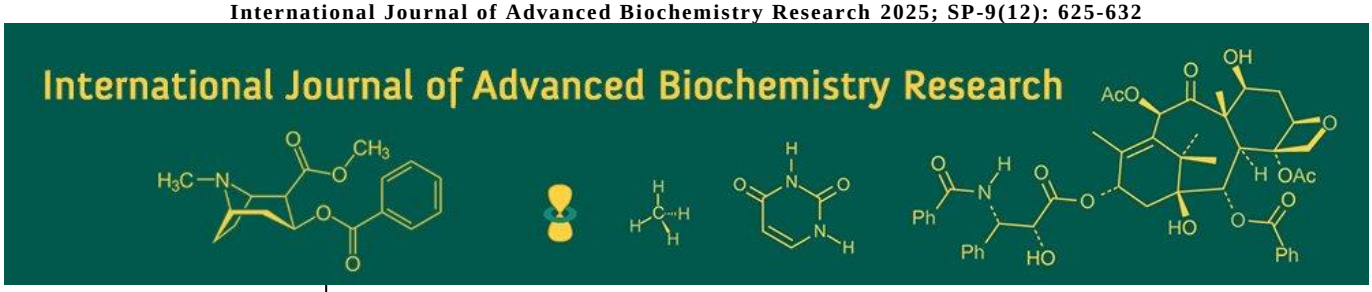

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Generation mean analysis studies in chickpea (*Cicer arietinum* L.) genotypes

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Abstract
The mean of six generations in the cross indicated that, the F_1 means were higher than mid parental mean values which is comparable to better parent mean values in significant direction with respects to all the traits in present investigation which indicating the presence of over dominance. In the cross, F_2 means were lower than the F_1 mean except some cases. The mean of backcross populations tended towards their respective parents. These results indicated that the predominance of non-additive gene action which includes both dominance as well as epistatic interactions. The F_1 and segregating generations evolved from the cross combination phule-G-1420-13-6 x RSG-888 exhibited the higher mean values for grain yield and its contributing characters. Based on the substantial information obtained from mean performance of parents and segregating generations the parents. In the cross, individual scaling test and joint scaling test were significant for all the characters indicating the inadequacy of simple additive-dominance model, justifying the use of six parameters model for detection of gene interactions. The generation mean analysis revealed the significance of additive, dominance and epistasis gene effects were found operating the gene actions for grain yield and its contributing traits in chickpea in the cross.
The estimates of A, B, C and D scaling tests and joint scaling test were significant in the cross for sixteen characters with few exceptions. The significance of these cross for various characters indicated inadequacy of additive-dominance model.

1. For grain yield and yield components, the dominant component (h) and dominance x dominance (l) gene interaction was found significant for most of the characters *viz*, days to maturity, plant height, number of primary branches per plant, seeds per pod, grain yield per plant and relative water content, chlorophyll stability index, glycine betaine and stomatal frequency these characters can be improved by hybrid development or by recurrent selection for SCA.
2. Additive gene action along with additive x additive (i) followed by dominance (h) was found significant for the characters *viz*. days to maturity, plant height, number of primary branches per plant, yield per plant, relative water content, chlorophyll stability index, proline, glycine betaine and stomatal frequency. For improvement of these characters, one should follow the simple selection in early segregating generations.

Keywords: Chickpea, generation mean analysis, additive gene interaction, dominance gene interaction, epistasis gene interaction

Introduction
Pulses hold an important place in human diets and also serve as nutritious green fodder and valuable livestock feed. One unique feature of pulse crops is their natural ability to fix atmospheric nitrogen through Rhizobium bacteria present in their root nodules. This enables them to meet much of their own nitrogen requirement and enrich the soil for subsequent crops. However, pulse production has not kept pace with population growth over the past two decades, causing a decline in per capita availability from 69 grams per day in 1961 to 37 grams per day in 2004 (Ali and Shivkumar, 2005) [1].
Chickpea ranks as the second most significant cool-season legume globally and is cultivated in more than 33 countries across Central and West Asia, Southern Europe, Ethiopia, North Africa, the Americas and Australia (Ladizinsky, 1976) [9]. It is a major source of dietary protein for India's predominantly vegetarian population and also contributes to livestock feed.
Botanically, chickpea (*Cicer arietinum* L.) is a self-pollinated species belonging to the Fabaceae family and has 2n = 16 chromosomes. It is commonly known as Bengal gram, chana or harbhara. In India, chickpea is grown on about 10.17 million hectares with a

production of 11.35 million tonnes and an average productivity of 1116 kg/ha (Anonymous, 2019-20). The major producing states—Madhya Pradesh, Uttar Pradesh, Rajasthan, Maharashtra, Andhra Pradesh, Tamil Nadu and Telangana—account for more than 88% of national production. Madhya Pradesh alone contributes over 40%. During 2019-20, Maharashtra recorded 43.87 lakh hectares under pulses with a production of 40.27 lakh tonnes (productivity 918 kg/ha). As a rabi pulse crop, chickpea occupies about 98.86 lakh hectares in India, producing 107.37 lakh tonnes with a productivity of 1086 kg/ha (Anonymous, 2024).

Despite its importance, chickpea productivity remains low due to constraints such as the use of low-quality seeds, cultivation on marginal and rainfed lands, and the absence of stable, high-yielding and disease-resistant varieties. Since chickpea is predominantly self-pollinated, developing extra-early (60-70 days) and medium-maturing (75-90 days), non-photosensitive lines with desirable grain quality and dual-purpose potential is a major breeding goal.

Chickpea is mainly grown on conserved soil moisture in the post-monsoon season, and because soil moisture declines progressively during crop growth, plants frequently face terminal drought stress. This makes moisture stress one of the principal yield-limiting factors. Physiological responses to stress in chickpea have been widely studied, and significant progress has been made in understanding drought tolerance mechanisms. Knowledge of gene action controlling yield and related traits is crucial for plant breeders to develop appropriate breeding strategies, especially because seed yield is a complex trait influenced by many genes and environmental factors.

Losses caused by abiotic stresses in chickpea (6.4 million tonnes) exceed those from biotic stresses (4.8 million tonnes) (Ryan, 1997). Drought, heat, cold and salinity result in massive economic losses globally. Given the complexity of genetic control and the strong genotype × environment interactions, breeding for abiotic stress tolerance remains challenging.

Drought impacts several physiological and biochemical processes including germination, photosynthesis, osmotic adjustment, chlorophyll stability, water potential and flowering behaviour. For instance, every 1 °C increase above optimal temperature may reduce yield by 10-15%, and even a 0.1 °C rise coupled with reduced rainfall can significantly decrease productivity. Under rainfed conditions, terminal drought can reduce chickpea yields by up to 50%. Physiological traits such as high relative water content, reduced stomatal frequency and greater chlorophyll stability are valuable for screening drought-tolerant genotypes.

Osmoprotectants like glycine betaine, proline and soluble sugars play critical roles in maintaining cellular stability under drought, protecting proteins and membranes and supporting photosynthetic machinery.

Developing pure-line varieties adapted to diverse agro-ecological zones and possessing desirable plant type, maturity duration and seed characteristics requires selecting promising genotypes from germplasm, using them in hybridization programmes and identifying superior segregants. Transgressive segregation—where offspring outperform both parents—offers valuable opportunities to combine favourable alleles and enhance traits such as branching, plant height, pod number, seed weight and overall yield.

Material and Methods

The present investigation entitled "Genetic analysis for Drought Tolerance in Chickpea [*Cicer arietinum* (L.)] "aimed at studying, gene action for grain yield contributing traits, transgressive segregation and Physiological and biochemical characters in chickpea was conducted during *Rabi*-2022 and *Rabi*-2023 at Pulse Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri. The details of the materials used, the experimental approach and statistical methods followed for conduct of experiment are described below.

The experimental material for generation mean analysis for present study comprised P_1 P_2 F_1 F_2 B_1 B_2 of one cross Phule -G 1420-13-6 × RSG-888 from Pulse Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri

The experiment was conducted in randomised block design with three replications, six generations consisting parents (P_1 and P_2), F_1's, F_2's, B_1's and B_2's of the cross Phule -G 1420-13-6 × RSG-888. Sowing was carried out during *rabi* 2023 at Pulse Improvement Project, Mahatma Phule Krishi Vidyapeeth, Rahuri. Among the six generations each of the parents (P_1 and P_2) and F_1's was represented by single row, B_1's and B_2's represented by two rows and F_2's by four rows of 3 m length spaced at 30 cm apart with 10 cm distance between plants in a row.

Results and Discussion

Analysis of variance

Analysis of variance was carried out for traits associated with grain yield for sixteen different generations of chickpea in a cross *viz*., Phule-G-1420-13-6 × RSG-888 (Table 4.1).

4.1.2 Mean performance of parents and generations for grain yield and its components traits

The mean values for parents, F_1, F_2, B_1 and B_2 generations of a cross *viz.*, Phule-G-1420-13-6 × RSG- 888 for sixteen different characters of chick pea have been presented in Table 4.2.

4.1.2.1 Days to 50% first flowering

The trait exhibited a variation ranging from 48.60 to 57.60 days in the cross. Among the parents, Phule-G-1420-13-6 flowered earliest (48.60 days), whereas RSG-888 was comparatively late (57.60 days). In the segregating generations, the means recorded were F_1 (54.20) days,,F_2(51.43) days, B_1(49.10) days, B_2(54.93) days for cross Phule-G-1420-13-6 × RSG-888.These values indicate the expression of both early and late flowering tendencies in the progenies.

4.1.2.2 Days to Maturity

Days to maturity ranged between 109.33 and 129.53 days in the cross. Among the parents, Phule-G-1420-13-6 matured earlier (109.33 days), while RSG-888 was late-maturing (129.53 days). Mean values for the segregating generations were F_1 (115.40 days), F_2(111.69) days, B_1 (112.43) days, B_2 (125.40) days for days to maturity. The results suggest wide variation in maturity duration among derived generations.

4.1.2.3 Plant height (cm)
Plant height varied from 66.00 to 87.56 cm in the cross. Among the parents, Phule-G-1420-13-6 was taller (75.27 cm), whereas RSG-888 recorded a height of 66.00 cm. In the segregating generations F_1 (71.18) cm, F_2 (87.56) cm, B_1(73.40) cm, B_2(68.67) cm. The F_2 generation showed the maximum height, indicating increased variability due to segregation.

4.1.2.4 Number of primary branches per plant
The number of primary branches ranged from 3.67 to 5.13 in the cross. Among the parents Phule-G-1420-13-6 had the highest number (5.13) RSG-888 showed fewer branches (3.67) Mean values in the progeny were F_1 (4.33), F_2(4.46) B_1(4.40), B_2 (3.78). These results reflect moderate variation in branching pattern across generations.

4.1.2.5 Number of secondary branches per plant (No.)
The number of secondary branches per plant showed a variation from 9.40 to 14.87 in the cross Phule-G-1420-13-6 × RSG-888. Among the parents, Phule-G-1420-13-6 produced the highest number of secondary branches (12.93), whereas RSG-888 recorded the lowest (9.40). In the segregating generations, the mean values were F_1(14.27), F_2(14.87), B_1(14.15),B_2 (12.85) These results indicate considerable improvement in branching among the progenies.

4.1.2.6 Number of Pods per Plant (No.)
The number of pods per plant ranged from 77.53 to 93.47 in the cross. Among the parents, Phule-G-1420-13-6 produced the maximum pods (93.47), while RSG-888 recorded fewer pods (77.53). The means of segregating generations were F_1 (87.40) F_2 (88.66), B_1(92..18), B_2(84.78).These values suggest substantial pod-bearing ability among derived generations.

4.1.2.7 Number of seeds per pod (No.)
The number of seeds per pod varied between 1.20 and 1.83. Among the parents, Phule-G-1420-13-6 had more seeds per pod (1.53) than RSG-888 (1.20). The progeny generations recorded F_1 (1.33), F_2 (1.83), B_1 (1.35), B_2 (1.28). The F_2 generation exhibited the highest value, showing enhanced segregation for seed set.

4.1.2.8 100-Seed weight (g)
The 100-seed weight varied from 20.58 to 27.79 g in the cross. Among the parents, Phule-G-1420-13-6 recorded the highest seed weight (27.79 g), while RSG-888 had the lowest (20.58 g).
The corresponding values in segregating generations were F_1 (24.71), F_2(23.90) B_1(25.60) B_2(22.33). This indicates moderate variation in seed size across generations.

4.1.2.9 Grain Yield per Plant (g)
Grain yield per plant ranged from 54.15 to 60.84 g. Among parents, Phule-G-1420-13-6 produced the highest yield (60.84 g), while RSG-888 produced the least (54.15 g). The segregating generations showed F_1(57.17), F_2(44.70), B_1(59.20), B_2(56.74) . The lower yield in F_2 reflects greater segregation and variability in this generation.

4.1.2.10 Relative water content (%)
Relative water content (RWC) varied from 74.56% to 85.67%. Among parents, Phule-G-1420-13-6 showed higher RWC (85.67%), compared to RSG-888 (74.56%).The segregating generations recorded F_1 (77.82), F_2 (75.78), B_1(84.87), B_2(76.28). The B_1 generation displayed values similar to the high-RWC parent.

4.1.2.11 SPAD (Chlorophyll Meter) reading (%)
SPAD values ranged from 51.58 to 55.92. Among the parents, Phule-G-1420-13-6 had a higher SPAD reading (55.51), while RSG-888 had a lower value (51.58). Values in derived generations were F_1(54.50), F_2(55.92),B_1(54.87) B_2 (54.48). The F_2 generation showed the highest SPAD level, indicating better chlorophyll retention.

4.1.2.12 Chlorophyll stability index (%)
Chlorophyll stability index (CSI) ranged from 0.58 to 0.74. Parent Phule-G-1420-13-6 registered a higher value (0.74), while RSG-888 had a lower CSI (0.58). The progeny means were F_1(0.65), F_2(0.48), B_1(0.66), B_2(0.63) Variability in CSI indicates differences in tolerance to stress conditions.

4.1.2.13 Membrane injury index (%)
The membrane injury index varied from 12.17 to 13.50%. Among parents, Phule-G-1420-13-6 exhibited the lowest membrane injury (12.17%), whereas RSG-888 showed the highest (13.50%).
In progenies, the values recorded were F_1(12.25), F_2(11.97), B_1(12.20) B_2(12.26). Lower values in F_2 suggest improved membrane stability under stress.

4.1.2.14 Stomatal frequency (No./mm²)
Adaxial Surface (ADAX)
Variation ranged between 49.13 and 54.40. Phule-G-1420-13-6 had 54.40 (higher) while RSG-888 showed 49.13. Generational means F_1 (51.73), F_2(45.44), B_1(53.02),B_2(50.18)

Abaxial Surface (ABAX)
Values ranged from 54.60 to 61.07. Phule-G-1420-13-6 showed 61.07, while RSG-888 showed 54.60 Generations recorded F_1(55.53), F_2(51.13) B_1(58.47), B_2(54.63)

4.1.2.15 Proline content (µ moles g^{-1} fw)
Proline content varied from 1.75 to 3.48. The parent Phule-G-1420-13-6 had the lowest value (1.75), while RSG-888 showed the highest proline accumulation (3.48). Values among generations were F_1(2.37), F_2(2.40),B_1(1.86), B_2(2.86). Higher proline content in some progenies suggests improved drought response.

4.1.2.16 Glycine betaine (µ moles g^{-1} FW)
Glycine betaine ranged from 3.28 to 4.06. Among parents, Phule-G-1420-13-6 recorded more glycine betaine (4.06) compared to RSG-888 (3.28). In the generations F_1 (3.76), F_2(3.48) B_1(3.95), B_2(3.69) These values indicate stable inheritance of osmoprotectants.

4.1.3 Estimates of scaling tests for detecting non-allelic interactions of a cross for different traits of chickpea
4.1.3 Scaling tests for detecting non-allelic interactions
Scaling tests (A, B, C and D) as described by Mather (1949) were used to determine the presence of non-allelic gene

interactions in the inheritance of yield and related traits.
Significant values of A and B scales suggested interaction effects of:

- Additive × additive (i)
- Additive × dominance (j)
- Dominance × dominance (l)

Significance of the C scale specifically indicated dominance × dominance (l) interaction, while significance of the D scale confirmed additive × additive (i) interaction. The significance of any one of these scaling tests implied that the simple additive-dominance model was insufficient to explain inheritance. Chi-square (χ^2) values were significant for all characters, further supporting the presence of epistatic interactions.

4.1.3.1 Days to first flowering
For days to first flowering, the A scaling test (−4.60) showed a significant negative deviation in the cross *Phule-G-1420-13-6* × *RSG-888*. Similarly, scaling tests B (−1.93) and C (−8.87) were also significantly negative. The significance of the joint scaling test indicated that the additive-dominance model was inadequate, suggesting the involvement of non-allelic (epistatic) interactions for this trait.

4.1.3.2 Days to maturity
In the case of days to maturity, the B scaling test (5.87) was significantly positive, whereas scaling tests C (−22.90) and D (−14.45) showed significant negative deviations. The joint scaling test was significant, confirming that the simple additive-dominance model does not sufficiently explain the inheritance pattern for this trait.

4.1.3.3 Plant height
For plant height, scaling tests C (66.61) and D (33.05) exhibited significant positive deviations.
The significance of the joint scaling test implied that epistatic interactions are present, and the additive-dominance model alone is inadequate.

4.1.3.4 Number of primary branches per plant
The D scaling test (0.73) showed a significant positive value for number of primary branches. The joint scaling test was significant, demonstrating that the inheritance of this trait cannot be explained solely by the additive-dominance model.

4.1.3.5 Number of secondary branches per plant
Significant positive deviations were observed for scaling tests B (2.03), C (8.60) and D (2.73). These results, along with the significant joint scaling test, indicated that non-allelic interactions play an important role in governing this trait.

4.1.3.6 Number of pods per plant
The B scaling test (4.63) was significantly positive for number of pods per plant.
The joint scaling test was also significant, suggesting that the additive-dominance model is insufficient and epistasis contributes to trait expression.

4.1.3.7 Number of seeds per pod
For number of seeds per pod, scaling tests C (1.93) and D (1.03) recorded significant positive values.
The significant joint scaling test confirmed the presence of gene interactions, indicating the inadequacy of the additive-dominance model for this trait.

4.1.3.8 100-Seed weight
The A scaling test (−1.31) exhibited significant negative deviation for 100-seed weight.
The joint scaling test was significant, showing that inheritance involves epistasis, and the additive-dominance genetic model does not fully explain the variation.

4.1.3.9 Grain yield per plant
For grain yield per plant, scaling tests C (−50.53) and D (−26.54) were significantly negative.
As the joint scaling test was significant, it indicated that the additive-dominance model is inadequate, and gene interactions are influencing yield.

4.1.3.10 Relative water content (%)
Relative water content showed a significant positive deviation for the A scaling test (6.25), whereas C (−12.74) and D (−9.59) were significantly negative.
The joint scaling test was significant, confirming that epistatic gene action is involved and the additive-dominance model cannot account fully for genetic expression of RWC.

4.1.3.11 SPAD (Chlorophyll Meter) Reading
Significant positive deviations were noted for scaling tests B (2.88) and C (7.58) for SPAD values.
The significant joint scaling test showed that inheritance of SPAD is influenced by non-allelic interactions, making the additive-dominance model insufficient.

4.1.3.12 Chlorophyll stability index
For chlorophyll stability index (CSI), scaling tests A (−0.07) and C (−0.69) were significantly negative, while D (0.33) was significantly positive.
With the joint scaling test being significant, it was concluded that epistatic interactions are involved, and the additive-dominance model alone cannot explain the observed genetic variation.

4.1.3.13 Membrane injury index (%)
For membrane injury index, the scaling tests B (−1.23), C (−2.32), and D (−0.53) showed significant negative deviations in the cross *Phule-G-1420-13-6* × *RSG-888*.
Because the joint scaling test was significant, it indicates that the simple additive-dominance model does not sufficiently describe the genetic variation, confirming the involvement of non-allelic interactions.

4.1.3.14 Proline (µ moles g^{-1} FW)
The joint scaling test for proline revealed significant deviation, suggesting that the additive-dominance model is inadequate for explaining the genetic control of this trait, thereby implicating epistatic interactions.

4.1.3.15 Glycine betaine (µ moles g^{-1} FW)
For glycine betaine, the scaling test D (−0.67) was significantly negative.
The joint scaling test was also significant, indicating the

inability of the additive-dominance model to explain genetic variation, implying the presence of gene interactions.

4.1.3.16 Stomatal frequency

Adaxial Surface (ADAX)

Scaling tests C (−25.23) and D (−12.32) showed significant negative deviations.

The significant joint scaling test indicates that epistatic interactions contribute to stomatal frequency inheritance, making the additive-dominance model insufficient.

Abaxial Surface (ABAX)

Scaling tests C (−22.23) and D (−10.85) showed significant negative deviations.

The joint scaling test confirmed the presence of non-allelic interactions, as reflected by significant chi-square values, pointing again to the inadequacy of the additive-dominance model.

4.1.4 Estimation of gene effects

The six generations of the cross were used to estimate the gene effects viz., (m), (d), (h), (i), (j) and (l) for grain yield and its contributing traits in chickpea. Wherever, the scaling tests and joint scaling test were highly significant indicating inadequacy of the simple additive-dominance model to explain the genetic control.

The estimates of m (mean), major genetic effects additive [d] and dominance [h] and non-allelic gene interactions (i, j and l) based on six parameter model (Hayman, 1958) for grain yield and its contributing traits (Table 4.4).

The gene effects estimated by using perfect fit model in respect of traits associated with grain yield in chickpea has been presented in Table (4.4) and discussed traits wise below.

4.1.4.1 Days to first flowering

In the cross *Phule-G-1420-13-6* × *RSG-888*, the additive component d (−5.83) was significantly negative, while the dominance effect h (3.43) was positive but non-significant. Interaction terms i (2.33) and l (4.20) were significantly positive, whereas j (−1.33) was significantly negative.

The strong significance of the additive effect shows that additive gene action is predominant for this trait. Significant positive i and l and negative j indicate the presence of non-allelic interactions, with dominance × dominance (l) showing the largest magnitude. Similar findings were reported by several earlier researchers.

4.1.4.2 Days to maturity

For days to maturity, d (−12.97) was significantly negative, and h (24.87) was significantly positive. Interaction component i (28.90) was significantly positive, while j (−2.87) and l (−34.90) were significantly negative. The opposite signs of h and l indicate duplicate epistasis.

Dominance effects were larger than additive effects, suggesting dominance-driven inheritance.

All three interaction components were significant, confirming a non-additive gene action pattern.

4.1.4.3 Plant height

For plant height, d (4.73) was significantly positive, whereas h (−65.55) was significantly negative. Interaction components showed i (−66.10) significantly negative, j (0.10) non-significant, and l (65.59) significantly positive. The opposite signs of h and l again confirmed duplicate epistasis. Dominance gene action predominated, and inheritance was governed by non-additive effects.

4.1.4.4 Number of primary branches

Additive effect d (0.62) was significant and positive; dominance effect h (−1.23) was significantly negative. Interactions showed i (−1.47) significant negative, j (−0.12) non-significant, and l (2.57) significant positive. Dominance × dominance interaction was of higher magnitude. Overall inheritance involved non-additive gene action, and duplicate epistasis was present.

4.1.4.5 Number of secondary branches

Additive effect d (1.30) was significant; dominance h (−2.37) was negative but non-significant.

Interaction i (−5.47) was significantly negative; j (−0.47) and l (2.33) were non-significant Additive effects dominated, with significant i indicating involvement of additive × additive epistasis.

4.1.4.6 Number of pods per plant

Additive effect d (7.40) was significant; dominance h (1.20) was non-significant.

All interaction components (i, j, l) were non-significant. This indicates that additive gene action predominates for this trait.

4.1.4.7 Number of seeds per pod

Additive d (0.07) was non-significant; dominance h (−2.10) was significantly negative.

Interaction i (−2.07) was significant; j (−0.10) non-significant; and l (2.20) significantly positive. Opposite signs of h and l indicate duplicate epistasis, and inheritance is largely non-additive.

4.1.4.8 100-Seed weight

Additive effect d (3.27) was significantly positive; dominance h (0.75) was non-significant.

All interaction components (i, j, l) were non-significant. Thus, additive gene action governs 100-seed weight.

4.1.4.9 Grain yield per plant

Both additive d (2.47) and dominance h (52.75) were significantly positive. Interaction i (53.07) was significant positive, l (−55.61) significant negative, while j (−0.88) was non-significant.

The opposing signs of h and l characterized duplicate epistasis, with strong non-additive gene action influencing yield.

4.1.4.10 Relative water content

Additive d (8.59) and dominance h (16.87) were both significant. Interaction terms: i (19.17) and j (3.04) were significantly positive; l (−25.60) significantly negative. Duplicate epistasis was evident, and inheritance was governed by non-additive gene effects.

4.1.4.11 SPAD reading

Additive d (0.39) and dominance h (−4.02) were both non-significant.

Interaction i (−4.98) was non-significant, j (−1.58) significant, and l (2.38) non-significant. The overall pattern suggests dominance gene action, with additive × dominance interaction (j) contributing significantly.

4.1.4.12 Chlorophyll stability index

Additive d (0.03) and dominance h (0.64) were significantly positive. Interaction i (0.65) was significant, whereas j (−0.05) and l (−0.61) were significantly negative. The opposite signs of h and l indicate duplicate epistasis, and inheritance is influenced mainly by non-additive gene action.

4.1.4.13 Membrane injury index (%)

Both additive d (−0.06) and dominance h (0.48) were non-significant. Interaction components: i (1.06) and j (0.60) were significantly positive, while l (0.20) was non-significant. This suggests a general preponderance of dominance gene action, with additive × additive epistasis contributing most strongly.

4.1.4.14 Proline content

Additive d (−1.00) was significantly negative; dominance h (−0.42) was non-significant.

Interaction terms (i, j, l) were all non-significant. Hence, additive gene action plays a major role in inheritance of proline content.

4.1.4.15 Glycine betaine

Additive d (0.25) and dominance h (1.44) were both significant. Interaction i (1.35) was significant positive; j (−0.14) non-significant; l (−1.76) significant negative. The opposite signs of h and l confirm duplicate epistasis, with non-additive gene action dominating inheritance.

4.1.4.15 Stomatal frequency (ADAX & ABAX)

ADAX

Both additive d (2.83) and dominance h (24.60) were significantly positive.

Interaction i (24.63) was significant, j (0.20) non-significant, and l (−24.03) significantly negative. Duplicate epistasis was evident, and inheritance was non-additive.

ABAX

Additive d (3.83) and dominance h (19.40) were significantly positive. Interaction i (21.70) significant, j (0.60) non-significant, and l (−21.17) significantly negative. Again, duplicate epistasis dominated inheritance.

Table 1: Analysis of variance

Sr. No.	Name of characters		Phule-G-1420-13-6 × RSG-888	
			Mean sum of squares	
			Treatments	Error
	DF		5	10
1.	Days to First flowering(No.)		27.67**	0.49
2.	Days to maturity (No.)		204.38**	14.42
3.	Plant height (cm)		169.03**	12.08
4.	Primary branches(No.)		0.83**	0.05
5.	Secondary branches(No.)		13.70**	0.54
6.	Pods per plant(No.)		99.24**	11.35
7.	Seeds per pod (No.)		0.14**	0.02
8.	100 seed weight (gm)		19.06**	0.88
9.	Yield per plant(gm)		101.36**	7.52
10.	Relative water content (%)		73.68**	0.98
11.	SPAD chlorophyll meter reading (%)		7.86**	0.59
12.	Chlorophyll stability index (%)		0.02**	0.00
13.	Membrane injury index (%)		0.92**	0.03
14.	Proline (µ moles g-1 FW)		1.15**	0.01
15.	Glycine betaine (µ moles g-1 FW)		0.26**	0.03
16.	Stomatal frequency	ADAX(No./mm^2)	30.27**	1.94
		ABAX(No./mm^2)	35.62**	0.42

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

Table 2: Mean performance of parents and generations for grain yield and its components traits

Name of cross	Generations	Days to first flowering	Days to maturity	Plant height	Primary branches	Secondary branches	Pods per plant	Seeds per pod	100 seed weight	Yield per plant
Phule-G-1420-13-6 × RSG-888	P_1	48.60 (0.13)	109.33 (0.13)	75.27 (0.18)	5.13 (0.13)	12.93 (0.30)	93.47 (0.66)	1.53 (0.13)	27.79 (0.13)	60.84 (0.39)
	P_2	57.60 (0.13)	129.53 (0.29)	66.00 (0.20)	3.67 (0.13)	9.40 (0.24)	77.53 (0.58)	1.20 (0.11)	20.58 (0.23)	54.15 (0.70)
	F_1	54.20 (0.11)	115.40 (0.13)	71.18 (0.18)	4.33 (0.16)	14.27 (0.45)	87.40 (0.65)	1.33 (0.13)	24.71 (0.24)	57.17 (1.04)
	F_2	51.43 (0.47)	111.69 (1.33)	87.56 (1.88)	4.46 (0.11)	14.87 (0.45)	88.66 (2.33)	1.83 (0.03)	23.90 (0.32)	44.70 (1.39)
	B_1	49.10 (0.10)	112.43 (0.12)	73.40 (0.23)	4.40 (0.15)	14.15 (0.11)	92.18 (0.88)	1.35 (0.06)	25.60 (0.09)	59.20 (0.52)
	B_2	54.93 (0.13)	125.40 (0.08)	68.67 (0.26)	3.78 (0.13)	12.85 (0.23)	84.78 (0.81)	1.28 (0.06)	22.33 (0.14)	56.74 (0.82)

Table 2: Contd….

Name of cross	Generations	Relative water content (%)	SPAD chlorophyll meter reading (%)	Chlorophyll stability index (%)	Membrane injury index (%)	Proline (µ moles g^{-1} FW)	Glycine betaine (µ moles g^{-1} FW)	Stomatal frequency (No./mm^2)	
								ADAX (No./mm^2)	ABAX (No./mm^2)
Phule-G-1420-13-6 × RSG-888	P_1	85.67 (0.85)	55.51 (0.16)	0.74 (0.03)	12.17 (0.14)	1.75 (0.05)	4.06 (0.11)	54.40 (0.13)	61.07 (0.25)
	P_2	74.56 (0.67)	51.58 (0.21)	0.58 (0.01)	13.50 (0.12)	3.48 (0.23)	3.28 (0.12)	49.13 (0.31)	54.60 (0.46)
	F_1	77.82 (1.16)	54.50 (0.26)	0.65 (0.00)	12.25 (0.20)	2.37 (0.16)	3.76 (0.16)	51.73 (0.36)	55.53 (0.17)
	F_2	75.78 (0.81)	55.92 (0.67)	0.48 (0.03)	11.97 (0.08)	2.40 (0.07)	3.48 (0.11)	45.44 (0.78)	51.13 (0.61)
	B_1	84.87 (0.85)	54.87 (0.38)	0.66 (0.01)	12.20 (0.09)	1.86 (0.04)	3.95 (0.03)	53.02 (0.18)	58.47 (0.17)
	B_2	76.28 (0.85)	54.48 (0.40)	0.63 (0.01)	12.26 (0.06)	2.86 (0.06)	3.69 (0.09)	50.18 (0.22)	54.63 (0.15)

Table 3: The results on scaling test (A, B, C and D) in respect of yield and yield contributing traits

Sr. No.	Name of characters	Scaling test				Chi square (χ^2)
		A	B	C	D	
1	Days to First flowering (No.)	-4.60**	-1.93**	-8.87**	-1.17	332.09**
2	Days to maturity (No.)	0.13	5.87**	-22.90**	-14.45**	309.31**
3	Plant height (cm)	0.35	0.15	66.61**	33.05**	78.74**
4	Primary branches (No.)	-0.67	-0.43	0.37	0.73*	7.00*
5	Secondary branches (No.)	1.10	2.03**	8.60**	2.73**	20.91**
6	Pods per plant (No.)	3.50	4.63*	8.83	0.35	9.01**
7	Seeds per pod (No.)	-0.17	0.03	1.93**	1.03**	102.16**
8	100 seed weight (g)	-1.31**	-0.64	-2.18	-0.12	16.52**
9	Yield per plant (g)	0.39	2.15	-50.53**	-26.54**	81.95**
10	Relative water content (%)	6.25**	0.17	-12.74**	-9.59**	27.98**
11	SPAD chlorophyll meter reading (%)	-0.27	2.88**	7.58**	2.49	17.97**
12	Chlorophyll stability index (%)	-0.07*	0.03	-0.69**	0.33**	38.48**
13	Membrane injury index (%)	-0.02	-1.23**	-2.32**	-0.53**	37.50**
14	Proline (µ moles g^{-1} FW)	-0.40*	-0.14	-0.36	0.08	5.35*
15	Glycine betaine (µ moles g^{-1} FW)	0.07	0.34	-0.94	-0.67**	8.82**
16	Stomatal frequency					
	ADAX (No./mm^2)	-0.10	-0.50	-25.23**	-12.32**	62.94**
	ABAX (No./mm^2)	0.33	-0.87	-22.23**	-10.85**	80.96**

Table 4: Estimates of genetic effects of a cross for gain yield and its component traits in chickpea

Name of characters		Genetic components						Type of epistasis
		M	D	H	i	J	L	
Days to First flowering (No.)		51.43**	-5.83**	3.43	2.33	-1.33**	4.20*	-
Days to maturity (No.)		111.69**	-12.97**	24.87**	28.90**	-2.87**	-34.90**	Duplicate
Plant height (cm)		87.56**	4.73**	-65.55**	-66.10**	0.10	65.59**	Duplicate
Primary branches (No.)		4.46**	0.62**	-1.23*	-1.47*	-0.12	2.57*	Duplicate
Secondary branches (No.)		14.87**	1.30**	-2.37	-5.47**	-0.47	2.33	-
Pods per plant (No.)		88.66**	7.40**	1.20	-0.70	-0.57	-7.43	-
Seeds per pod (No.)		1.83**	0.07	-2.10**	-2.07**	-0.10	2.20**	Duplicate
100 seed weight (gm)		23.90**	3.27**	0.75	0.24	-0.34	1.71	-
Yield per plant (gm)		44.70**	2.47**	52.75**	53.07**	-0.88	-55.61**	Duplicate
Relative water content (%)		75.78**	8.59**	16.87**	19.17**	3.04*	-25.60**	Duplicate
SPAD chlorophyll meter reading (%)		55.92**	0.39	-4.02	-4.98	-1.58**	2.38	-
Chlorophyll stability index (%)		0.48**	0.03**	0.64**	0.65**	-0.05**	-0.61**	Duplicate
Membrane injury index (%)		11.97**	-0.06	0.48	1.06*	0.60**	0.20	-
Proline (µ moles g^{-1} FW)		2.40**	-1.00**	-0.42	-0.17	-0.13	0.70	-
Glycine betaine (µ moles g^{-1} FW)		3.48**	0.25**	1.44**	1.35**	-0.14	-1.76**	Duplicate
Stomatal frequency	ADAX(No./mm^2)	45.44**	2.83**	24.60**	24.63**	0.20	-24.03**	Duplicate
	ABAX(No./mm^2)	51.13**	3.83**	19.40**	21.70**	0.60	-21.17**	Duplicate

Conclusion

The estimates of A, B, C and D scaling tests and joint scaling test were significant in the cross for sixteen characters with few exceptions. The significance of these cross for various characters indicated inadequacy of additive-dominance model.

1. For grain yield and yield components, the dominant component (h) and dominance x dominance (l) gene interaction was found significant for most of the characters *viz*, days to maturity, plant height, number of primary branches per plant, seeds per pod, grain yield per plant and relative water content, chlorophyll stability index, glycine betaine and stomatal frequency these characters can be improved by hybrid development or by recurrent selection for SCA.
2. Additive gene action along with additive x additive (i) followed by dominance (h) was found significant for the characters *viz*. days to maturity, plant height, number of primary branches per plant, yield per plant, relative water content, chlorophyll stability index, proline, glycine betaine and stomatal frequency. For improvement of these characters, one should follow the simple selection in early segregating generations.

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References

1. Ali, Shivkumar. Chickpea (*Cicer arietinum* L.) research in India: accomplishment and future strategies. Indian Journal of Agricultural Science. 2005;75(3):125-133.
2. Girase VS, Deshmukh RB. Gene action for yield and its components in chickpea. Indian Journal of Genetics and Plant Breeding. 2000;60(2):185-189.
3. Hayman BI. The separation of epistatic from additive and dominance variation in generation means. Heredity. 1958;12(3):371.
4. Hayman BI. The separation of epistatic from additive and dominance variation in generation means. Heredity. 1958;12(3):371.
5. Karami E, Sabaghpour SH, Naghavi MR, Taeb M. Genetic analysis of earliness in chickpea (*Cicer arietinum* L.) using generation mean analysis. Iranian Journal of Pulses Research. 2011;2(2):63-68.
6. Kempthorne O. An introduction to genetic statistics. New York: John Wiley and Sons Inc.; 1957. 545 p.
7. Kumar M, Patel M, Rani K. Delineating genetic inheritance and non-allelic genic interactions for grain iron and zinc concentration, yield and its attributes by generation mean analysis in pearl millet [*Pennisetum glaucum* (L.) R. Br.]. Genetic Resources and Crop Evolution. 2020;69:117-143.
8. Kumar M, Patel M, Rani K. Delineating genetic inheritance and nonallelic genic interactions for grain iron and zinc concentration, yield and its attributes by generation mean analysis in pearl millet [*Pennisetum glaucum* (L.) R. Br.]. Genetic Resources and Crop Evolution. 2022;69:117-143.
9. Ladizinsky G, Adler A. The origin of chickpea *Cicer arietinum* L. Euphytica. 1976;25(1):211-217.
10. Pujar M, Govindaraj M, Gangaprasad S, Kanatti A, Gowda TH, Kumar D, Satish KM. Generation mean analysis reveals the predominant gene effects for grain iron and zinc contents in pearl millet. Frontiers in Plant Science. 2022;12:1-13.
11. Shora HEE, Ali AS. Enhancement the activity of L-asparaginase and antioxidant enzymes in *Cicer arietinum* L. cotyledons under stress conditions. International Journal of Agronomy and Plant Production. 2013;4:3724-3735.