0.31	9.26** ± 1.42	8.90** ± 0.23	10.75**±0.27	9.81** ± 0.24
d	-0.13 ± 0.46	-1.46** ± 0.49	0.13 ± 0.55	1.40* ± 0.54	1.93** ± 0.37	1.70** ± 0.52	-0.53 ± 0.48	0.26 ± 0.39
h	3.53* ± 1.43	1.66 ± 1.38	3.43* ± 1.66	-0.79 ± 1.73	2.73 ± 3.75	5.96** ±1.50	1.53 ± 1.59	3.50* ± 1.35
i	3.13* ± 1.29	0.60 ± 1.30	2.06 ± 1.55	-1.33 ± 1.65	-	4.86** ±1.41	1.13 ± 1.45	1.93 ± 1.26
j	0.53 ± 0.57	-0.93 ± 0.53	-0.76 ± 0.64	-0.06 ± 0.66	-	0.20 ± 0.60	0.01 ± 0.64	0.56 ± 0.46
l	-7.00** ± 2.42	-2.46 ± 2.34	-5.46* ± 2.73	-1.60 ± 2.72	-	-6.46* ±2.52	1.93 ± 2.58	-0.66 ± 2.09

	Duplicate	--	Duplicate	--	--	Duplicate	--	--
Pod per plant								
m	42.78** ± 0.74	37.33** ±4.19	44.16** ± 0.7	39.68** ±0.96	40.23**±0.96	32.66**±1.31	47.25** ± 0.72	39.76**±1.12
d	-0.23 ± 1.27	2.26 ± 1.15	2.10 ± 1.58	1.76 ± 1.41	9.86** ± 2.07	12.73**±1.95	4.59** ± 1.43	8.03** ± 2.16
h	9.10* ± 4.34	8.39 ± 10.61	4.26 ± 4.78	13.76** ±5.21	6.90 ± 6.00	14.76* ±6.80	10.33* ± 4.38	19.96**±6.63
i	8.53* ± 3.91	-	3.00 ± 4.22	10.00* ± 4.77	1.20 ± 5.68	11.20 ± 6.56	8.33* ± 4.06	15.80* ±6.23
j	-2.26 ± 1.78	-	1.90 ± 1.99	-0.93 ± 2.04	-0.36 ± 2.29	6.16** ± 2.31	1.79 ± 1.83	1.66 ± 2.41
l	-10.93 ± 6.99	-	7.06 ± 8.25	-0.13 ±8.01	29.79**±9.96	4.33 ± 10.08	19.93** ± 7.20	10.60 ±10.75
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Table 4. Estimates of gene effects using six generations of four crosses for 100-seed weight, seed yield per plant, and biological yield per plant.

	RSG-973 × HC-5 (C1)		RSG-963 ×RSG-973 (C2)		CSJD-884 ×Avrodhi (C3)		RSG-974 × CSJ-515 (C4)	
	E1	E2	E1	E2	E1	E2	E1	E2
Gene effects (Three or six parameter model) and type of epistasis								
100-seed weight								
m	18.77** ± 0.15	16.68** ± 0.23	18.1** ± 0.28	16.54** ±0.25	17.83**±0.16	15.86** ± 0.12	17.48** ± 0.25	16.35**±0.23
d	-1.96** ± 0.38	-1.31** ± 0.39	0.07 ± 0.78	0.21 ± 0.56	-0.18 ± 0.34	-0.85* ± 0.33	-0.28 ± 0.51	0.26 ± 0.48
h	5.24** ± 1.05	7.52** ± 1.28	3.09 ± 1.98	1.32 ± 1.59	2.06 ± 1.08	3.08** ± 0.93	-2.20 ± 1.52	-5.26** ±1.43
i	4.81** ± 0.98	7.97** ± 1.22	2.78 ± 1.94	0.53 ± 1.54	0.46 ± 0.95	1.05 ± 0.84	-2.47 ± 1.43	-4.99** ±1.33
j	-1.50** ± 0.46	-0.49 ± 0.47	2.11* ± 0.80	1.58* ± 0.61	-0.03 ± 0.42	-1.09** ± 0.38	-0.80 ± 0.60	-1.18* ± 0.55
l	-5.90** ± 1.81	-11.05** ±1.98	-7.13* ± 3.43	-0.21 ± 2.64	3.10 ± 1.83	4.92** ± 1.63	6.50* ± 2.50	9.29** ± 2.39
	Duplicate	Duplicate	--	--	--	Complementary	--	Duplicate
Seed yield per plant								
m	7.94** ± 0.16	7.4** ± 0.14	7.17** ± 0.16	6.41** ± 0.15	7.15** ±0.16	6.78** ± 0.13	7.52** ± 0.13	6.91** ±0.12
d	0.14 ± 0.28	0.87** ± 0.26	0.42 ± 0.329	0.89** ± 0.32	-0.35 ± 0.34	0.35 ± 0.39	-0.57 ± 0.38	0.14 ± 0.34
h	2.68** ± 0.91	-0.97 ± 0.80	0.82 ± 1.10	-0.20 ± 0.97	-1.93 ± 1.02	-3.37** ± 0.99	5.05** ± 0.98	4.70** ±0.87
i	2.05* ± 0.87	-1.45 ± 0.77	0.69 ± 1.03	-0.67 ± 0.90	-2.63** ±0.95	-3.93** ± 0.94	4.04** ± 0.94	3.21** ±0.84
j	0.21 ± 0.35	1.22** ± 0.31	0.58 ± 0.47	0.59 ± 0.38	-0.83* ±0.39	0.06 ± 0.43	-0.83 ± 0.43	-0.72 ± 0.37
l	-2.07 ± 1.43	3.27* ± 1.27	2.43 ± 1.87	5.81** ± 1.61	10.28**±1.68	8.42** ± 1.75	-1.05 ± 1.72	-0.25 ± 1.53
	--	--	--	--	--	Duplicate	--	--
Biological yield per plant								
m	22.07** ± 0.35	20.82** ±0.38	19.92** ±0.36	18.63** ±0.27	20.87**±0.44	19.85** ± 0.35	27.91** ± 3.03	22.58**±0.68
d	-1.96** ± 0.65	-0.57 ± 0.56	0.19 ± 0.72	2.08* ± 0.85	1.30 ± 0.85	0.86 ± 0.6	0.85 ± 0.47	2.27** ± 0.83
h	9.30** ± 2.02	3.87 ± 2.06	11.19** ±2.17	9.46** ± 2.19	-1.40 ± 2.67	-1.81 ± 2.08	-13.07 ± 7.14	-9.27** ±3.27
i	6.81** ± 1.92	3.36 ± 1.89	11.33** ±2.06	7.18** ± 2.03	-1.45 ± 2.45	-3.54 ± 1.85	-	-9.98** ±3.21
j	-2.19** ± 0.77	0.62 ± 0.7	1.99* ± 0.86	1.70 ± 0.92	2.66* ± 1.03	1.65* ± 0.77	-	1.50 ± 0.93
l	-0.29 ± 3.21	-10.53** ±3.19	-12.76**±3.52	-7.49 ± 3.93	4.01 ± 4.38	6.47 ± 3.36	-	15.79** ± 4.5
	--	--	Duplicate	--	--	--	--	Duplicate

*,** Significant at 5 per cent and 1 per cent, respectively

al. 2022). Attaining optimal yield may involve either recurrent selection in these crosses for the specified traits and conditions mentioned earlier, where improvements through selection are constrained, or preserving substantial heterozygosity through interbreeding of early segregating generations' chosen genotypes (Parlevliet and Van Ommeren 1988). This approach enhances the probability of diverse recombinants, potentially resulting in the accumulation of advantageous genes in the final homozygous lines that exhibit higher yield. Consequently, employing pedigree breeding and a series of recurrent selections can prove effective in augmenting the seed yield per chickpea plant.

CONCLUSION

Based on the comprehensive findings, it can be inferred that most of the studied characteristics, considering seed yield, were affected by a combination of additive and non-additive gene effects, with a notable prevalence of non-additive effect of the gene in both situations. Consequently, in the process of enhancing these traits within a population, it is essential to concurrently maintain heterozygosity while incorporating beneficial additive genes.

REFERENCES

Allard RW and Bradshaw AD. 1964. Implications of genotype environmental interaction in applied plant breeding. Crop Science **4**: 503-508

Berger JD, Milroy SP, Turner NC, Siddique KHM, Imtiaz M and Malhotra R. 2011. Chickpea evolution has selected for contrasting phonological mechanisms among different habitats. Euphytica **180**: 1-15.

Deshmukh RA and Gawande VL. 2016. Generation mean analysis for seed yield and its contributing traits in chickpea (*Cicer arietinum* L.). Electronic Journal of Plant Breeding **7**(1): 86-93.

Devasirvatham V, Gaur PM, Mallikarjuna N, Tokachichu RN, Trethowan RM and Daniel KY. 2012. Effect of high temperature on the reproductive development of chickpea genotypes under controlled environments**.** Functional Plant Biology **39**(12): 1009-1018.

Devasirvatham, V and Tan DKY. 2018. Impact of High Temperature and Drought Stresses on Chickpea Production. Agronomy **8**: 145.

Gaur PM, Kumar J, Gowda CLL, Pande S, Siddique KHM, Khan TN, Warkentinm TD, Chaturvedi SK, Than AM and Ketema, D. 2008. Breeding chickpea for early phenology: perspectives progress and prospects. In: Kharkwal MC (ed.) Food Legumes for Nutritional Security and Sustainable Agriculture. New Delhi: Indian Society of Genetics and Plant Breeding. Pp. 39-48.

Ghasemi P, Karami E and Talebi R. 2022. Study of heterosis, genetic depression and estimation of genetic parameters of some morphological traits in chickpea genotypes by generation mean analysis. Central Asian Journal of Plant Science Innovation **2**(1): 19-36.

Gowda CLL, Parthasarathy RP, Tripathy S, Gaur PM and Deshmukh RB. 2009. Regional shift in chickpea production in India. In: Ali Masood and Kumar Shiv (eds) Milestones in Food Legumes Research. Indian Institute of Pulses Research, Kanpur. Pp. 21-35.

Graham PH and Vance CP. 2003. Legumes: importance and constraints to greater use. Plant Physiology **131**: 872-877.

Hayman BI. 1958. The separation of epistasis from additive and dominance variation in generation means. Heredity **12**: 371-390.

Hayman BI and Mather K. 1955. The description of genetic interactions in continuous variation. Biometrics **11**: 69-82.

Jameel S, Hameed A and Shah TM. 2021. Investigation of Distinctive Morpho-Physio and Biochemical Alterations in Desi Chickpea at Seedling Stage under Irrigation, Heat, and Combined Stress. Frontiers in Plant Science **12**: 692745.

Jinks JL and Jones RM. 1958. Estimation of the components of heterosis. Genetics **43**: 223-224.

Khetarpal S, Pal M and Snehlata. 2009. Effect of elevated temperature on growth and physiological characteristics in chickpea cultivars. Indian Journal of Plant Physiology **14**(4): 377-383.

Kumhar BL, Singh D, Bhanushally TB and Koli NR. 2013. Gene effects for yield and yield components in chickpea (*Cicer arietinum* L.) under irrigated and rainfed conditions. Journal of Agricultural Science **5**(3): 1-13.

Mohapatra C, Chand R, Tiwari JK and Singh AK. 2020. Effect of heat stress during flowering and pod formation in pea (*Pisum sativum* L.). Physiology and Molecular Biology of Plants **26**(6): 1119-1125.

Mujjassim NE, Nehru SD and Gowda J. 2018. Heterosis for quantitative traits in wide crosses of chickpea (*Cicer arietinum* L.). International Journal of Pure and Applied Bioscience **6**(6): 1204-1209.

Najan BR and Kadam DD. 2018. Generation mean analysis for seed yield and its components in kabuli chickpea (*Cicer arientinum* L.). Trends in Biosciences **11**(21): 2986-2991.

Nehra M, Panwar RK, Verma SK, Arora A, Bhardwaj R and Choudhary R. 2020. Generation mean analysis for seed yield and it's contributing quantitative traits in chickpea (*Cicer arietinum* L.). International Journal of Chemical Studies **8**(6): 172-175.

Parlevliet JE and Van Ommeren A. 1988. Recurrent selection for grain yield in early generations of two barley populations. Euphytica **38**: 175-184.

Prasad SN, Sinha T, Kumari A and Rakshit A. 2018. High temperature stress in chickpea: Effects on physiological processes, nitrogen fixation, pollination and reproductive growth. Current Journal of Applied Science and Technology **31**(2): 1-8.

Prasanthi G, Jayalakshmi V, Reddy AT and Khayumahammed S. 2023. Genetic variability parameters and character association studies among phenological traits, yield traits and quality traits under different dates of planting in chickpea (*Cicer arietinum* L.). Journal of Food Legumes **36**(2 & 3): 126-135.

Samad MA, Sarker N and Deb AC. 2016. Generation mean analysis of quantitative traits in chickpea. Bangladesh Journal of Botany **45**(2): 277-281.

Sundaram P, Samineni S, Sajja SB, Singh SP, Sharma RN and Gaur PM. 2018. Genetic studies for seed size and grain yield traits in kabuli chickpea. Euphytica **214**(4): 63.

Thombre SV, Goud VV, Darade GA, Saoji BV and Tupe AR. 2019. Effect of sowing dates on growth and yield of chickpea varieties under delayed planting condition. Journal of Pharmacognosy and Phytochemistry **8**(5): 801-805.

Varol IS, Kardes YM, Irik HA, Kirnak H and Kaplan M. 2020. Supplementary irrigations at different physiological growth stages of chickpea (*Cicer arietinum* L.) change grain nutritional composition. Food Chemistry **303**: 125402.

Yegrem L. 2021. Nutritional composition, antinutritional factors, and utilization trends of Ethiopian chickpea (*Cicer arietinum* L.). International Journal of Food Science 2021: 5570753.