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GENETIC VISION OF SOME QUANTITIVE TRAITS IN MUNG BEAN (*VIGNA RADIATA* L.) SUBJECTED TO CONTRASTING IRRIGATION SITUATIONS

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ABSTRACT

Mung bean is an important legume and pulse crop of semi-arid regions of Pakistan. Therefore, studies were carried out to determine the inheritance of important agronomic traits under contrasting water regimes, Study showed significant genetic variability among parents and their direct and reciprocal crosses. Scaling test showed partially adequacy of additive-dominance model. Genotypes MN-51, MN-92, MN-96, MN-98 and 00TM-12 contained dominant and recessive genes for different quantitative traits**,** days to first flowering, days to first pod maturity, pod length and Number of grains per pod.

Key words. Diallel, Dominant, additive, recessive, quantitative, scaling, water stress

INTRODUCTION

The continuing global population growth will increase food demand. The future challenge is to feed 9 billion peoples in coming decades and ensuring food equitable availability to everybody in the world so that nobody goes to bed hungry. The balanced diet necessary for healthy nourishment requires handsome amount of proteins and vitamins. The animal source of protein is becoming short and expensive, however, the pulses offer an excellent substitute of meat, which is reliable and comparatively cheaper, rich in fiber, low in fat, and source of complex carbohydrates (Thrikawela and Bandara,1992). Mungbean grains contains 51% carbohydrates, 26% protein, 10% moisture, 4% mineral and 3% vitamins (Khan, 1981; Ali, *et al*. 2010)

In Pakistan, pulses are used as a part of daily food consumption by rich and poors and their consumption is increasing day by day.Total cropped area of Pakistan in year 2010-11 was 21.22 m ha. Area under Pulse crops is 1.492 m ha (7%), Cereals 12.603 m ha (56%), Cash crops 4.343 m ha (19%), Edible oilseeds 0.694 mha (3%)(GOP, 2011). Although pulses hold a sound value in terms of proteins provision but pulses-cereals ratio is still 1:8.5. Per capita availability of pulses in Pakistan is 6.44 kg annum^{-1}. Mung bean occupies only 18% of total area which is under pulses cultivation, however, it contributes 16% of the total pulses production. (GOP, 2011).

In arid and semi-arid regions, due to the deficiency of water the crops performance remains very low (Abdel *et al.*, 2011).Unexpected and non-reliable rainfall situation and limited resource management causes severe decline in crops yield. (Eack, 1996; Hussain *et al.*, 2012; Zare *et al.*, 2012).Therefore, water stress is an emerging issue that needs keen attention. (Rfiei *et al.*, 2009; Ranawake *et al.* 2011). To cope up with stagnant yield, increasing food demand and limited water; it is pertinent to develop water stress tolerant Mung been geno types (Mahajan and Tuteja, 2005; Mahmood *et al.*, 2012).

The aim of present study was to make viable Mung bean crosses and to investigate the inheritance pattern and effects of water stress on in Mung bean plants and response of different genotypes to tolerate water stress and so that a feasible genetic infrastructure may be designed for further research.

MATERIALS AND METHODS

The present study was conducted in the research area of Plant Breeding & Genetics, University College of Agriculture, University of Sargodha, Sargodha during the crop season of 2009-2011.The experimental material comprised of five Mungbean varieties i.e MN-51, MN-92, MN-96, MN-98 and 00TM-12. These Mung bean varieties were sown in March, 2011 and all combination crosses were developed by using 5×5 diallel fashion during the month of April, 2011. During June 2011, the F_1seeds were sown in the field using a triplicated randomized complete block design (RCBD) keeping plant to plant and row to row distances as 30cm and 75cm, respectively, with controlled application of water (T1) as normal irrigation. In T2, irrigation was applied as 50% of normal irrigation while no irrigation was applied in T3. Each experimental unit comprised of single row of 4 meter length having 12 plants.

The data were recorded from ten random plants throughout their growth period to maturity for the traits viz., days to first Flowering, days to first pod maturity, Pod Length, Grains yield plant^{-1}. The data were further subjected to analysis of variance technique (Steel *et al.*, 1997) to calculate the differences among the different genotypes. The genetic improvement of characters and to investigate gene action behavior across the water stress conditions, the diallel analysis technique was employed (Hayman, 1954 and Jinks, 1954). The graphical presentation provides an appropriate and precise mechanism of gene action for quantitative traits.

RESULTS AND DISCUSSION

Presence of adequate genetic variation associated with traits of interest is pre-requisite to achieve diverse plant breeding objectives (Noorka and Tabasum, 2013). On the other hand type of genetic variability will determine the breeding methods adopted to achieve these objectives (Rauf, 2008; Kalyar *et al*. 2013).Therefore, magnitude of genetic variability along with its types was determined in important agronomic traits in Mung bean populations.

Days to First Flowering: Analysis for days to first flowering showed significant ($P \leq 0.05$) differences among the genotypes and water regimes, however the interaction of genotype into water regime was insignificant (Table 1a). This shows genotype ranking was not affected across the water regimes, therefore the genotype performance was averaged over the water regimes and re-analysis of varieties was carried out (Table 1b).On the other hand Wr –Vr and Wr+Vr array co-variance were significant ($P \geq 0.05$)showing that model was inadequate and not valid for the estimation of genetic component.

However, genetic effect could be estimated through graphical approach. Wr/Vr graph of the days to first flowering depicted over-dominance type of gene action as Wr line cut the Vr line below the point of origin (Fig. 1A). The genotype MN-92 and MN-51 were closest to the point of origin, thereby containing the highest no of dominant gene while MN-98 contained the similar proportion of dominant and recessive genes. The genotype MN-96 contained the highest number of recessive genes being furthest from the origin (Fig. 1A). This genotype also showed the lowest mean value for days to first flowering showing that lower value under control of recessive genes. Contrastingly, genotype MN-92 showed significant high mean value. Genotypes i.e. MN-98 and MN-96 may be intermated due to distinct genetic background as well as contrasting mean values to establish segregating populations for the evolution of early maturing varieties.

Time to flowering in mungbean is genotype dependent and or temperature and day length. The days to first flowering is an index of early maturity and genotype with lower values may be preferred in selection. Mean value ranged from 36-44 days for this trait

Days to First Pod Maturity: Pod maturity is an important trait in Mung bean and a uniform pod maturity within population is highly desirable. Analysis for days to first pod maturity within water regime was carried out which shows significant differences among genotypes and water regimes, however the genotype interaction into water were non-significant showing that the ranking of genotypes were not affectedby the different water regimes (Table 1a). Therefore the genotypes performance was averaged over the water regimes and re-analysis of variance was carried out. (Table 1 b).By the scaling test model was found inadequate due to arrays analysis (Table 2)

The environmental variance (E) was non-significant ($P \geq 0.05$) and additive variance (D) was significant ($P \leq 0.05$) and positive. A positive additive genetic component means homozygote carried the increasing alleles. H1 was negative and significant showing that heterozygotes were similar to the lower valued parents. H2 was non-significant ($P \geq 0.05$) showing dissimilar weightage for the allelic distribution. “F” was positive but non-significant ($P \geq 0.05$). Degree of dominance was lesser than unity showing partial dominance variation toward the lower parent (Table 3). Proportion of dominant and recessive allele in parents was lesser than unity, showing that recessive genes were in excess (Table 3). The proportion of positive and negative alleles showed asymmetrical distribution of these alleles in the parents.The graphical representation of the distribution of genesin parents is shown in Fig: 1B.The regression lines cuts the Wr axis showing the partial dominance. TheParents genotypes MN-98closer to their point of origin carried maximum number of dominant genes while parents MN-92 present further away have recessive genes while parents in middle MN-96, MN-51 and 00 TM-12having equal proportion of dominance and recessive genes.

The bar chart for days to first pod maturity depicted that hybrid MN-98×MN-51 attained maturity in minimum days showingbetter performance and hybrid MN-92×00TM-12 attained maturity in maximum days at normal irrigation condition (Figure 1B). The results indicated significant genetic variability for this trait. Similar results were revealed by (Khattak *et al*., 2004; Ranawake *et al.*, 2011) who indicated that additive and non-additive gene action was important in the inheritance of this trait. In our study, additive component was of higher magnitude and it is concluded that transgressive segregants may be isolated which show lower mean values than parents.

Pod Length (cm): The analysis of variance for pod length showed significant variation due to genotypes (G) water regimes (W) and their interaction G×W showing that genotypes change their ranking over the genotypes. (Table 1). The ordinary analysis of variance of pod length showed the highly significance of genotype comprising male, female and their interactions showing that each genotype has much potential to contribute for pod length and ultimately to contribute for grain yield.(Table 2). The scaling test showed that additive-dominance model was partially adequate for further analysis while estimates of components of variation for pod length showed that the environmental variance was non-significant, additive variance was significant and the magnitude of H1 variance was smaller than the additive variance showing preponderance of additive effect but the heterozygote similar to the lower parent values (Table 3).

Graphical representing data (Figure 1C) showed partial dominance as regression lines cuts at Wr axis. The predicted regression lines showed complete dominance as just apart through point of origin therefore estimates for the types of dominant selection are not reliable.

It was depicted that (Figure 1C) the genotype MN-98 showed the maximum pod length at normal irrigation condition but in hybrids MN-96×00TM-12 and MN-98×MN-96 showed minimum pod length at 0% level of irrigation while the genotype MN-98×00TM-12 showed equal pod length at all levels of irrigation showing that water stress has played a negative role however some hybrid showed potential for water stress tolerance breeding for future breeding programmes

Number of grains per pod: Grain yield always remained an ultimate goal of the breeder. Analysis for number of grains per pod within water regimes were carried out which showed significant differences among genotypes and water regimes.(Table 1a) The genotype interaction into water regimes was non-significant showing that ranking of genotype was not affected across the water regimes. Therefore the genotypes performances were averaged over the water regimes and reanalysis of variance was carried out. (Table 1b) which showed significant ($P \leq 0.05$) differences among the genotypes, in male and female parents and their interaction while the analysis of variance of diallel showed non- significance ($P \geq 0.05$) of additive variance, directional dominance as the item a and b1 were non-significant. Dominance ratio was greater than unity showing over dominance type of gene action. Negative genes were higher in proportion similarly the recessive alleles were higher than dominant alleles and scaling test showed that the additive dominant was partially adequate (Table 2). Additive variance was positive and significant while dominance variance was negative. Dominance variance was higher in magnitude than the additive. H1 was greater than the H2 showing that the alleles with positive and negative effect were unequal to additive loci while the value of H1 showed that heterozygote were more like to the low valued parents (Table 3).

Table 1a. Analysis of variance for different traits of mungbean genotypes as affected by different water regimes

S.O.V.	d.f.	Mean sum of square			
		DFF	DPM	PL	NGP
Replications	2	0.73	0.97	1.78	13.66
Water regimes (W)	2	4.99^{NS}	1.66^{ns}	3.34^{NS}	26.05*
Error a	4	2.13	6.10	1.10	7.42
Genotypes (G)	24	46.73*	41.59*	2.12*	2.15*
G x W	48	6.56^{NS}	4.45^{NS}	1.37^{NS}	1.78^{NS}
Error b	144	4.87	4.63	0.76	1.33

DFF= Days to first flowering, DPM=Days to first pod maturity, PL= Pod length, GYP= Number of Grains per pod

* = $P \leq 0.05$

Table 1b: Ordinary analysis of variance for days to first flowering (DFF), days to first pod maturity (DPM), pod length (PL) and Number of grains per pod (NGP) over water regimes

S.O.V.	d.f.	Mean sum of sqaure			
		DFF	DPM	PL	NGP
Replication	2	2.61	0.35	0.06*	1.21
Genotypes	24	20.67*	43.08**	0.56**	1.04**
Male (M)	4	13.02*	155.58*	1.09**	1.17**
Female (F)	4	42.18*	81.55**	1.70**	0.82**
M x F	16	17.20*	5.34	0.15**	1.06**
Error	48	1.35	0.69	0.01	0.26

Where * = $P \leq 0.05$, ** = $P \leq 0.01$

Table 2. Scaling tests of additive-dominance model

Parameters	(Regression analysis) (t value of b)			Analysis of Var. of arrays (F ratios)		Conclusion
	b/S.E.	b_o,	b_1	Wr+Vr	Wr-Vr	
Days to Ist flowering	1.06±0.30	6.14**	0.95^{NS}	6.14*	0.95^{NS}	Model was partially adequate.
Days to first pod maturity	0.84±0.11	7.36**	1.45^{NS}	20.27**	6.56*	Model was inadequate due to arrays analysis
Pod length (cm)	0.72±0.13	5.60*	2.14^{NS}	15.01**	1.83^{NS}	Model was partially adequate
Number of GrainsPer Pod	1.56±0.50	3.14*	-1.12^{NS}	6.12*	1.50^{NS}	Model was partially adequate

Where ^{ns} is non-significant; * is significant at P≤ 0.05 and ** is significant at P≤ 0.01

Wr / Vr graph of number of grains per pod the regressive lines cut the Wr axis below the point of origin showing the presence of over dominance effect. Parents MN-92 and MN-98 showed the highest dominant genes while genotype OOTM-12 showed equal proportion of dominant and recessive genes. The genotype MN-51 contained the highest proportion of recessive genes (Fig. 1D). Among the parental genotypes, MN-98 showed the highest number of grains per pod followed by MN-51. The cross combination MN-96 × 00TM-12 showed the highest number of grains per pod followed by MN-51× 00TM-12. Array mean was greater than parental mean showing crosses were superior in their performance as compared to their parents for number of grains per pod. Grains per pod is an important yield component, however its influence over the yield is debatable issue among the Mungbean breeders. Studies have indicated non-significant ($P \geq 0.05$) influence of this trait over yield per plant (Haqqani and Pandey 1994; Jansen and Charnnarongkul 1995; Moradi *et al.*, 2008; Ranawake *et al.*, 2011).In contrast, Khajudparn and Tantasawa, 2011 showed its positive influence over the grain yield per hectare. It may be concluded from these contrasting results that influence of this trait over yield is subjected to specific germplasm understudy. Results of the present study indicated the preponderance of dominance effect in the inheritance of this trait. These results get confirmation from previous finding which showed non-additive gene action in the inheritance of number of grain per pod however additive, dominance and non-allelic interaction was reported by (Khattak, 2002). Ikramullah*et al.*, (2011), Noorka *et al.*, (2013) linked the differential heritability and selectionresponses with simultaneous evaluation and selection of genotypes across environments.

The hybrid MN-98×MN-96 shows the maximum number of grains per pod that was 12 at the level of normal irrigation conditions, hybrid 00TM-12×MN-92 showed the minimum number of grains per pod at 50% level of irrigation and the genotype 00TM-12 showed the maximum number grains per pod on an average at all level of irrigations (Figure1D) Ali *et al.*, (2013), Noorka and Schwarzacher (2013).

Table3. Estimation of component variations for days to first flowering (DFF), days to pod maturity (DPM), pod length (PL) and Number of grains per pod (NGP) of mungbean.

Components	DFF	DPM	PL	NGP
D	25.26*±1.22	31.89*±1.10	0.17*±0.02	0.44* ± 0.14
H1	14.76*±3.28	-9.16*±2.96	-14.83*±0.04	-13.87* ± 0.37
H2	18.51*±2.98	5.47^{NS}±2.68	0.12*±0.04	1.18* ± 0.34
F	31.55*±3.04	2.30^{NS}±2.74	-0.13^{NS}±0.04	0.42^{NS} ± 0.34
E	0.47^{NS}±0.50	0.23^{NS}±0.45	0.01^{NS}±0.01	1.10* ± 0.06
$(\frac{H1}{D})_{0.5}$	0.76	-0.54	-9.33	5.06
$4DH1^{0.5}$ + $F/4DH1^{0.5}$-F	9.92	0.87	1.09	0.84
$(H2/4H1)$	0.08	-0.15	-0.01	-0.02
h^2 (ns)	0.08NS±2.01	0.26*±0.14	0.01^{NS}±0.04	0.06^{NS}±0.23

D= additive variance; H1=dominance variance; H2= proportion of positive and negative genes in parents; F= relative frequency of dominant and recessive alleles in parents; E= environmental variance; √H1/D= mean degree of dominance; √4DH1+ F/√4DH1-F proportion of dominant and recessive genes in the parents; H2/4H1 proportion of genes with positive and negative effects in the parents; h^2 (ns) heritability narrow sense

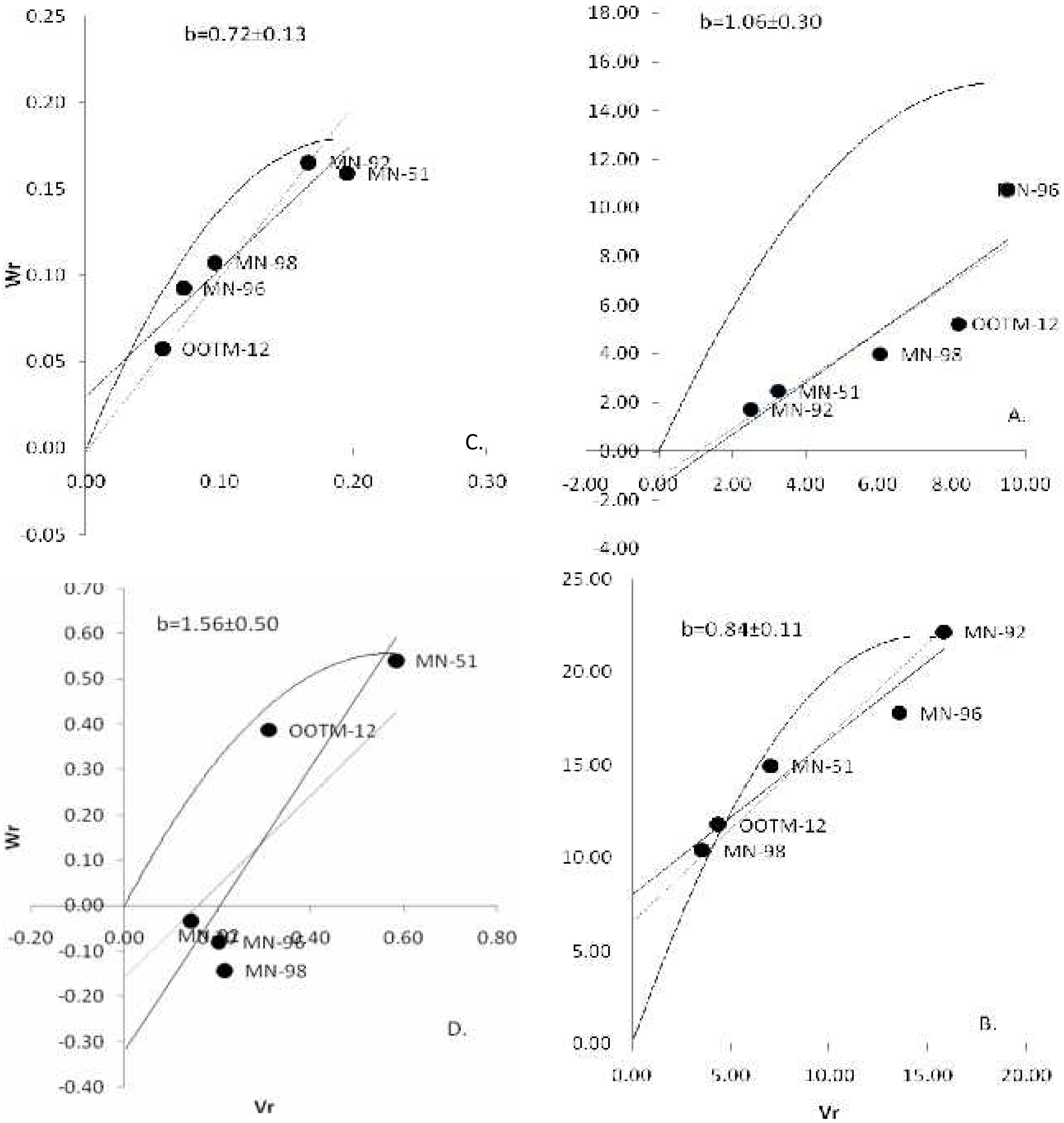

Figure 1.Wr/Vr graph for A.days to firstflowering B. Days to pod maturity C. pod length D. Number of grains per pod^1

Conclusion: The scaling test of additive dominance model the analysis of variance and regression analysis showed that the difference were present among the quantitative traits of Mung bean genotypes but mostly the model was partially adequate which may be due to arrays analysis. The results showed that different genotypes and cross combinations have dominant gene for different traits. That would be used to bridge the gap prevailing in pulses breeding against abiotic stress. By the help of this genetic infrastructure the future breeding may be devised to ensure successful Mung bean crop production.

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