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Nature of gene action for yield and its components in mungbean (*Vigna radiata*)

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ABSTRACT

The assessment of gene effect for some yield characters and detection of epistasis in mungbean [*Vigna radiata* (L.) Wilczek] was studied in four crosses involving five parents through generation mean analysis during *kharif* 2012 at Banaras Hindu University (BHU), Varanasi, UP. Six populations, viz. P_1, P_2, F_1, F_2, B_1 and B_2 of four crosses involving five parents were evaluated. The nature and magnitude of gene effects for yield and its components in mungbean was studied using six parameter model of generation mean analysis. The presence of epistasis was detected by joint scaling test and inadequacy of additive-dominance model was established except seeds/pod. Additive (*d*), dominance (*h*) gene effects along with one or more type of non-allelic interactions (*i, j, l*) contributed significantly towards the inheritance of all the quantitative characters in majority of the crosses. Duplicate type of epistasis and predominant dominance effects was also prevalent in most of the cases except in days to maturity in HUM 8 × ML 713 cross. Thus, postponement of selection in later generations may be suggested to obtain transgressive segregants for improvement of mungbean populations.

Key words: Epistasis, Gene effects, Joint scaling test, Mungbean, V*igna radiata*, Yield

Among pulses, greengram or mungbean [*Vigna radiata* (L.) Wilczek] is an ancient and well known leguminous crop of Asia, on account of its nutritional quality and the suitability to cropping systems. The lower productivity in greengram is mainly attributed to low genetic yield potentiality, indeterminate growth habit, canopy architecture, low partitioning efficiency, cultivation in marginal land including biotic and abiotic stresses. Seed yield is an important trait as it measures the economic productivity in mungbean but its inheritance is extremely complex. Seed yield is closely associated with many traits that make direct or indirect contribution towards this trait. The choice of appropriate breeding procedure depends on the type of gene action involved in the expression of these characters. Gene action is measured in terms of components of genetic variance. Three type of genetic variance, viz. additive, dominance and epistatic variance. In natural plant breeding population, epistatic variance has the lowest magnitude. Breeder cannot oversight the role of epistasis; otherwise he would obtain biased estimates of additive and dominance components of genetic variation which would lead to faulty breeding procedure (Singh and Singh 1974). The presence and absence of epistasis can be detected by the analysis of generation means using the scaling test. Generation mean analysis provides information about the component of genetic variation and provides the information about the predominant type of gene action for important traits of a crop species. This help deciding on a suitable breeding procedure for the improvement of the various quantitative traits of the species. In the present studies, the detection of epistasis, and estimates of additive and dominance components of variation for yield components in five sets of mungbean crosses were carried out by using generation mean analysis of Hayman (1958).

MATERIALS AND METHODS

Three testers (HUM 8, HUM 9 and HUM 12) and two lines (ML 713 and TM 96-2) of mungbean genotypes were hybridized in line × tester fashion to obtain seeds of four cross combinations (Table 1). The genotypes obtained from AICRP on Pulses, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The testers used in this study as a female and line as a male. A bud of approximately 1 cm in length and light green in colour was emasculated in the evening (4 to 6 pm) and pollinated in the next morning (6:30 am to 8:00 am) (Pathak *et al.* 2014). Colored threads were used for marking of different cross combinations. All the genotypes used in this study were photoperiod insensitive.

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Table 1 Distinctive characteristics of genotypes used in this study

Lines	Pedigree	Place of origin	Height	Maturity	100-seed weight (g)
HUM 8	HUM 2 × DPM 90-1	I.Ag.Sc.,BHU, Varanasi	Medium in height	Medium in duration	3.53
HUM 9	Pusa 9131 × F_5(BHU M1 × Pant U 30)	I.Ag.Sc.,BHU, Varanasi	Medium in height	Medium in duration	4.63
HUM 12	HUM 5 × DPM 90-1	I.Ag.Sc.,BHU, Varanasi	Medium in height	Medium in duration	4.9
ML 713	15127 × ML 5	PAU, Ludhiana	Medium in height	Medium in duration	3.40
TM 96-2	Kopergaon × TARM 2	BARC, Mumbai	Medium in height	Medium in duration	4.85

The descriptive characteristics of all genotypes used in this study are presented in Table 1.

The experiments involved the six basic generations of each cross, viz. six parents, their F_1, F_2 and back crosses (BC_1 and BC_2). The segregating and non-segregating generations were planted in completely randomized block design with three replications during *kharif* 2012 at the Genetics and Plant Breeding Research Farm, Institute of Agricultural Sciences, BHU, Varanasi (UP). Each plot was 2 meter row length with spacing of 40cm between rows and 10cm between plants. Each experimental unit comprised of parents and F_1 three rows; 10 rows for the B_1 and B_2 and 20 rows for the F_2. The experimental material was bordered by a mungbean variety HUM 16 to avoid border effect. The experimental field soil was alluvial. Fertilizer was applied at sowing at the rate of 20N: 60P kg/ha. Weeds were removed manually. In the *kharif* season no irrigation is required due to monsoon. Observations were recorded on 20 randomly selected plants from parents and F_1's, 50 plants from back crosses (B_1 and B_2) and 300 plants from F_2 generations for 8 quantitative traits namely, days to 50 per cent flowering, days to maturity, plant height (cm), number of primary branches/plant, number of pods/plant, number of seeds/pod, 100-seed weight (g) and yield/plant (g). The joint scaling test (Cavalli 1952) was used to detect epistasis for all the measured characters. In the presence of epistasis the estimation of additive (d), dominant (h) and non-allelic component (i, j and l) of generation mean were calculated by using six parameter model of Hayman (1958). The type of epistasis was determined only when dominance (h) and dominance × dominance (l) were significant, when these effects had the same sign the effects were complementary while different signs indicated duplicate type of epistasis (Kearsey and Pooni 1996).

RESULTS AND DISCUSSION

The estimates of joint scaling test and magnitudes of components of genetic mean variation for the yield characters studied during *kharif* 2012 are presented in Table 2. The expected mean (m) was significant and positive in all the crosses for all the traits.

Days to 50% flowering

For all the crosses, an epistatic digenic interaction was found to be a suitable fit because the chi-square (χ^2) values were found significant. All the crosses showed significant value of additive and non-additive gene action. The dominance (*h*) effects were higher than the additive (*d*) effects in all the crosses as well as dominance × dominance (*l*) effects were higher than other non-additive interactions indicating dominance gene effects were found to be relatively more important in the inheritance of this trait. All crosses showed duplicate type of non-allelic gene interaction in inheritance this trait. Positive and negative significant value of additive × additive (*i*) effect show association and dispersion of alleles in parents, respectively. The significance but negative value of additive × additive (*i*) effect in cross HUM 9 × TM 96-2 indicated negative additive alleles present in parent, so the selection should be done in later segregating generations, while for other crosses additive × additive (*i*) effects significant and positive indicated positive additive alleles present in parent, so the selection should be done in early segregating generations.

Days to maturity

A simple additive-dominance model was adequate in cross HUM 8 × TM 96-2 because χ^2 value was non-significant. For the remaining crosses the χ^2 values were significant indicating presence of non-allelic gene interaction with significant values *d*, *h*, *i*, *j* and *l* effects. The dominance gene effects were found to be relatively more important because dominance (*h*) and dominance × dominance (*l*) effects were higher than the additive (*d*) and other non-additive effects in all crosses. The significant but negative additive × additive (*i*) effects in crosses HUM 9 × TM 96-2 indicating the possibilities of obtain desirable segregates in later segregating generations, while crosses HUM 12 × TM 96-2 and HUM 8 × ML 713 showed positive significant values. This trait also showed duplicate type epistasis in crosses HUM 9 × TM 96-2 and HUM 12 × TM 96-2, while cross HUM 8 × ML 713 showed complimentary type epistasis in the inheritance of this trait.

Plant height (cm)

The chi-square (χ^2) values were significant in crosses HUM 9 × TM 96-2 and HUM 12 × TM 96-2 indicating presence of epistasis for plant height. For the remaining crosses chi-square (χ^2) values were non-significant,

Table 2 Estimate of gene effects for yield characters in mungbean crosses during *Kharif* 2012

Crosses	$[\hat{m}]$	$[\hat{d}]$	$[\hat{h}]$	$[\hat{i}]$	$[\hat{j}]$	$[\hat{l}]$	Chi square (χ^2)	Epistasis
Days to 50 % flowering								
HUM 8 × TM 96-2	34.00**	1.67**	6.83**	8.67**	3.50**	-11.00**	148.63**	Duplicate
HUM 9 × TM 96-2	38.67**	1.00**	–15.00**	–12.67**	1.67**	16.67**	16.00**	Duplicate
HUM 12 × TM 96-2	35.33**	2.00**	8.67**	12.00**	3.00**	–22.67**	50.40**	Duplicate
HUM 8 × ML713	32.33**	3.00**	13.00**	14.00**	3.33**	–19.33**	16.11**	Duplicate
Days to maturity								
HUM 8 × TM 96-2	65.33**	7.00**	–8.33**					
HUM 9 × TM 96-2	68.00**	8.00**	–16.67**	–14.67**	6.00**	22.67**	313.69**	Duplicate
HUM 12 × TM 96-2	66.33**	11.33**	17.50**	17.33**	10.83**	–36.33**	7.87**	Duplicate
HUM 8 × ML713	64.33**	4.33**	6.33**	8.67**	4.33**	–18.00**	16.27**	Complementary
Plant height (cm)								
HUM 8 × TM 96-2	58.67**	–0.30**	–20.85**				2.91	
HUM 9 × TM 96-2	54.90**	7.10**	–23.68**	–18.87**	10.98**	25.37**	10.84**	Duplicate
HUM 12 × TM 96-2	49.10**	1.83	43.40**	47.80**	3.50*	–75.07**	8.82*	Duplicate
HUM 8 × ML713	53.47**	5.67**	–6.98*				4.09	
Number of Primary branches/plant								
HUM 8 × TM 96-2	3.50**	0.83**	–1.42**	–1.67**	0.55**	2.57**	53.48**	Duplicate
HUM 9 × TM 96-2	2.13**	0.20**	4.93**	5.47**	0.10**	–8.53**	8.64**	Duplicate
HUM 12 × TM 96-2	3.50**	–0.13**	1.25**	0.67**	–0.38**	–1.57**	8.87**	Duplicate
HUM 8 × ML713	2.30**	**0.25****	3.08**	2.93**	–0.25**	–1.90**	9.66**	Duplicate
Number of seeds/pod								
HUM 8 × TM 96-2	10.33**	–0.33	1.50**				7.00	
HUM 9 × TM 96-2	9.00**	–1.00**	5.17**				1.75	
HUM 12 × TM 96-2	10.33**	1.00**	**3.17****				1.75	
HUM 8 × ML713	10.67**	–1.00**	–2.17**				0.28	
Number of pods/plant								
HUM 8 × TM 96-2	21.67**	0.33	–15.67**				0.85	
HUM 9 × TM 96-2	25.00**	1.00	–14.67**				1.09	
HUM 12 × TM 96-2	26.00**	–7.67**	–11.50*				2.23	
HUM 8 × ML713	18.33**	–1.33	–5.50*	–8.00**	–2.83*	12.33**	6.78**	Duplicate
100-seed weight (g)								
HUM 8 × TM 96-2	4.30**	1.20**	–0.13**	–0.27**	1.87**	0.40**	47.09**	Duplicate
HUM 9 × TM 96-2	4.47**	–0.17**	1.55**	1.27**	–0.05*	–0.83**	4.06*	Duplicate
HUM 12 × TM 96-2	4.60**	0.17**	–0.33**					
HUM 8 × ML713	3.83**	–0.13**	–1.07**	–1.33**	–0.20**	1.73**	28.00**	Duplicate
Seed yield/plant (g)								
HUM 8 × TM 96-2	9.00**	3.33**	–3.83**	–5.73**	5.00**	6.87**	15.72**	Duplicate
HUM 9 × TM 96-2	9.30**	–0.9	3.35*	–0.2	–0.72	3.83*	6.70**	Duplicate
HUM 12 × TM 96-2	11.73**	–3.10**	0.15	–6.47**	–3.35**	18.50**	1.24**	Duplicate
HUM 8 × ML713	6.90**	–1.37**	–5.78**				0.01	

* Significant at $P<0.05$ and **significant at $P<0.01$

indicating adequacy of additive-dominance model to explain the inheritance of plant height. The dominance gene effects were found to be relatively more important because dominance (*h*) and dominance × dominance (*l*) effects were higher than the additive (*d*) and other non-additive effects in crosses HUM 9 × TM 96-2 and HUM 12 × TM 96-2. The trait also showed duplicate type of epistatic in cross HUM 9 × TM 96-2 and HUM 12 × TM 96-2. For cross HUM 9 × TM 96-2 selections should be done in later segregating generations because additive × additive (*i*) effect is significant and negative, while HUM 12 × TM 96-2 had significant and positive additive × additive (*i*) effect indicating selection should be done in earlier segregating generations.

Number of primary branches/plant

Additive dominant and non-allelic interactions were found significant for number of primary branches/plant in all crosses. In this trait dominance (*h*) effects were found to be relatively more important because of the *h* values were higher than the *d* values in all crosses. The significant positive values of additive × additive (*i*) effects in all the crosses except HUM 8 × TM 96-2 indicated that alleles with positive effects were more often dominant. The significant and opposite values of dominance (*h*) and dominance × dominance (*l*) effects for this trait in all the crosses indicated duplicate type of non-allelic gene interaction in the expression of this trait.

Number of seeds/pod

For all the crosses chi-square (χ^2) values were non-significant, indicating adequacy of additive-dominance model to explain the inheritance of this trait. Dominance gene effects were found to be relatively more important because the dominance (*h*) effects values were higher than additive (*d*) effects in all the crosses.

Number of pods/plant

The chi-square (χ^2) value was significant for cross HUM 8 × ML 713 indicating presence of non-allelic gene interaction in inheritance of this trait. For the remaining crosses chi-square (χ^2) values were non-significant, indicating adequacy of additive-dominance model to explain the inheritance of this trait. Similar results were also reported by Alghamdi (2009) in faba bean and Kunkaew *et al.* (2010) in adzuki bean. The *h* gene effect was found to be predominant in the expression of these traits because values of *h* were in all the crosses higher than the values of *d*. The significant and negative sign of *h* effect in all the crosses showed accumulation of negative dominant gene in parents therefore postponement of selection in later segregating generations to obtain transgressive segregants. The significant but negative value of *d*, *i* and duplicate epistasis in cross HUM 8 × ML 713 indicated that alleles with negative effects were more often dominant in the parents involved in the cross. Thus, the possibilities are obtaining transgressive segregants in later generations.

100-seed weight (g)

The estimate of chi-square (χ^2) value was found significant in cross HUM 12 × TM 96-2 indicating adequacy of additive-dominance model to explain the inheritance of this trait. For the remaining crosses chi-square (χ^2) values were significant, indicating presence of non-allelic gene interaction. The significant but opposite signs of *h* and *l* indicated duplicate type of non-allelic interaction present in crosses HUM 8 × TM 96-2, HUM 9 × TM 96-2 and HUM 8 × ML 713 for the expression of this trait. Both additive and non-additive gene effects were also found for this trait in mungbean by some earlier researchers (Joseph and Kumar 2000, Khattak *et al.* 2001, Khattak *et al.* 2002, Singh *et al.* 2007, Alam *et al.* 2014).

Seed yield/plant (g)

The estimates of *d, h, i, j,* and *l* were found significant in crosses HUM 8 × TM 96-2, HUM 9 × TM 96-2 and HUM 12 × TM 96-2 for seed yield/plant showing presence of epistatic effect for this trait. In all these three crosses the significant but opposite sign values of *h* and *l* indicated that role duplicate dominant type of non-allelic interaction in the inheritance of this trait. The dominant × dominant (*l*) values were higher than other non-allelic gene interaction indicating predominant role of dominant gene effect for the inheritance of seed yield/plant. The significant but negative values of *i* in above three cross combinations of this trait indicated that negative alleles are dispersed in the parents involved in this crosses. Therefore, the selection for the improvement of seed yield should be delayed to the later generation in segregating population.

In this study, epistasis for all the characters was duplicate type except in days to maturity in HUM 8 × ML 713 cross combination. Duplicate type of non-allelic interaction also reported for plant height, pods/plant and 100-seed weight in mungbean (Singh *et al.* 2007); for plant height, number of primary branches, seeds/pod, pods/plant, 100-seed weight and seed yield/plant in lentil (Khodambashi *et al*. 2012). Prevalence of dominance genetic variance was observed in almost all the traits. Similar findings were also reported by Singh *et al.* (2007) in mungbean and Dahiya and Waldia (1982) in blackgram for plant height, number of primary branches, pods per plant and 100-seed weight. Predominant role of dominance genetic variance in almost all the characters were also observed by Payasi *et al.* (2010), Baradhan and Thangavel (2011) in blackgram, Khodambashi *et al*. (2012) in lentil, Meshram *et al.* (2013) and Pandey *et al.* (2014) in pigeonpea.

An overview the results indicated that yield and its contributed characters showed all the three types of gene actions, i.e. additive, dominant and epistasis. Epistasis is integral part of genetic materials and breeder cannot ignore it. Predominant role of non-additive gene actions and duplicate epistasis was involved in expression of almost all the characters indicating that postponement of selection in later generations or intermating among the selected segregants followed by one or two generations of selfing could be suggested to break the undesirable linkage and allow the accumulation of favorable alleles for the improvement of these traits.

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