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Evaluation of P₁, P₂, F₁, F₂, B₁ and B₂ generations of ML 267 × LGG 528 cross of Mung bean for yield, yield attributes along with WUE and heat stress tolerance related traits using generation mean analysis

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Abstract

The mean data obtained from six generations (P₁, P₂, F₁, F₂, B₁ and B₂) of selected superior cross ML 267 × LGG 528 for yield, yield components, WUE and heat stress tolerance related traits were subjected to generation mean analysis. Partitioning of generation means into six components revealed that the component mean $[m]$ was positive and highly significant for all the traits. The results of scaling tests revealed that additive-dominance model was not sufficient to explain the inheritance of the characters studied. The inadequacy of additive-dominance model suggested the possible involvement of di-genic or higher order epistatic gene action in the expression of all the traits. It also indicated that presence of positively significant proportion of epistatic $\{[i], [j]$ and $[l]\}$ effects besides main $\{[d]$ and $[h]\}$ effects for yield, yield attributes, WUE and heat stress tolerance related traits. The findings divulged that both additive and the dominance components were important in the inheritance of yield, water use efficiency and heat stress tolerance related components.

Keywords: mungbean, generation mean analysis, water use efficiency

Introduction

Green gram, popularly known as mungbean is the third important legume after chickpea and pigeon pea. It is a self pollinating, short duration legume that belongs to family Fabaceae with a chromosome number of $2n=22$. Our national production and productivity levels of mungbean are low, which indirectly affects the nutrient availability of people resulting in malnutrition. Among several reasons for low productivity, various biotic and abiotic factors play a major role. Among the abiotic stresses, drought stress and heat stress are prominent, which seriously influences the mungbean productivity. Water deficits and high temperature occur together in many environments and both stresses can interact to reduce yields. Although intensive research work has been done on genetic architecture of yield and yield attributes of mungbean but limited work was done on yield attributes along with water use efficiency (WUE) and heat stress tolerance related traits. Realizing the significance of drought and heat stress on yield components there is an immediate need to enhance the genetic potential of mungbean genotypes with high yield and drought and heat stress tolerance.

Water use efficiency is one of the genetic characters which can contribute to higher productivity under scarce water resources. Hence, a proper understanding and appreciation of the differences in water use efficiency and relationship of water use efficiency with other parameters are essential to plan strategies for yield improvement in water scarce areas. Assessment of inter-relationship among surrogate traits of water use efficiency with yield and its components is essential for formulating selection strategy to combine water use efficiency conferring traits with higher yield.

So far, the approach to breeding cultivars with superior yield performance under water limited conditions has remained empirical, *via*; selection for yield under stress conditions. More rapid progress may be achieved by a prior knowledge of the physiological basis of surrogate traits related to WUE, such as specific leaf area (SLA), soil and plant analytical development chlorophyll meter reading (SCMR) and specific leaf weight (SLW). SLA is negatively correlated with WUE whereas SCMR is positively associated with WUE (Nageswara Rao *et al.*, 2001) ^[13, 15]. Hence, these traits could be used for selecting higher water use efficient green gram genotypes.

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This provides sufficient justification for the use of SLA and SCMR as potential surrogate traits for selecting genotypes with enhanced WUE (Nageswara Rao *et al.*, 2001) [13, 15]. Cultivars with more SLW had thick leaves (reduced surface area to volume ratio) and exhibit improved water use efficiency (Brown and Byrd, 1997; Thumma *et al.*, 1998) [2, 20].

High temperature stress during germination and flowering causes considerable yield losses in mungbean. Temperature is rising day by day, which highly affects the crop at different phenophases, ultimately yield. It causes cell death, burning, flower drop, pollen abortion, shortening the grain filling duration etc. (Khalil *et al.*, 2009) [9]. Thus there is a dire need to develop heat tolerant varieties in this challenging era. Heat tolerance is determined by measuring relative injury percentage. Cell membrane integrity is tested by exposing leaves to high temperature and computing relative injury to the membranes in terms of electrolytes leakage. Lower leakage indicates lower the injury and higher the thermo tolerance.

The knowledge of gene action involved in the expression of various polygenic characters is essential to a plant breeder. It is useful in deciding the plant breeding procedure for genetic improvement of various polygenic characters. Generation mean analysis technique provides information about the genetic components of variance (d, h, i, j, l). Such information helps in deciding a suitable breeding procedure for improvement of various metrical traits of a crop species. This also provides information about the type of epistasis, which depends on the sign of two components only, *viz.*, h and l. Those crosses in which h and l have similar sign indicate presence of complementary epistasis, and opposite sign reveal duplicate epistasis. Hayman's generation mean analysis could be considered as one of the best options available to gain the information on nature and magnitude of gene action as it partitions the gene effects into additive, dominance and epistatic effects involved in the expression of traits.

The significance of A and B scales indicates the presence of all the three types of non-allelic interactions *viz.*, additive \times additive (i), additive \times dominance(j) and dominance \times dominance (l). The significance of C scale suggests dominance \times dominance (l) type of interaction. The significance of D scale reveals additive \times additive (i) type of gene interaction and significance of both C and D scales indicates additive \times additive and dominance \times dominance type of gene interactions. The significance of any one of the scaling tests indicates inadequacy of simple additive - dominance model.

In the present investigation, an attempt has been made to understand the genetics of yield, yield attributes along with WUE and heat stress tolerance related traits in the selected mungbean cross. Hayman's six parameter model of generation mean analysis was carried out utilizing mean data of six basic generations *viz.*, P₁, P₂, F₁, F₂, B₁ and B₂ of selected cross ML 267 \times LGG 528. The estimates of generation mean analysis helps in deciding a suitable breeding procedure for improvement of various quantitative traits of a crop species.

Materials and methods

The experimental material consisted of six generations *viz.*, P₁, P₂, F₁, F₂, B₁ and B₂ of cross ML 267 \times LGG 528 were grown at the dry land farm, S.V. Agricultural College, Tirupati during *rabi*, 2017 in compact family block design with two replications. The P₁, P₂, F₁, B₁ and B₂ generations were sown in two rows of three meter length while F₂ populations were raised in 10 rows of three meter length following a spacing of 30 cm between the rows and 10 cm between the plants within a row. After 15 days of sowing, the seedlings were thinned to maintain 10 cm between plants within a row.

As a basal dressing, fertilizers *viz.*, urea and single super phosphate to supply 20 kg N and 40 kg P₂O₅ha⁻¹ were applied respectively to experimental plots. Thinning was done to leave single seedling per hill after 15 days of sowing. Irrigation, weeding and plant protection measures were taken up as and when needed during the crop growth period, as per the standard recommended package of practices to raise a good and healthy crop.

Data for seed yield, yield attributes, water use efficiency and heat stress tolerance related traits were collected on 10 randomly selected plants in each F₁ and parents, 80 plants in each F₂ and 20 plants in each backcross population from each replication for 14 quantitative traits. The means and variances of means for six basic generations (P₁, P₂, F₁, F₂, B₁ and B₂) were computed using individual plant data. The variation among the plants within each replication was used for calculating the sampling variances (variances of mean). The generation mean analysis was carried out by following the methodology of Hayman (1958) [7].

Results and discussion

The data on mean performance and gene effects for yield, water use efficiency and heat stress tolerance related traits in the cross ML 267 \times LGG 528 were presented in the Table 1 to 8.

Table 1: Estimates of mean on parental, first filial, second filial and backcross generations of ML 267 \times LGG 528 cross of mungbean for days to 50% flowering, days to maturity, plant height, number of branches per plant

Generation	Days to Flowering	Days to Maturity	Plant Height	Number of branches per plant
P ₁	32.05 \pm 0.17	72.60 \pm 0.23	52.55 \pm 0.33	2.85 \pm 0.17
P ₂	33.10 \pm 0.19	74.25 \pm 0.24	48.25 \pm 0.38	2.05 \pm 0.15
F ₁	29.70 \pm 0.26	70.00 \pm 0.19	57.35 \pm 0.26	3.00 \pm 0.16
F ₂	33.99 \pm 0.11	72.59 \pm 0.13	55.39 \pm 0.57	1.94 \pm 0.07
B ₁	33.00 \pm 0.13	70.03 \pm 0.17	55.82 \pm 0.51	2.32 \pm 0.13
B ₂	33.33 \pm 0.14	69.35 \pm 0.15	55.52 \pm 0.90	2.02 \pm 0.11

Table 2: Estimates of scaling test and gene effects for days to 50% flowering, days to maturity, plant height, number of branches per plant in ML 267 \times LGG 528 cross of mungbean

Generation	Days to Flowering	Days to Maturity	Plant Height	Number of branches per plant
A	4.25** \pm 0.41	-2.55** \pm 0.45	1.75 \pm 1.10	-1.20** \pm 0.35
B	3.85** \pm 0.42	-5.55** \pm 0.43	5.45** \pm 1.86	-1.00** \pm 0.32
C	11.43** \pm 0.73	3.50** \pm 0.74	6.07* \pm 2.40	-3.12** \pm 0.49

D	1.66** ± 0.29	5.80** ± 0.35	-0.56 ± 1.54	-0.46* ± 0.22
Gene effects				
[<i>m</i>]	33.99** ± 0.11	72.58** ± 0.13	55.39** ± 0.57	1.94** ± 0.07
[<i>d</i>]	-0.33 ± 0.19	0.68** ± 0.22	0.30 ± 1.03	0.30 ± 0.17
[<i>h</i>]	-6.20** ± 0.65	-15.03** ± 0.74	8.07** ± 3.11	1.47** ± 0.49
[<i>i</i>]	-3.33** ± 0.58	-11.60** ± 0.70	1.12 ± 3.08	0.92* ± 0.45
[<i>j</i>]	0.20 ± 0.23	1.50** ± 0.28	-1.85 ± 1.06	-0.10 ± 0.20
[<i>l</i>]	-4.78** ± 1.05	19.70** ± 1.16	-8.32 ± 4.79	1.27 ± 0.85
Type of epistasis	Complementary	Duplicate	Duplicate	Complementary

* Significant at 5% level of probability, ** Significant at 1% level of probability

Table 3: Estimates of mean on parental, first filial, second filial and backcross generations of ML 267 × LGG 528 cross of mungbean for number of clusters per plant, number of pods per cluster, Number of pods per plant

Generation	Number of clusters per plant	Number of pods per cluster	Number of pods per plant
P ₁	5.65 ± 0.17	4.55 ± 0.16	25.30 ± 0.49
P ₂	5.85 ± 0.17	4.86 ± 0.11	28.25 ± 0.66
F ₁	6.45 ± 0.23	5.55 ± 0.18	35.15 ± 0.60
F ₂	5.23 ± 0.12	4.93 ± 0.17	24.12 ± 0.69
B ₁	5.35 ± 0.14	4.87 ± 0.19	25.77 ± 1.05
B ₂	5.52 ± 0.17	4.62 ± 0.21	25.25 ± 1.28

Table 4: Estimates of scaling test and gene effects for number of clusters per plant, number of pods per cluster, Number of pods per plant in ML 267 × LGG 528 cross of mungbean

Generation	Number of clusters per plant	Number of pods per cluster	Number of pods per plant
A	-1.40** ± 0.40	-0.36 ± 0.46	-8.90** ± 2.24
B	-1.25** ± 0.45	-1.17* ± 0.46	-12.90** ± 2.71
C	-3.45** ± 0.71	-0.80 ± 0.80	-27.35** ± 3.11
D	-0.40 ± 0.32	0.36 ± 0.44	-2.78 ± 2.15
Gene effects			
[<i>m</i>]	5.23 ** ± 0.12	4.93** ± 0.17	24.12** ± 0.69
[<i>d</i>]	-0.17 ± 0.22	0.25 ± 0.28	0.52 ± 1.65
[<i>h</i>]	1.50* ± 0.70	0.11 ± 0.91	13.92** ± 4.37
[<i>i</i>]	0.80 ± 0.66	-0.73 ± 0.90	5.55 ± 4.31
[<i>j</i>]	-0.07 ± 0.25	0.40 ± 0.30	2.00 ± 1.70
[<i>l</i>]	1.85 ± 1.14	2.27 ± 1.39	16.25* ± 7.33
Type of epistasis	Complementary	Complementary	Complementary

* Significant at 5% level of probability, ** Significant at 1% level of probability

Table 5: Estimates of mean on parental, first filial, second filial and backcross generations of ML 267 × LGG 528 cross of mungbean for 100-seed weight (g), Harvest index (%), SCMR, SLA (cm² g⁻¹)

Generation	100-seed weight (g)	Harvest index (%)	SCMR	SLA (cm ² g ⁻¹)
P ₁	3.28 ± 0.04	33.46 ± 0.37	45.14 ± 0.60	205.32 ± 1.88
P ₂	3.41 ± 0.04	32.57 ± 0.51	46.02 ± 0.48	153.75 ± 1.37
F ₁	4.00 ± 0.06	34.64 ± 0.45	49.18 ± 0.49	185.31 ± 0.85
F ₂	3.44 ± 0.02	33.57 ± 0.52	37.65 ± 0.50	156.54 ± 2.25
B ₁	3.33 ± 0.04	32.56 ± 0.53	42.79 ± 1.22	173.98 ± 2.73
B ₂	3.33 ± 0.04	32.91 ± 0.84	41.86 ± 1.23	172.94 ± 1.98

Table 6: Estimates of scaling test and gene effects for 100-seed weight (g), Harvest index (%), SCMR, SLA (cm² g⁻¹) in ML 267 × LGG 528 cross of mungbean

Generation	100-seed weight (g)	Harvest index (%)	SCMR	SLA (cm ² g ⁻¹)
A	-0.62** ± 0.11	-2.98* ± 1.22	-8.73** ± 2.56	-42.66** ± 5.84
B	-0.75** ± 0.11	-1.38 ± 1.82	-11.48** ± 2.55	6.82 ± 4.28
C	-0.91** ± 0.17	-1.03 ± 2.36	-38.94** ± 2.35	-103.53** ± 9.46
D	0.22** ± 0.08	1.66 ± 1.44	-9.36** ± 2.00	-33.85** ± 5.63
Gene effects				
[<i>m</i>]	3.44* ± 0.02	33.57** ± 0.52	37.65** ± 0.50	156.44** ± 2.25
[<i>d</i>]	-0.00 ± 0.06	-0.35 ± 1.00	0.93 ± 1.73	1.04 ± 3.38
[<i>h</i>]	0.19 ± 0.18	-1.70 ± 2.94	22.32** ± 4.05	73.48** ± 11.35
[<i>i</i>]	-0.46** ± 0.17	-3.33 ± 2.89	18.72** ± 4.00	67.70** ± 11.26
[<i>j</i>]	0.06 ± 0.07	-0.79 ± 1.05	1.37 ± 1.78	-24.74** ± 3.57
[<i>l</i>]	1.83** ± 0.31	7.70 ± 4.65	1.49 ± 7.33	-31.86 ± 16.50
Type of epistasis	Complementary	Duplicate	Complementary	Duplicate

* Significant at 5% level of probability, ** Significant at 1% level of probability

Table 7: Estimates of mean on parental, first filial, second filial and backcross generations of ML 267 × LGG 528 cross of mungbean for SLA (g cm⁻²), Relative injury (%), Seed yield per plant (g)

Generation	SLA (g cm ⁻²)	Relative injury (%)	Seed yield per plant (g)
P ₁	0.0049 ± 0.00	35.74 ± 0.39	6.01 ± 0.11
P ₂	0.0065 ± 0.00	41.48 ± 0.37	6.93 ± 0.16
F ₁	0.0054 ± 0.00	34.41 ± 0.46	8.86 ± 0.16
F ₂	0.0066 ± 0.00	34.87 ± 0.31	5.52 ± 0.17
B ₁	0.0058 ± 0.00	40.14 ± 1.11	5.87 ± 0.24
B ₂	0.0058 ± 0.00	36.30 ± 0.81	6.10 ± 0.32

Table 8: ML 267 × LGG 528 Estimates of scaling test and gene effects for SLA (g cm⁻²), Relative injury (%), Seed yield per plant (g) in ML 267 × LGG 528 cross of mungbean

Generation	SLA (g cm ⁻²)	Relative injury (%)	Seed yield per plant (g)
A	0.001** ± 0.00	10.11** ± 2.31	-3.11** ± 0.52
B	0.001* ± 0.00	-3.30 ± 1.73	-3.58** ± 0.68
C	0.004** ± 0.00	-6.58** ± 1.64	-8.55*8 ± 0.76
D	0.002** ± 0.00	-6.70** ± 1.51	-0.93 ± 0.52
Gene effects			
[<i>m</i>]	0.007** ± 0.00	34.87** ± 0.31	5.52** ± 0.16
[<i>d</i>]	0.000 ± 0.00	3.84** ± 1.38	-0.22 ± 0.40
[<i>h</i>]	-0.003** ± 0.00	9.20** ± 3.08	4.25** ± 1.06
[<i>i</i>]	-0.003** ± 0.00	13.40** ± 3.03	1.86 ± 1.05
[<i>j</i>]	0.001** ± 0.00	6.70** ± 1.40	0.23 ± 0.41
[<i>l</i>]	0.002** ± 0.00	-20.22** ± 5.77	4.83** ± 1.80
Type of epistasis	Duplicate	Duplicate	Complementary

* Significant at 5% level of probability, ** Significant at 1% level of probability

Days to 50 per cent flowering

The F₁ of the cross ML 267 × LGG 528 has exhibited desired early flowering than their respective means of parents. The F₂, B₁ and B₂ generations exhibited later in flowering than their parents. The partitioning of generation means and estimation of genetic components revealed highly significant and positive mean [*m*] value. Among interaction effects, the cross exhibited significant values for additive × additive [*i*] and dominance × dominance (*l*) gene interactions in negative direction. Negative sign of '*i*' in the cross indicate that selection should be deferred to later generations when desirable recombinants become available. The similar sign between dominance [*h*] and dominance × dominance [*l*] components indicated the predominance of complementary type of gene action for this trait. Presence of complementary epistasis for days to 50 per cent flowering was reported by Hegde *et al.* (1994)^[8] and Murthy (2000)^[12].

Days to maturity

The mean of F₁ was lower than their both parents and the F₂ generation had mean values intermediate between their corresponding parents. The back cross generations had lower number of days to maturity than the both parents. The partitioning of generation means and estimation of genetic components revealed that [*m*] was significant. Additive effects [*d*] were positively significant and the dominance effects [*h*] were negative and significant. The additive × dominance [*j*] and dominance × dominance [*l*] components were significant and positive. The opposite signs of [*h*] and [*l*] components indicated predominance of duplicate type of gene action in governing this trait. Negative and significant effects of '*i*' indicates that selection may be deferred to later generations till desirable recombinants become available. Hence, selection in early generations may not be effective and it is always better to go for selection in advanced generations as possibility of transgressive segregants being more in the later stages. These results were in agreement with Hegde *et al.* (1994)^[8], Singh *et al.* (2007)^[18], Gawande and Patil (2007)^[5],

Narasimhulu *et al.* (2016)^[14] and Swarnalatha *et al.* (2018)^[19] who reported duplicate type of epistasis.

Plant height (cm)

The F₁, F₂ and back crosses mean were higher than both of its parental means which could be due to the presence of large number of transgressive segregants. Estimation of genetic components revealed that [*m*] and [*h*] effects were highly significant and positive. The opposite signs of [*h*] and [*l*] components revealed duplicate type of epistasis and hence, selection could be delayed until later generations. Predominance of duplicate epistasis was also reported by Hegde *et al.* (1994)^[8], Ram (1997)^[17], Gawande and Patil (2007)^[5], Devendra *et al.* (2010)^[3].

Number of branches per plant

The F₁ cross showed higher mean value than their parents and the F₂ mean was lower than their parental mean. The mean of B₁ and B₂ generations was intermediate between their corresponding parents. For this trait, the [*m*], (*h*) and [*i*] components were positive and significant. Gawande and Patil (2007)^[5], Singh *et al.* (2007)^[18] also reported the importance of dominance effect for this trait. The cross has exhibited complementary type of epistasis.

Number of clusters per plant

The F₁ mean was higher than their parental means and all segregating generations (F₂, B₁ and B₂) had mean values intermediate between their corresponding parents. The partitioning of generation means into six components revealed that [*m*] and (*h*) effects were positive and highly significant. The complementary type of gene interaction was recorded.

Number of pods per cluster

The mean values of F₁s for number of pods per cluster were higher than their respective parents and mean performance of F₂ generation was lower than F₁ mean. Mean values of the backcrosses were intermediate to their corresponding parental means. The partitioning of generation means into six

components revealed that the mean $[m]$ and $[h]$ components were positive and highly significant. Complementary nature of gene action was exhibited and these results were in conformity with those reported by Aher and Dahat (1999)^[1], Kute and Deshmukh (2002)^[10], Gawande and Patil (2007)^[5], Devendra *et al.* (2010)^[3].

Number of pods per plant

F₁ generation produced higher mean values than the corresponding parents of the crosses. The F₂ and both back cross generation means were lower than F₁ mean value. The $[m]$ and $[h]$ effects were significantly positive. It has recorded positive and significant dominance \times dominance $[I]$ gene effects. Dominance $[h]$ and dominance \times dominance $[I]$ effects had similar sign suggesting the involvement of complementary type of epistasis. Predominance of dominance effects for number of pods was also reported by Godhani *et al.*, (1978), Hegde *et al.*, (1994)^[8], Singh *et al.* (1994), Ram (1997)^[17], Murthy (2000)^[12], Gawande and Patil (2007)^[5], Singh *et al.* (2007)^[18], Devendra *et al.* (2010)^[3], Narasimhulu *et al.* (2016)^[14] and Swarnalatha *et al.* (2018)^[19].

100-seed weight (g)

A small difference was observed among all generations for this trait. Both F₁ and F₂ mean performance was slightly higher than their parents and mean of backcross recorded lower seed weight than parents. All the scaling tests were significant and complementary type of gene action was predominant., Aher and Dahat (1999)^[1] reported complementary type of epistasis for this trait.

Harvest index (%)

The mean performance of F₁ generation exhibited increased harvest index than their respective parental means. The F₂ populations expressed lower mean values than their respective F₁s. The mean of B₂ populations was intermediate between their corresponding parents. The $[m]$ component was highly significant and exhibited duplicate type of epistasis. These results are in agreement with the findings of Singh *et al.* (2007)^[18], Devendra *et al.* (2010)^[3], and Swarnalatha *et al.* (2018)^[19].

SPAD Chlorophyll Meter Reading (SCMR)

The mean values for SCMR in F₁ generation was higher than their respective parents which clearly suggests possible involvement of over-dominance in the expression of SCMR. The F₂ population exhibited lower mean values than F₁ generation. In backcross populations, the mean appeared to be lower than their corresponding parents. The components $[m]$ and $[h]$ were found to be positive and highly significant. Among the three interaction components, the magnitude of additive \times additive (i) gene effects were highly significant and positive and exhibited complimentary gene action.

Specific leaf area (cm² g⁻¹)

The F₁ and back cross populations (B₁ and B₂) mean for specific leaf area was intermediate to their parental means. Fitting of six parameter model revealed that mean $[m]$ and $[h]$ effects were significant and positive. Among interaction effects, the cross exhibited significant and positive additive \times additive $[i]$ type of epistasis. Based on opposite signs of $[h]$ and $[I]$ components, duplicate type of gene action was observed in governing this trait. Duplicate type of epistasis for specific leaf area was also reported by Nigam *et al.* (2001)^[15], Pavitradevi *et al.* (2013)^[16] and Govardhan (2015)^[6].

Therefore selection of this character should be deferred to later generations when desirable segregants become available.

Specific leaf weight (g cm⁻²)

The mean specific leaf weight was intermediate between their corresponding parents and the F₂ progenies mean were higher than their F₁s. All the backcross populations recorded mean value intermediate to their parents. The cross recorded significant positive additive \times dominance (j) effects and significant dominance \times dominance (l) effects. The direction for dominance (h) and dominance \times dominance (l) gene effects were dissimilar which indicated the presence of duplicate epistasis. Biparental mating in early generations followed by selection in advanced generations would be more effective than direct selection in early segregating generations.

Relative injury (%)

Comparatively F₁ and F₂ progenies exhibited low relative injury than their parents. With respect to backcross progenies, it was intermediate to their parents. The additive $[d]$ and dominance (h) gene effects were found to be significant and positive. Among the interaction effects, significant and positive additive \times additive $[i]$ and additive \times dominance $[j]$ interaction effects were found. These results were similar to Lal *et al.* (2014)^[11] and Govardhan (2015)^[6]. The $[h]$ and $[I]$ components were in opposite sign indicating duplicate type of gene action. For exploitation of all types of genetic effects biparental approach *inter se* crossing may be practiced for developing elite population for selection of high yielding lines along with high WUE and heat stress tolerance in advanced generations.

Seed yield per plant (g)

The mean seed yield per plant of all the F₁ crosses was higher than their respective parents while F₂ means were lower than F₁ s and their corresponding parents. Backcross progenies exhibited lower seed yield when compared to F₁ seed yield. The partitioning of generation means into six components revealed that the component $[m]$ was positive and highly significant. The dominance (h) effects and dominance \times dominance $[I]$ genic effects were positive and significant with higher magnitude. It indicated that $[I]$ type of interaction had more influence on seed yield per plant. The similar signs of $[h]$ and $[I]$ components indicated complementary type of gene action in governing seed yield per plant. Complementary type of epistasis was also reported by Kute and Deshmukh (2002)^[10].

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