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Evaluation of P_1, P_2, F_1, F_2, B_1 and B_2 generations of LM 95 × EC 362096 cross of mung bean for yield and yield attributes along with water use efficiency and heat stress tolerance related traits using generation mean analysis

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ABSTRACT

In mung bean, limited work has been 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 need to enhance the genetic potential of mung bean genotypes with high yield and drought and heat stress tolerance. The experimental material comprising six populations viz P_1, P_2, F_1, F_2, B_1 and B_2 of the cross LM 95 × EC 362096 was grown at the dryland farm of SV Agricultural College, Tirupati, Andhra Pradesh during rabi 2017 in compact family block design with two replications. The mean data obtained from six generations (P_1, P_2, F_1, F_2, B_1 and B_2) of selected superior cross LM 95 × EC 362096 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 the 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, WUE and heat stress tolerance related components.

Keywords: Mung bean; generation mean analysis; water use efficiency

INTRODUCTION

Green gram, popularly known as mung bean 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. The national production and productivity levels of mung bean are low, which indirectly affect 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 influence the mung bean 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 mung bean, yet limited work has been 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 mung bean genotypes with high yield and drought and heat stress tolerance.

WUE 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 WUE and relationship of WUE with other parameters are essential to plan strategies for yield improvement in water scarce areas. Assessment of inter-relationship among surrogate traits of WUE with yield and its components is essential for formulating selection strategy to combine WUE 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 (Rao et al 2001). Hence, these traits could be used for selecting higher water use efficient green gram genotypes. This provides sufficient justification for the use of SLA and SCMR as potential surrogate traits for selecting genotypes with enhanced WUE (Rao et al 2001). Cultivars with more SLW had thick leaves (reduced surface area to volume ratio) and exhibited improved WUE (Brown and Byrd 1997, Thumma et al 1998).

High temperature stress during germination and flowering causes considerable yield losses in mung bean. 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 of the grain filling duration etc (Khalil et al 2009). 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 that lower is the injury, higher is 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 and 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 reveals duplicate epistasis. Hayman's generation mean analysis may 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 × additive (i), additive × dominance (j) and dominance × dominance (l). The significance of C scale suggests dominance × dominance (l) type of interaction. The significance of D scale reveals additive × additive (i) type of gene interaction and significance of both C and D scales indicates additive × additive and dominance × dominance type of gene interactions. The significance of any one of the scaling tests indicates inadequacy of simple additive-dominance model.

In the present investigations, 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 mung bean cross. Hayman's six parameter model of generation mean analysis was carried out utilizing mean data of six basic generations viz P_1, P_2, F_1, F_2, B_1 and B_2 of selected superior cross LM 95 × EC 362096. The estimates of generation mean analysis helps in deciding a suitable breeding procedure for improvement of various quantitative traits of a crop species.

MATERIAL and METHODS

The experimental material consisted of six generations viz P_1, P_2, F_1, F_2, B_1 and B_2 of cross LM 95 × EC 362096 and were grown at the dryland farm of SV Agricultural College, Tirupati, Andhra Pradesh during rabi 2017 in compact family block design with two replications. The P_1, P_2, F_1, B_1 and B_2 generations were sown in two rows of three meter length while F_2 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 distance between plants within a row.

As a basal dressing, fertilizers viz urea and single super phosphate to supply 20 kg N and 40 kg P_2O_5/ha respectively were applied 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 on seed yield, yield attributes, WUE and heat stress tolerance related traits were collected on 10 randomly selected plants in each F_1 and parents, 80 plants in each F_2 and 20 plants in each backcross population from each replication for 14 quantitative traits. The means and variances of means for six basic generations (P_1, P_2, F_1, F_2, B_1 and B_2) 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).

RESULTS and DISCUSSION

The data on mean performance and gene effects for yield, WUE and heat stress tolerance related traits in the cross LM 95 × EC 362096 are presented in Tables 1 to 8.

Days to 50 per cent flowering: The F_1, B_1 and B_2 generations of the cross LM 95 × EC 362096 exhibited desired early flowering than their respective means of parents. The F_2 had mean values intermediate to their corresponding parents. The partitioning of generation means and estimation of genetic components revealed highly significant and positive mean [*m*] value. Duplicate type of epistasis was observed. Rao et al (1984), Govardhan (2015)and Narasimhulu et al (2018) also reported duplicate epistasis for days to 50 per cent flowering.

Days to maturity: The mean of F_1 was lower than both its parents and the F_2 generation had mean values intermediate between its corresponding parents. The backcross generation had lower number of days to maturity than both the parents. The partitioning of generation means and estimation of genetic components revealed that [*m*] 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'* indicate 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 are in agreement with the work of Hegde et al (1994), Singh et al (2006), Singh et al (2007), Gawande and Patil (2007), Narasimhulu et al (2018) and Latha et al (2018) who reported duplicate type of epistasis.

Plant height (cm): The F_1 mean was higher than both of its parental means while F_2 and backcrosses had mean values intermediate between parents. Estimation of genetic components revealed that [*m*], [*d*] and [*j*] effects were highly significant and positive. The cross has shown similar signs of [*h*] and [*l*] components which indicated the presence of complementary type of gene action. Therefore, selection may be practiced in early generations followed by single plant selection so as to exploit both additive and non-additive gene effects.

Number of branches per plant: The F_1 cross showed higher mean value for number of branches per plant than their parents, whereas, F_2, B_1 and B_2 generations had intermediate mean between their corresponding parents. For this trait, the [*m*] and (*h*) components were positive and significant. Gawande and Patil 2007), Singh et al (2007) and Yadav et al (2017) also reported the importance of dominance effect for this trait. The cross exhibited complementary type of epistasis.

Number of clusters per plant: The F_1 mean was higher than its parental means and all segregating generations (F_2, B_1 and B_2) 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 F_1, F_2 and backcrosses for number of pods per cluster were higher than their respective parents. The partitioning of generation means into six components revealed that the mean [*m*] and [*l*] components were positive and highly significant. The opposite signs of dominance gene effects [*h*] and dominance × dominance gene effects [*l*] indicated duplicate type of epitasis.

Number of pods per plant: F_1 generation produced higher mean values for number of pods per plant than the corresponding parents of the crosses. The F_2 and

Table 1. Estimates of mean on parental, first filial, second filial and backcross generations of LM 95 × EC 362096 cross of mung bean for days to 50% flowering, days to maturity, plant height and number of branches per plant

Generation	Days to 50% flowering	Days to maturity	Plant height	Number of branches/plant
P_1	35.20 ± 0.21	73.15 ± 0.30	50.00 ± 0.30	1.35 ± 0.11
P_2	34.75 ± 0.30	75.25 ± 0.29	53.15 ± 0.39	1.65 ± 0.17
F_1	31.25 ± 0.23	70.45 ± 0.20	55.35 ± 0.41	2.15 ± 0.18
F_2	34.66 ± 0.12	74.70 ± 0.10	51.96 ± 0.52	1.45 ± 0.06
B_1	31.85 ± 0.16	70.85 ± 0.17	53.55 ± 0.88	1.57 ± 0.13
B_2	33.30 ± 0.17	71.52 ± 0.18	50.95 ± 0.85	1.52 ± 0.14

Table 2. Estimates of scaling test and gene effects for days to 50% flowering, days to maturity, plant height and number of branches per plant in LM 95 × EC 362096 cross of mung bean

Generation	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches/plant
A	-2.75** ± 0.44	-1.90** ± 0.50	1.75 ± 1.82	-0.35 ± 0.34
B	0.60 ± 0.51	-2.65** ± 0.51	-6.60 ± 1.79	-0.75 ± 0.38
C	6.17** ± 0.77	9.50** ± 0.72	-6.00** ± 2.30	-1.47** ± 0.49
D	4.16** ± 0.34	7.02** ± 0.11	-0.57** ± 1.60	-0.18 ± 0.23
Gene effect				
[*m*]	34.66** ± 0.12	74.70** ± 0.10	51.96** ± 0.52	1.45** ± 0.06
[*d*]	-1.45** ± 0.23	-0.67** ± 0.25	2.60* ± 1.22	0.05 ± 0.20
[*h*]	-12.05** ± 0.74	-17.80** ± 0.72	4.92 ± 3.24	1.02* ± 0.51
[*i*]	-8.3** ± 0.68	-14.05** ± 0.66	1.15 ± 3.21	0.37 ± 0.47
[*j*]	-1.67** ± 0.30	0.37 ± 0.32	4.17** ± 1.24	0.20 ± 0.22
[*l*]	10.47** ± 1.21	18.60** ± 1.23	3.70 ± 5.40	0.72 ± 0.92
Type of epistasis	Duplicate	Duplicate	Complementary	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 LM 95 × EC 362096 cross of mung bean for number of clusters per plant, number of pods per cluster and number of pods per plant

Generation	Number of clusters/plant	Number of pods/cluster	Number of pods/plant
P_1	5.70 ± 0.17	4.24 ± 0.08	23.95 ± 0.45
P_2	6.15 ± 0.26	4.16 ± 0.09	25.15 ± 0.55
F_1	7.25 ± 0.32	4.42 ± 0.10	31.45 ± 0.85
F_2	5.93 ± 0.16	4.54 ± 0.07	26.31 ± 0.65
B_1	6.00 ± 0.27	4.50 ± 0.13	26.67 ± 1.25
B_2	5.62 ± 0.26	4.67 ± 0.13	26.12 ± 1.30

both backcross generation means were lower than F_1 mean value. The [*m*] effect was significantly positive. Dominance [*h*] and dominance × dominance [*l*] effects had similar sign suggesting the involvement of complementary type of epistasis.

100-seed weight (g): A small difference was observed among all generations for this trait. F_1 mean performance was slightly higher than its parents while F_2 mean was lower than its parents. Mean of backcross recorded higher 100-seed weight than parents. The components [*m*], [*h*] and [*i*] were positively significant. Duplicate type of epistasis was recorded. Khattak et al (2004), Singh et al (2006), Narasimhulu et al (2018) and Latha et al (2018) reported duplicate type of epistasis.

Table 4. Estimates of scaling test and gene effects for number of clusters per plant, number of pods per cluster and number of pods per plant in LM 95 × EC 362096 cross of mung bean

Generation	Number of clusters/plant	Number of pods/cluster	Number of pods/plant
A	-0.95 ± 0.65	0.35 ± 0.30	-2.05** ± 2.68
B	-2.15** ± 0.66	0.76* ± 0.30	-4.35** ± 2.79
C	-2.62** ± 0.95	0.94* ± 0.40	-6.72** ± 3.21
D	0.23 ± 0.49	-0.08 ± 0.25	-0.16* ± 2.23
Gene effect			
[*m*]	5.93** ± 0.15	4.54** ± 0.07	26.31** ± 0.65
[*d*]	0.37 ± 0.37	-0.16 ± 0.19	0.55 ± 1.80
[*h*]	0.85 ± 1.04	0.38 ± 0.76	7.22 ± 4.56
[*i*]	-0.47 ± 0.98	0.16 ± 0.49	0.32 ± 4.46
[*j*]	0.60 ± 0.40	-0.20 ± 0.20	1.15 ± 1.84
[*l*]	3.57* ± 1.78	-1.28 ± 0.87	6.07 ± 7.90
Type of epistasis	Complementary	Duplicate	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 LM 95 × EC 362096 cross of mung bean for 100-seed weight, harvest index, SCMR and SLA

Generation	100-seed weight (g)	Harvest index (%)	SCMR	SLA (cm^2/g)
P_1	3.50 ± 0.06	34.93 ± 0.47	44.21 ± 0.33	185.41 ± 1.12
P_2	3.87 ± 0.04	36.02 ± 0.47	44.54 ± 0.34	156.23 ± 0.85
F_1	4.00 ± 0.05	38.28 ± 0.52	47.22 ± 0.47	167.87 ± 0.90
F_2	3.45 ± 0.02	34.88 ± 0.31	44.36 ± 0.37	165.93 ± 1.36
B_1	3.52 ± 0.05	36.06 ± 0.57	46.83 ± 0.42	171.45 ± 2.13
B_2	3.90 ± 0.07	35.10 ± 0.57	46.74 ± 0.40	166.27 ± 2.42

Table 6. Estimates of scaling test and gene effects for 100-seed weight, harvest index, SCMR and SLA in LM 95 × EC 362096 cross of mung bean

Generation	100-seed weight (g)	Harvest index (%)	SCMR	SLA (cm^2/g)
A	-0.46** ± 0.14	-1.09 ± 1.35	2.23* ± 1.02	-10.38* ± 4.50
B	-0.07 ± 0.17	-4.11** ± 1.34	1.71 ± 0.99	8.44 ± 5.00
C	-1.57** ± 0.16	-7.98** ± 1.77	-5.77** ± 1.82	-13.67* ± 5.91
D	-0.52** ± 0.11	-1.38 ± 1.02	-4.86** ± 0.94	-5.86 ± 4.22
Gene effect				
[*m*]	3.45** ± 0.02	34.89** ± 0.31	44.36** ± 0.37	165.93*8 ± 1.36
[*d*]	-0.37** ± 0.09	0.96 ± 0.81	0.09 ± 0.58	5.17 ± 3.22
[*h*]	1.35** ± 0.22	5.57** ± 2.14	12.56** ± 1.96	8.78 ± 8.52
[*i*]	1.04** ± 0.22	2.77 ± 2.05	9.72** ± 1.88	11.73 ± 8.44
[*j*]	-0.19 ± 0.10	1.50 ± 0.88	0.25 ± 0.63	-9.41** ± 3.30
[*l*]	-0.50 ± 0.42	2.43 ± 3.70	-13.67** ± 2.96	-9.79 ± 14.20
Type of epistasis	Duplicate	Complementary	Duplicate	Duplicate

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

Harvest index (%): The mean performance of F_1 generation exhibited increased harvest index than its respective parental means. The F_2 populations expressed lower mean values than their respective F_1s. In B_1 populations, the means appeared to be higher than their corresponding parents, whereas, the means of B_2 populations were intermediate between their corresponding parents. The [*m*] and [*h*] components were highly significant and exhibited complementary type of epitasis.

Table 7. Estimates of mean on parental, first filial, second filial and backcross generations of LM 95 × EC 362096 cross of mung bean for SLA, relative injury and seed yield per plant

Generation	SLA (g/cm^2)	Relative injury (%)	Seed yield/ plant (g)
P_1	0.0054 ± 0.00	40.13 ± 0.72	6.65 ± 0.17
P_2	0.0064 ± 0.00	38.67 ± 0.64	7.11 ± 0.27
F_1	0.0060 ± 0.00	35.48 ± 0.56	9.95 ± 0.27
F_2	0.0061 ± 0.00	33.92 ± 0.21	7.03 ± 0.19
B_1	0.0059 ± 0.00	37.16 ± 0.50	7.35 ± 0.38
B_2	0.0061 ± 0.00	33.78 ± 0.51	6.95 ± 0.33

Table 8. Estimates of scaling test and gene effects for SLA, relative injury and seed yield per plant in LM 95 × EC 362096 cross of mung bean

Generation	SLA (g/cm^2)	Relative injury (%)	Seed yield/plant (g)
A	0.001* ± 0.00	-1.29 ± 1.36	-1.89* ± 0.83
B	0.000 ± 0.00	-6.59** ± 1.34	-3.15** ± 0.77
C	0.001** ± 0.00	-14.08** ± 1.71	-5.51** ± 0.99
D	0.000 ± 0.00	-3.09** ± 0.84	-0.23 ± 0.63
Gene effect			
[*m*]	0.006** ± 0.00	33.92** ± 0.21	7.03** ± 0.19
[*d*]	0.000 ± 0.00	3.38** ± 0.72	0.40 ± 0.50
[*h*]	0.000 ± 0.00	2.27 ± 1.83	3.53** ± 1.31
[*i*]	-0.001 ± 0.00	6.19** ± 1.68	0.46 ± 1.27
[*j*]	0.000 ± 0.00	2.65** ± 0.87	0.63 ± 0.53
[*l*]	0.001** ± 0.00	1.68 ± 3.36	4.59* ± 2.26
Type of epistasis	Complementary	Complementary	Complementary

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

SPAD chlorophyll meter reading (SCMR): The mean values for SCMR in F_1 generation were higher than their respective parents which clearly suggested possible involvement of over-dominance in the expression of SCMR. The F_2 population exhibited lower mean values than F_1 generation. In backcross populations, the mean appeared to be higher than their corresponding parents. The components [*m*], [*h*] and [*i*] were found to be positive and highly significant. Among the three interaction components, the magnitude of additive × additive (*i*) gene effects was highly significant and positive and exhibited duplicate gene action.

Specific leaf area (cm^2/g): The F_1 and backcross populations (B_1 and B_2) means for specific leaf area were intermediate to their parental means. Fitting of six parameter model revealed that mean [*m*] was significant and positive. Based on opposite signs of [*h*] and [*l*] 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), Pavitradevi et al (2013) and Govardhan (2015). 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 its corresponding parents and the F_2 progenies mean was higher than their F_1s. All the backcross populations recorded mean values intermediate to their parents. The cross recorded significant positive dominance × dominance (*l*) effect. The direction for dominance (*h*) and dominance × dominance (*l*) gene effects were similar which indicated the presence of complementary epistasis.

Relative injury (%): Comparatively, F_1 and F_2 progenies exhibited low relative injury than their parents. With respect to backcross progenies, it was intermediate to their parents. The additive [*d*] gene effect was found to be significant and positive. Among the interaction effects, significant and positive additive × additive [*i*] and additive × dominance [*j*] interaction effects were found. The [*h*] and [*l*] components were in similar sign indicating complementary type of gene action.

Seed yield per plant (g): The mean seed yield per plant of all the F_1 crosses was higher than their respective parents while F_2 means were lower than F_1s and their corresponding parents. Backcross progenies exhibited lower seed yield as compared to F_1 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 × dominance [*l*] genic effects were positive and significant with higher magnitude. It indicated that [*l*] type of interaction had more influence on seed yield per plant. The similar signs of [*h*] and [*l*] 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) and Khattak et al (2004).

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