Original Research Article

Generation Mean Analysis for Yield and Drought Related Traits in Maize (*Zea mays* L.)

ABSTRACT

Six generations of two maize crosses were used for computation of generation mean analysis under moisture stressed and non-stressed conditions for yield and drought related traits. Epistasis was observed for all the traits studied in two crosses in both the moisture conditions. The traits number of kernel rows per cob, number of kernels per row, number of grains per cob, grain yield, chlorophyll content and anthesis to silking interval depicted the duplicate gene action under both non stress and moisture stress condition for both the crosses. However relative water content depicted complementary gene action for the cross CIL1221×ZL11243 under both the moisture regimes. Although leaf area index exhibit complementary gene action for cross CAL1411×CZL0713 under both the moisture regimes. In the presence of epistasis, complementary type of gene interaction situation, additive component is often relatively underestimated while dominance effects tend to be overestimated. Duplicate type of epistasis generally hinders improvement through selection and selection of these traits will be difficult in the early generations. Therefore selection should be delayed after several generations of selection (single seed descent) until a high level of gene fixation is attained. Such genotypes could stand better under drought conditions to get maximum yield in maize.

Comment [u1]: Introduce the abstract by stating the overall objective of the study (a sentence or two)

Keywords: Drought tolerance, Epistasis, Generation mean, Gene action, Maize

1. INTRODUCTION

Maize (2n=20) belong to family Poaceae andis the most important cereal crop in the world after wheat and rice. Drought is an important abiotic stress causing the major yield losses in maize in India as well as worldwide. Despite recent agricultural advances, climate play key role in today's agricultural production. In the light of climate changes and global warming, where some areas are expected to be more subjected to frequent severe drought, the development of drought tolerant cultivars is the most efficient and cost effective strategy for fighting drought stress in low-value cropping systems. Therefore, understanding the genetic control of drought tolerance is of a great importance for the applic breeding methods in the development of cultivars with improved tolerance. Since maize seems to be relative adapted to water deficit, it necessary to understand the genetic control and mechanisms of drought stress tolerance.

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Drought tolerance is a complex polygenic trait involved withpowerful epistatic interactions among loci and genotype × environment interactions. However, limited genetic, physiological, and biochemical studies have been carried out in the past two decades to explore the genetic control of drought tolerance and its mechanism in maize. A significa improvement is possible through the development of high yielding cultivars, having wide genetic base and cap producing higher yield under various agro-climatic conditions. For this purpose, basic knowledge of genetic architecture of yield and yield components and nature of gene action is required. Therefore, the present study is aimed to understand the gene action of quantitative traits related to yield and drought tolerance through generation mean analysis.

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2. MATERIAL AND METHODS

For the purpose of gene action study, crosses were made between diverse parents. The seed of six generation **(**F_1, F_2, P_1, P_2, B_1 and B_2) from the crosses CIL1221×ZL11243 and CAL1411×CZL0713 were used in the experiment. Detail of six generation developed for generation mean analysis ~~was given in the following~~is shown intable 1. Six generations *viz.,* F_1, F_2, P_1, P_2, B_1 and B_2 of the two crosses were raised in randomized block design (RBD) during Rabi/summer 2018 at agricultural research farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, consisted of five rows of each parent, five rows of F_1s, 20 rows of F_2s and 10 rows of B_1 and B_2 with 4 m length. The genotypes under non-stress received recommended cultural practices besides regular irrigation (furrow) at an interval of 10-12 days so that they did not experience any moisture stress. Under stress environment, drought stress was applied to the crop ~~during~~ throughout the flowering phase by withholding irrigation. When the flowering was over, the irrigation was again resumed *i.e.,* following 21 days of stress close to the development stage so as to permit grain filling of the pollinated embryos and keep the plants alive. A four-meter buffer zone wasmaintained alongside these trials to separate moisture stressed and control plots. Each genotype was sown in a row with a length of 4m. Rows and plants ~~are~~werespaced by 60 cm and 20 cm, respectively. Pheontypic data was recorded on 16 morpho-physiological traits (*viz.,* plant height, days to 50% tasseling, days to 50%silking, number of cobs per plant, cob length, number of kernel rows per cob, number of kernels per row, number of grains per cob, hundred grain weight, grain yield per plant, plant survival % in drought, leaf area index, relative water content, total chlorophyll content, anthesis silking interval and drought susceptible index) on six generations (*viz.,* F_1, F_2, P_1, P_2, B_1 and B_2) of two crosses.

Statistical analysis

Generation mean analysis was performed using Mather and Jinks method. In this method the mean of each character is indicated as follows:

$Y = m + \alpha [d] + \beta [h] + \alpha^2 [i] + 2 \alpha \beta [j] + \beta^2 [l]$

Where: Y = the mean of one generation. m = the mean of all generation. d = the sum of additive effects. h = the sum of dominance effects. i = the sum of additive × additive interaction. 1 = the sum of dominance × dominance interaction. j = sum of additive × dominance and α, 2αβ and β^2 are the coefficients of genetic parameters.

Simple scaling test adequacy of scale must satisfy two conditions namely, additive of gene effects and independence of heritable components from non-heritable ones. The test of first condition provides information regarding absence or presence of gene interactions. The test of adequacy of scales is important because in most of the cases the estimation of additive and dominance components of variances is made assuming the absence of gene interaction. Mather gave following three tests for scale effects:

$A = 2 B_1 – P_1 – F_1$

$B = 2 B_2 – P_2 – F_1$

$C = 4 F_2 – 2 F_1 - P_1 – P_2$

When the scale is adequate, the values of A, B and C should be zero within the limit of their respective standard errors.

Variances of the above scales

$V_A = 4 V_{B1} + V_{P1} + V_{F1}$

$V_B = 4 V_{B2} + V_{P2} + V_{F1}$

$V_C = 16 V_{F2} + 4 V_{F1} + V_{P1} + V_{P2}$

Standard errors of the above scale:

Where, standard error (SE) is the square root of respective variance.

SE (A) = (VA) ½.

SE (B) = (VB) ½.

SE (C) = (VC) ½.

Now, the 't' values are calculated as follows:

t (A) = A/SE (A)

t (B) = B/SE (B)

t (C) = C/SE (C)

Where, standard error (SE) is the square root of respective variance.

The calculated value of 't' are to be compared with tabulated value of 't' at 5% level of significance. In each test, the degree of freedom is sum of the degrees of freedom of various generations (total number of observations - total number of replications) involved.

Components of generation means

The results of scaling test showing inadequacy of additive-dominance model indicated presence of higher order interaction. Such situation warranted the scope of analysis of data in six parameter model

Six parameter model:

Estimates of various gene effects and non allelic interaction were computed following Jinks and Jones, and Hayman. Formula for estimating both three and six parameter models were derived by solving the equations of expectation of means of generation by simple elimination method.

$F_1 = m + (h) + (1)$

$F_2 = m + ½ (h) + ¼ (l)$

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P_1 = m + (d) + (i)
P_2 = m – (d) + (i)
B_1 = m + ½ (d) + ½ (h) + ¼ (i) + ¼ (j) + ¼ (l)
B_2 = m – ½ (d) + ½ (h) + ¼ (i) + ¼ (j) + ¼ (l)
Where, P_1 = Mean of higher parent P_2 = Mean of lower parent F_1 = Mean of progenies of first generation F_2 = Mean of progenies of second generation B_1 = Mean of backcrosses (F_1 × P_1) progenies B_2 = Mean of backcrosses (F_1 × P_2) progenies. The perfect fit solution is given by formulae of Jinks and Jones
Mean = m = F_2
Additive effect = (d) = $B_1 – B_2$
Dominance effect = (h) = $2B_1 + 2 B_2 + F_1 – 4 F_2 – ½ P_1 – ½ P_2$
Additive × additive epistatic effect = (i) = $2 B_1 + 2 B_2 – 4 F_2$
Additive × dominance epistatic effect = (j) = $B_1 - ½ P_1 – B_2 + ½ P_2$
Dominance × dominance interaction effect = (l) = $P_1 + P_2 + 2 F_1 + 4 F_2 – 4 B_1 – 4 B_2$
Variances of gene effects were computed using following formulae.
$V_m = V_{F2}$
$V_d = V_{B1} + V_{B2}$
$V_h = V_{F1} + 16 V_{F2} + ¼ V_{P2} + 4 V_{B1} + 4 V_{B2}$
$V_i = 4 V_{B1} + 4 V_{B2} + 16 V_{F2}$
$V_j = 4 V_{B1} + 4 V_{B2} + V_{P1} + V_{P2}$
$V_l = V_{P1} + V_{P2} + 4 V_{F1} + 16 V_{F2} + 16 V_{B1} + 16 V_{B1}$
Where,
V_m = Variance of mean effect
V_d = Variance of additive effect
V_h = Variance of dominance effect
V_i = Variance of additive × additive interaction effect
V_j = Variance of additive × dominance interaction effect
V_l = Variance of dominance × dominance interaction effect
B_1 = Back cross 1 and B_2 = Back cross 2. Square roots of the variance provided respective standard errors. The standard errors were used to calculate the 't' values for testing significance of the corresponding variances.
t (m) = √2 SE (m), where, SE (m) = [V (m)]½
t (d) = √2 SE (d), where, SE (d) = [V (d)]½
t (h) = √2 SE (h), where, SE (h) = [V (h)]½
t (i) = √2 SE (i), where, SE (i) = [V (i)]½
t (j) = √2 SE (j), where, SE (j) = [V (j)]½
t (l) = √2 SE (l), where, SE (l) = [V (l)]½
The calculated value of 't' are to be compared with tabulated value of 't' at 5% level of significance. In each test, the degree of freedom is sum of the degrees of freedom of various generations (total number of observations - total number of replications) involved.

3. RESULTS AND DISCUSSION

The genetic studies have been conducted to understand the genetic control of grain yield and its component traits in Maize. These studies have shown that both additive and non additive genes control the grain yield in maize. The detection and estimation of epistasis would also enable the breeders to understand the genetic cause of heterosis with greater reliability. The presence or absence of epistasis can be detected by the analysis of generation means using the scaling test, which measures epistasis accurately whether it is complementary or duplicate at the digenic level reported by Sharmila *et al.* (2007).

The six parameter model of generation mean analysis provides information about all the six parameters (mean effects, additive, dominance, additive × additive gene interaction, additive × dominance gene interaction and dominance × dominance gene interaction) and thereby helps in formulating the guidelines for handling the segregating material in the subsequent generations by the exploitation of fixable component. The genetic feature of the characters would have a direct bearing on the breeding programme for further advancement of the crop.

Scaling test and gene action

In the present study~~revealed that all~~as presented in table…..scaling test were significant for all the sixteen traits under both moisture stress and normal condition of both the crosses. This implies that additive and dominance effects of genes (simple additive dominance model) are not satisfactory to explain the inheritance of characters being investigated. Hence, presence of digenic or higher order non-allelic interaction for all the 16 traits was indicated. It was found necessary to incorporate parameters specifying non-allelic gene interaction effects as explained by Hayman (1958) in six parameter model.

Studies on six generation mean analysis to elucidate information on gene actions governing the inheritance morpho-physiological traits responsible for drought tolerance revealed that the additive variance [d] was positive and significant in respect of plant height under stress and chlorophyll content under non stress for the cross of CIL1221×ZL11243. On the

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other hand cross CAL1411×CZL0713 revealed positive and significant additive variance [d] for plant height, days to 50 per cent anthesis, days to 50 per cent silking and chlorophyll content under both non-stress and stress conditions. However, number of kernel rows per cob, number of kernels per row and number of grains per cob exhibited positive with significant additive variance under non stress condition. The existence of additive variance for these traits has also been reported by Kassem *et al.* (1978a and 1978b), Perez-Velasquez *et al.* (1996) , Saeed *et al.* (2000), Hema *et al.* (2001), Amer *et al.* (2002), Kumar *et al.* (2005) and Singh and Roy (2007).

The variances prevailed due to additive gene actions for above mentioned traits could be well exploited by going for simple selection in the early segregating generations of a cross. However, one should be cautious to know that how for the traits are also influenced by the dominance portion or their interaction component of genetic variance, before initiation of any selection process.

The dominant component [h] variance was positive and significant for the characters like days to 50 per cent anthesis, number of kernel rows per cob, number of kernels per row, number of grains per cob, grain yield, plant survival % in drought, relative water content and chlorophyll content under both stress and non stress condition and plant height, days to 50 per cent silking, number of cobs per plant and hundred seed weight under non-stress condition for the cross CIL1221×ZL11243. On the other hand cross CAL1411×CZL0713 exhibited the dominance variance was positive and significant for 100 seed weight, relative water content and drought susceptibility index under non-stress. However, plant height, cob length, number of kernel rows per cob, number of kernels per row, number of grains per cob and grain yield showed the positive and significant of predominance of dominant variance under both non-stress and stress conditions.

Therefore, it is evident that non-additive gene actions prevailed in two crosses CIL1221×ZL11243 and CAL1411×CZL0713 for most of the traits. The results clearly indicate that seed yield and some of its important determinant traits are under the influence of both additive and non-additive gene actions. Similar results were reported by Saeed *et al.* (2000), Vidal Martinez *et al.* (2001) , Amer *et al.* (2002), Rezai and Rochi (2004), Kumar *et al.* (2005), Sofi *et al.* (2006), Alam *et al.* (2008), Akbar *et al.* (2008). Since maize is a cross pollinated crop, exploitation of both additive and non-additive gene actions is essential in heterosis breeding programmes to surpass the yield level of commercial check hybrids.

Among the fixable epistatic component of genetic variance additive× additive effects found to be positive and significant for days to 50 per cent silking, number of grains per cob, hundred seed weight and grain yield under non-stress condition and cob length, number of grains per cob and chlorophyll content under stress. However, days to 50 per cent anthesis and number of kernel rows per cob exhibited significant positive additive× additive interaction effects under both conditions for the cross CIL1221×ZL11243. On the other hand, The cross CAL1411×CZL0713 revealed significant positive additive × additive interaction effects for cob length and number of kernels per row under non-stress condition and plant height, number of kernel rows per cob and drought susceptibility index under stress. However, number of grains per cob and grain yield exhibited significant positive additive × additive interaction effects under both conditions.

Thus, these crosses can be advanced by selfing to exploit fixable portion of additive interactions especially for seed yield and its major yield traits when objective is to develop superior inbred lines. The significant additive × additive interaction effects for above mentioned traits were reported by Gamble (1962a and 1962b), Kassem *et al.* (1978a and 1978b), Melchinger *et al.* (1986) and Kumar *et al.* (2005). Therefore, selection in an early segregating generation for the improvement of these traits could be advantageous.

The cross CAL1411×CZL0713 exhibited positive and significant dominance × dominance interaction effects for days to 50 per cent anthesis, days to 50 per cent silking, number of cobs per plant, cob length, number of kernel rows per cob, number of kernels per row, number of grains per cob, hundred seed weight, grain yield, chlorophyll content and anthesis to silking interval showed significant positive dominance × dominance interaction effects under both non-stress and stress conditions. On the other hand, the cross CAL1411×CZL0713 revealed significant positive dominance × dominance interaction effects for plant height under non-stress condition. However, hundred seed weight, leaf area index, relative water content, chlorophyll content and anthesis to silking interval under both conditions exhibited significant positive dominance × dominance interaction effects. While days to 50 per cent silking and plant survival % in drought exhibited significant positive dominance × dominance interaction effects under stress. The similar findings were reported by Gamble (1962a and 1962b), Kassem *et al.* (1978a and 1978b), Wolf and Hallauer (1977) and Iqbal *et al.* (2010). Therefore, traits were influenced by dominance (h) and dominance × dominance (l) gene action, selection of these traits will be difficult in the early generations.

In the cross CIL1221×ZL11243 dominance variance [h] and dominance × dominance [l] interaction exhibited opposite sign for plant height, days to 50 per cent anthesis, number of cobs per plant, cob length, number of kernel rows per cob, number of kernels per row, number of grains per cob, 100 seed weight, grain yield, chlorophyll content and anthesis to silking interval depicted the duplicate gene action under both non stress and stress condition. While relative water content exhibit complementary gene action by possessing positive values of both dominance variance [h] and dominance × dominance [l] interaction exhibited complementary gene action under both stress and non stress condition. However, days to 50 per cent silking, plant survival % in drought, leaf area index, relative water content and drought susceptibility index under stress condition depicted the complementary gene action while that trait exhibited duplicate gene action under non stress condition.

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Whereas the opposite sign for dominance variance (h) and dominance × dominance (l) interactions in cross CAL1411×CZL0713 for number of kernel rows per cob, number of kernels per row, number of grains per cob, grain yield, plant survival % in drought, relative water content, chlorophyll content, anthesis to silking interval and drought susceptibility index depicted the duplicate gene action under both non stress and stress condition. While leaf area index exhibit complementary gene action by possessing positive values of both dominance variance [h] and dominance × dominance [l] interaction exhibited complementary gene action under both stress and non stress condition. However plant height, days to 50 per cent anthesis, number of cobs per plant and cob length under stress condition depicted the duplicate gene action while these traits exhibited complementary gene action under non stress condition, while hundred seed weight under stress condition depicted the complementary gene action while that trait exhibited duplicate gene action under non stress condition. Similar results were reported by Wolf and Hallauer (1977), Ndu and Openshaw (1999) and Ishfaq (2011). The studies suggest that selection in the early segregating generations is not effective and it is always better to go for selection in the advanced generations with the possibility of transgressive segregants being more in the later stages.

In the presence of epistasis, complementary type of gene interaction situation additive component is often relatively underestimated while dominance effects tend to be overestimated. Duplicate type of epistasis generally hinders improvement through selection and hence, a higher magnitude of dominance and dominance × dominance type of interaction effects would not be expected. It also indicated that selection should be delayed after several generations of selection (single seed descent) until a high level of gene fixation is attained. Subsequent inter mating between promising lines may be important in accumulating favorable genes.

4. CONCLUSION

As selection based on progeny performance exploits only additive component of genetic variances, for these traits bi-parental mating followed by recurrent selection or diallel selective mating, which allows inter mating among the selected segregates in the different cycles, would be useful to recover superior homozygote in later generations normal breeding methods would not be fruitful and the methods which will exploit non-additive gene effect and take care of non-allelic interactions such as restricted recurrent selection by way of inter mating the most desirable segregates, followed by selection or diallel selective mating or multiple crosses or bi-parental mating in early segregating generations could be promising for genetic improvement of yield and associated traits. In addition, few cycles of recurrent selection, followed by pedigree method may also be useful for the effective utilization of all three types of gene effects simultaneously. It will lead towards an increased variability in later generations for effective selection by maintaining considerable heterozygozity through mating of selected plants in early segregating generations. These breeding approaches could be helpful in developing maize populations, which upon selection will result in the most desirable yield traits along with drought tolerant genotypes. Such genotypes could stand better under drought conditions to get maximum yield in maize.

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TABLE.1. DETAILS SIX GENERATIONS OF TWO CROSSES

SL. NO.	GENERATION	CROSS NUMBER 1	CROSS NUMBER 2	TOTAL NUMBER OF PLANTS SELECTED
1	P_1	CIL1221 (DROUGHT SUSCEPTIBLE)	CAL1411 (DROUGHT SUSCEPTIBLE)	30
2	P_2	ZL11243 (DROUGHT TOLERANT)	CZL0713 (DROUGHT TOLERANT)	30
3	F_1	CIL1221×ZL11243	CAL1411×CZL0713	30
4	F_2	CIL1221×ZL11243 (SELFING)	CAL1411×CZL0713 (SELFING)	120
5	B_1	F_1×CIL1221	F_1×CAL1411	60
6	B_2	F_1×ZL11243	F_1×CZL0713	60

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Table 2. Estimates of scaling tests and genetic components of cross CIL1221×ZL11243 for morpho-physiological characters under non-stress

Parameters	Plant height	Days to 50 per cent anthesis	Days to 50 per cent silking	No of cobs per plant	Cob length	Number of kernel rows per cob	No of kernels per row
P1	160.33±0.12	50.10±0.12	52.15±0.11	1.23±0.06	15.76±0.09	12.50±0.10	23.65±0.12
P2	164.12±0.20	54.18±0.10	57.12±0.13	1.60±0.09	18.20±0.09	12.96±0.09	37.98±0.12
F1	196.98±0.24	50.95±0.18	51.99±0.18	1.96±0.04	18.05±0.47	13.78±0.06	44.00±0.14
F2	193.12±0.50	51.96±0.48	55.54±0.21	1.70±0.04	18.58±0.24	12.50±0.17	41.97±0.25
B1	185.65±0.17	54.14±0.17	56.98±0.16	1.83±0.05	18.00±0.17	13.28±0.09	41.74±0.22
B2	189.77±0.19	54.77±0.19	57.03±0.26	1.69±0.06	17.68±0.13	13.18±0.08	42.05±0.16
Scaling tests (Mather, 1949)							
A	13.99±0.45**	7.22±0.42**	9.81±0.39**	0.47±0.12**	2.19±0.60**	0.28±0.23NS	15.84±0.49**
B	18.44±0.49**	4.41±0.43**	4.95±0.57**	-0.17±0.16NS	-0.88±0.55NS	-0.38±0.20NS	2.11±0.37**
C	54.08±2.09**	1.66±2.00NS	8.90±0.93**	0.06±0.22NS	4.24±1.36**	-2.99±0.71**	18.27±1.08**
Best fit model (Hayman, 1958)							
m	193.12±0.50**	51.96±0.48**	55.54±0.21**	1.70±0.04**	18.58±0.24**	12.50±0.17**	41.97±0.25**
(d)	-4.11±0.26**	-0.63 ±0.26*	-0.05±0.31NS	0.13±0.07NS	0.32±0.22NS	0.10±0.12NS	-0.3± 0.27NS
(h)	13.11±2.10**	8.77±2.03**	3.21±1.07**	0.78±0.24**	-1.86±1.17NS	3.94±0.73**	12.85±1.18**
(i)	-21.63±2.09**	9.96±2.02**	5.86±1.05**	0.24±0.23NS	-2.93±1.06**	2.89±0.72**	-0.32±1.16NS
(j)	-2.22±0.28**	1.40±0.27**	2.43±0.32**	0.32±0.09**	1.54±0.23**	0.33±0.14*	6.86±0.29**
(l)	-10.80±2.34**	-21.60±2.25**	-20.63±1.56**	-0.55±0.39NS	1.62±1.63NS	-2.79±0.87**	-17.63±1.55**
Gene effects	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate

* and **significance at 5 % and 1 % levels, respectively

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Comment [u7]: Remove vertical lines and borders

UNDER PEER REVIEW

Parameters	No of grains per cob	Hundred seed weight	Grain yield	LAI	RWC	Chlorophyll content	ASI
P1	295.46±0.35	26.28±0.17	77.67±0.53	1.70±0.0015	62.10±0.12	50.19±0.14	2.05±0.14
P2	492.17±0.42	30.01±0.10	147.74±0.55	1.74±0.0022	61.18±0.10	57.15±0.15	2.94±0.19
F1	606.39±0.50	38.18±0.15	231.68±0.50	2.87±0.0025	72.95±0.18	56.26±0.15	1.08±0.14
F2	525.54±0.40	34.90±0.24	183.25±0.81	2.53±0.0050	67.41±0.40	55.69±0.29	3.53±0.21
B1	554.37±0.35	35.97±0.19	199.03±0.54	1.96±0.0018	65.95±0.17	55.88±0.25	2.84±0.25
B2	554.30±0.53	35.77±0.19	198.61±0.58	2.06±0.0018	66.77±0.19	55.00±0.22	2.25±0.23
Scaling tests (Mather, 1949)							
A	206.88±0.93**	7.47±0.46**	88.71±1.31**	-0.65±0.0046**	-3.14±0.41**	5.3±0.56**	2.55±0.54**
B	10.04±1.25**	3.35±0.42**	17.81±1.38**	-0.48±0.0049**	-0.59±0.43NS	-3.40±0.49**	0.48±0.53NS
C	101.73±1.98**	6.94±1.05**	44.24±3.50**	0.93±0.0209**	0.46±1.68NS	2.89±1.25**	6.97±7.47**
Best fit model (Hayman, 1958)							
m	525.54±0.40**	34.90±0.24**	183.25±0.81**	2.5±0.0050**	67.41±0.40**	55.69±0.29**	3.53±0.21**
(d)	0.06±0.63NS	0.19±0.27NS	0.41±0.79NS	-0.10±0.0025**	-0.81±0.25**	0.88±0.34*	0.58±0.34NS
(h)	327.76±2.13**	13.90±1.14**	181.25±3.68**	-0.92±0.0210**	7.11±1.72**	1.61±1.38NS	-5.35±1.11**
(i)	115.19±2.05**	3.87±1.13**	62.28±3.63**	-2.06±0.0208**	-4.19±1.71*	-0.97±1.37NS	-3.93±1.09**
(j)	98.41±0.69**	2.06±0.29**	35.45±0.88**	-0.08±0.0029**	-1.27±0.27**	4.36±0.35**	1.03±0.36**
(l)	-332.12±3.22**	-14.69±1.52**	-168.81±4.73**	3.20±0.0233**	7.92±1.97**	-0.94±1.85NS	0.89±1.66NS
Gene effects	Duplicate	Duplicate	Duplicate	Duplicate	Complementary	Duplicate	Duplicate

* and **significance at 5 % and 1 % levels, respectively

UNDER PEER REVIEW

Table 3. Estimates of scaling tests and genetic components of cross CIL1221×ZL11243 for morpho-physiological characters under moisture stress

Parameters	Plant height	Days to 50 per cent anthesis	Days to 50 per cent silking	No of cobs per plant	Cob length	No. of kernel rows per cob	No. of kernels per row	No. of grains per cob
P1	143.50± 0.12	53.93±0.18	61.01±0.15	1.91±0.06	10.05±0.07	9.12±0.05	17.26±0.16	157.43±0.55
P2	160.13±0.14	55.92±0.18	59.92±0.12	2.05±0.06	13.10±0.06	11.30±0.06	30.72±0.12	347.47±0.67
F1	174.70±0.49	54.00±0.17	57.98±0.17	2.18±0.07	15.92±0.06	13.49±0.08	38.70±0.15	522.22±0.97
F2	174.03±0.46	56.86±0.34	62.94±0.34	2.12±0.05	12.28±0.29	11.40±0.15	38.16±0.17	440.98±1.17
B1	172.46±0.06	57.96±0.17	62.53±0.16	2.16±0.06	13.21±0.03	11.82±0.05	36.96±0.09	437.07±0.43
B2	163.85±0.11	58.92±0.14	63.34±0.17	2.07±0.04	13.16±0.06	12.43±0.05	37.08±0.10	461.11±0.33
Scaling tests (Mather, 1949)								
A	26.71±0.52**	7.99±0.43**	6.06±0.40**	0.23±0.15NS	0.45±0.12**	1.03±0.15**	17.94±0.29**	194.48±1.42**
B	-7.13±0.56**	7.92±0.39**	8.78±0.40**	-0.08±0.13NS	-2.71±0.16**	0.07±0.16NS	4.72±0.29**	52.52±1.36**
C	43.06±2.11**	9.59±1.45**	14.86±1.43**	0.18±0.27NS	-5.86±1.17**	-1.78±0.64**	27.25±0.80**	214.60±5.15**
Best fit model (Hayman, 1958)								
m	174.03±0.46**	56.86±0.34**	62.94±0.34**	2.12±0.05**	12.28±0.29**	11.40±0.15**	38.16±0.17**	440.98±1.17**
(d)	8.60±0.13**	-0.95±0.22**	-0.81±0.23**	0.09±0.07NS	0.05±0.075NS	-0.61±0.08**	-0.11±0.14NS	-24.04±0.55**
(h)	-0.59±1.94NS	5.39±1.47**	-2.50±1.47NS	0.17±0.28NS	7.95±1.17**	6.17±0.63**	10.13±0.78**	302.18±4.92**
(i)	-23.48±1.88**	6.3±1.45**	-0.013±1.46NS	-0.026±0.26NS	3.60±1.17**	2.89±0.63**	-4.57±0.76**	32.41±4.81**
(j)	16.92±0.16**	0.03±0.26NS	-1.36±0.25**	0.16±0.09NS	1.58±0.09**	0.48±0.09**	6.60±0.17**	70.97±0.70**
(l)	3.89±2.18NS	-22.23±1.71**	-14.83±1.72**	-0.12±0.41NS	-1.34±1.21NS	-3.99±0.71**	-18.10±0.98**	-279.42±5.60**
Gene effects	Duplicate	Duplicate	Complementary	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate

* and **significance at 5 % and 1 % levels, respectively

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UNDER PEER REVIEW

Parameters	100 seed weight	Grain yield	plant survival %	LAI	RWC	Chlorophyll content	ASI	DSI
P1	22.19±0.07	34.63±0.22	82.43±0.22	1.47±0.01	41.93±0.18	27.73±0.16	7.07±0.21	1.14±0.06
P2	26.67±0.10	92.68±0.43	89.10±0.37	1.68±0.0018	44.97±0.23	39.77±0.19	4.00±0.19	0.58±0.04
F1	28.91±0.22	151.08±0.49	99.96±0.03	2.00±0.0013	51.92±0.18	37.85±0.16	3.97±0.26	0.96±0.03
F2	28.11±0.34	123.54±1.12	95.52±0.16	1.94±0.0010	47.84±0.25	32.94±0.35	6.07±0.19	1.04±0.01
B1	25.96±0.08	113.48±0.41	91.90±0.35	1.82±0.0007	47.70±0.19	34.05±0.09	4.56±0.22	1.00±0.0023
B2	27.77±0.19	128.04±0.62	93.46±0.22	1.85±0.0132	47.74±0.20	36.18±0.14	4.42±0.23	0.99±0.0022
Scaling tests (Mather, 1949)								
A	0.81±0.29**	41.23±0.99**	1.40±0.73NS	0.17±0.0166**	1.55±0.46**	2.51±0.30**	-1.92±0.56**	-0.11±0.07NS
B	-0.03±0.45NS	12.30±1.41**	-2.13±0.58**	0.0177±0.0265NS	-1.40±0.50**	-5.25±0.39**	0.87±0.57NS	0.44±0.05**
C	5.76±1.45**	64.66±4.61**	10.63±0.79**	0.6057±0.0173**	0.62±1.13NS	-11.44±1.47**	5.28±0.98**	0.52±0.13**
Best fit model (Hayman, 1958)								
m	28.11±0.34**	123.54±1.12**	95.52±0.16**	1.9452 ±0.0010**	47.84±0.25**	32.94±0.35**	6.07±0.19**	1.0494±0.0193**
(d)	-1.81±0.20**	-14.56±0.75**	-1.56±0.41**	-0.0250±0.0132NS	-0.04±0.28NS	-2.13±0.17**	0.13±0.32NS	0.0018±0.0032NS
(h)	-0.50±1.46NS	76.30±4.76**	2.83±1.08**	0.0098±0.0280NS	7.99±1.19**	12.80±1.47**	-7.90±1.05**	-0.0912±0.0943NS
(i)	-4.98±1.44**	-11.11±4.72*	-11.36±1.06**	-0.4147±0.0267**	-0.46±1.17NS	8.70±1.45**	-6.33±1.01**	-0.1960±0.0774*
(j)	0.42±0.21NS	14.46±0.79**	1.76±0.47**	0.0778±0.0156**	1.47±0.31**	3.88±0.22**	-1.40±0.35**	-0.2763±0.0371**
(l)	4.20±1.68*	-42.43±5.51**	12.10±1.85**	0.2236±0.0556**	0.31±1.60NS	-5.96±-3.64**	7.39±1.63**	-0.1367±0.1331NS
Gene effects	Duplicate	Duplicate	Complementary	Complementary	Complementary	Duplicate	Duplicate	Complementary

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* and **significance at 5 % and 1 % levels, respectively

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Table 4. Estimates of scaling tests and genetic components of cross CAL1411×CZL0713 for morpho-physiological characters under non-stress

Parameters	Plant height	Days to 50 per cent anthesis	Days to 50 per cent silking	No of cobs per plant	Cob length	Number of kernel rows per cob	No of kernels per row
P1	140.63±0.19	54.74±0.30	59.25±0.12	1.33±0.05	14.61±0.16	11.25±0.14	35.44±0.18
P2	152.61±0.19	53.15±0.18	56.37±0.15	1.72±0.08	17.02±0.20	13.88±0.15	35.70±0.19
F1	167.78±0.19	50.33±0.14	51.40±0.15	1.90±0.06	25.57±0.19	13.55±0.18	42.90±0.19
F2	158.10±0.35	53.53±0.25	56.53±0.22	1.79±0.03	17.87±0.23	13.07±0.25	41.72±0.34
B1	157.81±0.30	53.97±0.28	56.07±0.19	1.70±0.05	18.54±0.14	13.69±0.14	44.50±0.22
B2	150.06±0.33	52.45±0.13	54.90±0.20	1.74±0.05	19.37±0.15	13.26±0.14	43.69±0.21
Scaling tests (Mather, 1949)							
A	7.21±10.90**	2.87±0.66**	1.47±0.43**	0.17±1.15NS	-3.10±0.38**	2.57±0.37**	10.66±0.53**
B	-20.25±-27.62**	1.42±0.36**	2.02±0.45**	-0.13±-0.83NS	-3.85±0.42**	-0.92±0.37*	8.78±0.50**
C	3.60±2.42*	5.58±1.12**	7.67±0.98**	0.30±1.39NS	-11.30±1.03**	0.05±1.10NS	9.96±1.46**
Best fit model (Hayman, 1958)							
m	158.10±0.35**	53.53±0.25**	56.53±0.22**	1.79±0.03**	17.87±0.23**	13.07±0.25**	41.72±0.34**
(d)	7.74±0.45**	1.51±0.31**	1.16±0.28**	-0.04±0.08NS	-0.82±0.21**	0.43±0.20*	0.80±0.31*
(h)	4.51±1.69**	-4.90±1.22**	-10.58±1.09**	0.11±0.23NS	14.10±1.04**	2.58±1.11*	16.81±1.53**
(i)	-16.64±1.67**	-1.28±1.20NS	-4.17±1.07**	-0.26±0.22NS	4.34±1.01**	1.59±1.09NS	9.48±1.51**
(j)	13.73±0.47**	0.72±0.36*	-0.27±0.29NS	0.15±0.09NS	0.37±0.25NS	1.74±0.22**	0.93±0.33**

(l)	29.68±2.34**	-3.01±1.69NS	0.67±1.49NS	0.22±0.39NS	2.61±1.34NS	-3.24±1.37*	-28.94±1.92**
Gene effects	Complementary	Complementary	Duplicate	Complementary	Complementary	Duplicate	Duplicate

* and **significance at 5 % and 1 % levels, respectively

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Parameters	No of grains per cob	Hundred seed weight	Grain yield	LAI	RWC	Chlorophyll content	ASI
P1	398.80±0.76	32.69±0.09	130.40±0.45	1.80±0.02	54.79±0.17	35.37±0.18	4.51±0.31
P2	495.28±0.79	35.17±0.17	174.22±0.61	1.78±0.017	55.96±0.21	42.39±0.22	3.22±0.09
F1	581.13±0.23	35.03±0.17	203.35±0.70	2.64±0.088	64.22±0.20	54.09±0.27	1.08±0.04
F2	545.49±1.53	30.13±0.47	164.31±0.91	2.20±0.038	62.25±0.54	54.06±0.31	3.02±0.09
B1	609.42±0.56	27.93±0.13	170.36±0.70	2.03±0.023	59.90±0.31	50.04±0.20	2.10±0.05
B2	579.30±0.52	30.81±0.18	178.91±0.67	2.10±0.015	60.04±0.23	49.22±0.18	2.45±0.19
Scaling tests (Mather, 1949)							
A	238.91±1.37**	-11.86±0.33**	6.98±1.63**	-0.38±0.10**	0.77±0.69NS	10.61±0.52**	-1.38±0.33**
B	82.20±1.34**	-8.57±0.44**	-19.74±1.64**	-0.22±0.09*	-0.10±0.56NS	1.96±0.50**	0.60±0.40NS
C	125.63±6.25**	-17.38±1.95**	-54.08±4.00**	-0.04±0.23NS	9.80±2.24**	30.31±1.39**	2.20±0.52**
Best fit model (Hayman, 1958)							
m	545.49±1.53**	30.13±0.47**	164.31±0.91**	2.20±0.03**	62.25±0.54**	54.06±0.31**	3.02±0.09**
(d)	30.11±0.76**	-2.88±0.22**	-8.54±0.97**	-0.06±0.02*	-0.14±0.39NS	0.81±0.27**	-0.34±0.20NS
(h)	329.56±6.35**	-1.94±1.97NS	92.35±4.23**	0.28±0.18NS	-0.27±2.34NS	-2.52±1.39NS	-5.76±0.59**
(i)	195.48±6.32**	-3.04±1.96NS	41.31±4.15**	-0.56±0.16**	-9.12±2.33**	-17.72±1.35**	-2.98±0.56**
(j)	78.35±0.94**	-1.64±0.24**	13.36±1.04**	-0.07±0.03*	0.43±0.42NS	4.32±0.30**	-0.99±0.26**
(l)	-516.59±6.97**	23.48±2.15**	-28.54±5.59**	1.18±0.26**	8.44±2.75**	5.14±1.76**	3.76±0.96**
Gene effects	Duplicate	Duplicate	Duplicate	Complementary	Duplicate	Duplicate	Duplicate

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* and **significance at 5 % and 1 % levels, respectively

Table 5. Estimates of scaling tests and genetic components of cross CAL1411×CZL0713 for morpho-physiological characters under moisture stress

Parameters	Plant height	Days to 50 per cent anthesis	Days to 50 per cent silking	No of cobs per plant	Cob length	No. of kernel rows per cob	No. of kernels per row	No. of grains per cob
P1	120.12±0.35	57.75±0.22	68.44±0.17	1.91±0.06	13.35±0.11	9.51±0.08	27.34±0.18	260.30±0.56
P2	144.85±0.23	55.28±0.21	61.60±0.15	2.05±0.06	14.15±0.14	12.15±0.05	27.99±0.20	340.11±0.49
F1	155.11±0.28	52.03±0.15	57.34±0.16	2.18±0.07	19.95±0.17	12.16±0.07	35.25±0.18	428.32±0.55
F2	143.62±0.46	55.81±0.29	61.79±0.31	2.10±0.03	16.19±0.29	12.10±0.17	37.11±0.28	449.46±0.93
B1	151.80±0.20	55.98±0.17	61.57±0.12	2.16±0.06	16.15±0.10	12.72±0.12	37.31±0.12	474.60±0.47
B2	143.8±0.18	53.99±0.16	60.29±0.11	2.07±0.04	17.41±0.12	12.61±0.06	37.68±0.13	475.58±0.60
Scaling tests (Mather, 1949)								
A	28.38±0.60**	2.18±0.44**	-2.64±0.35**	0.23±0.15NS	-1.00±0.29**	3.76±0.27**	12.02±0.35**	260.56±1.23**
B	-12.23±0.52**	0.66±0.43NS	1.64±0.31**	-0.08±0.13NS	0.71±0.33*	0.91±0.15**	12.12±0.37**	182.73±1.41**
C	-0.67±1.96NS	6.16±1.24**	2.45±1.32NS	0.06±0.23NS	-2.66±1.25*	2.44±0.73**	22.61±1.23**	340.77±3.95**
Best fit model (Hayman, 1958)								
m	143.62±0.46**	55.81±0.29**	61.79±0.31**	2.10±0.03**	16.19±54.35**	12.10±0.17**	37.11±0.28**	449.46±0.93**
(d)	7.94±0.27**	1.99±0.24**	1.27±0.16**	0.09±0.07NS	-1.25±-7.70**	0.10±0.14NS	-0.37±0.18*	-0.98±0.76NS
(h)	39.45±1.95**	-7.80±1.27**	-11.13±1.31**	0.28±0.23NS	8.58±6.86**	3.57±0.76**	9.13±1.22**	230.64±4.08**

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(i)	16.83±1.91**	-3.31±1.25**	-3.44±1.30**	0.08±0.21NS	2.37±1.92NS	2.24±0.76**	1.54±1.20NS	102.52±4.02**
(j)	20.30±0.34**	0.75±0.29**	-2.14±0.20**	0.16±0.09NS	-0.85±-4.57**	1.42±0.15**	-0.04±0.22NS	38.91±0.85**
(l)	-32.98±2.25**	0.47±1.58NS	4.44±1.48**	-0.24±0.38NS	-2.09±-1.47NS	-6.93±0.92**	-25.69±1.42NS	-545.82±5.00**
Gene effects	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate	Duplicate

* and **significance at 5 % and 1 % levels, respectively

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Parameters	100 seed weight	Grain yield	Plant survival % indrought	LAI	RWC	Chlorophyll content	ASI	DSI
P1	24.28±0.14	63.21±0.42	82.46±0.27	1.47±0.01	41.93±0.18	24.72±0.16	10.68±0.31	1.11±0.058
P2	25.86±0.13	87.97±0.47	88.33±0.23	1.68±0.0018	49.92±0.18	30.81±0.16	6.33±0.18	0.52±0.035
F1	28.50±0.22	122.37±0.48	99.96±0.03	2.00±0.0013	50.00±0.17	38.08±0.14	5.30±0.21	0.74±0.030
F2	23.94±0.31	107.62±1.41	99.05±0.02	1.94±0.0010	47.90±0.26	38.01±0.29	5.94±0.16	0.23±0.016
B1	23.32±0.14	110.85±0.53	90.50±0.28	1.82±0.0007	47.96±0.17	34.07±0.09	5.56±0.19	0.47±0.016
B2	24.17±0.15	114.74±0.56	93.46±0.22	1.85±0.0132	48.92±0.14	33.68±0.14	6.30±0.07	0.68±0.011
Scaling tests (Mather, 1949)								
	Ch 9	Ch 10	Ch 11	Ch 12	Ch 13	Ch 14	Ch 15	Ch 16
A	-6.13±0.38**	36.12±28.93**	-1.43±0.62*	0.17±0.0166**	3.99±0.43**	5.33±0.29**	-4.86±0.54**	-0.90±0.073**
B	-6.02±0.40**	19.13±14.58**	-1.36±0.51**	0.0177±0.0265NS	-2.07±0.39**	-1.53±0.36**	0.97±0.32**	0.09±0.052NS
C	-11.38±1.34**	34.57±5.98**	25.46±0.37**	0.60±0.0173**	-0.26±1.15NS	20.35±1.22**	-3.86±0.88**	-2.19±0.112**
Best fit model (Hayman, 1958)								
m	23.94±0.31**	107.62±1.41**	99.05±0.02**	1.9452 ±0.0010**	47.90±0.26**	38.01±0.29**	5.94±0.16**	0.23±0.016**
(d)	-0.84±0.21**	-3.88±0.77**	-2.96±0.36**	-0.0250±0.0132NS	-0.95±0.22**	0.39±0.17*	-0.74±0.20**	-0.20±0.019**

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(h)	2.65±1.34*	67.46±5.89**	-13.70±0.75**	0.0098±0.0280NS	6.26±1.18**	-6.24±1.22**	-3.22±0.84**	1.30±0.089**
(i)	-0.77±1.32NS	20.68±5.86**	-28.26±0.73**	-0.4147±0.0267**	2.18±1.16NS	-16.55±1.21**	-0.02±0.79NS	1.38±0.076**
(j)	-0.05±0.23NS	8.49±0.83**	-0.03±0.40NS	0.0778±0.0156**	3.03±0.26**	3.43±0.21**	-2.91±0.27**	-0.50±0.039**
(l)	12.92±1.58**	-75.95±6.55**	31.06±1.50**	0.2236±0.0556**	-4.10±1.47**	12.75±1.41**	3.91±1.21**	-0.57±0.137**
Gene effects	Complementary	Duplicate	Duplicate	Complementary	Duplicate	Duplicate	Duplicate	Duplicate

* and **significance at 5 % and 1 % levels, respectively

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