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GENETIC ANALYSIS OF HARVEST INDEX IN MUNGBEAN

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A diallel cross experiment involving eight parents was conducted to understand the genetic mechanism controlling harvest index in mungbean. Analysis of variance depicted highly significant differences for female, male parents and their interaction in F_1 and F_2 generations. The data for both the generations was found partially adequate when subjected to adequacy tests. Estimation of genetic components of variation revealed significance of both additive and non-additive components in both generations. In F_1 generation degree of dominance was less than 1, indicating preponderance of additive gene effects while in F_2 it was more than 1 showing over dominance type of gene action. Graphical differences revealed presence of additive gene action in both the generations

INTRODUCTION

Pulses productivity is relatively low for their poor dry matter partitioning in to grains as compared with vegetative matter. To improve yield potential of mungbean varieties capable of high biomass production and having ability to convert maximum of the dry matter in to grains are required. In order to develop such cultivars, comprehensive information on inheritance mechanism is required.

Ahuja and Chowdhrary (1981) reported significant differences for yield in mungbean which were mainly because of differences in harvest index values ranging from 25-45%. Additive component of variation was important for harvest index. Chand *et al* (1996) found that additive gene action was important for harvest index in wheat. Dijee *et al* (2000) reported preponderance of additive component of genetic variation in cowpeas. Khattak *et al* (2002) reported significance of both additive and non-additive components in mungbean.

MATERIALS AND METHODS

Eight lines/varieties viz. 562-1, 56-2, NM-95, NM-92, L.No.1, L. No.21, 6601 and E32-1 were sown during July, 2002 (kharif season) in the field and all possible crosses, including reciprocals were made.

Sixty-four entries (56 F_1's and 8 parents) were planted in the field during March 2003 (spring season). The experiment was conducted using a randomized complete block design with three replications. Row to row and plant to plant spacing were kept 30 cm and 10 cm, respectively. Seeds were dibbled at the rate of two seeds per hole, which were later thinned to single healthy seedling per hole after germination. Each treatment comprised single row of 2.5 m length with 26 plants. Twenty equally competent plants were selected for data recording.

The seed obtained from the F_1 plants was used to raise the F_2 generation during kharif 2003 in a randomized complete block design replicated thrice. The plot size was 5 x 1.2 m thus accommodating 204 plants. Observations were recorded from all the plants by leaving one plant on each side of the row.

Crop was raised following standard agronomic practices in each season. All the cultural operations including hoeing, weeding, irrigation, fertilizer etc were carried out identically to reduce experimental error. Data were recorded from all the plants by leaving one plant on each side of the row as non-experimental. At maturity each plant was harvested just above the ground level. After harvest each plant was sun dried and weighed at regular intervals. At the stage when further loss in the plant weight was ceased, dry weight of each plant was recorded in grams on an electronic balance and average dry weight was computed and taken as total plant dry matter. After threshing, the produce obtained from each plant was weighed in grams on electronic balance and average grain weight for each treatment was taken as grain yield per plant. Harvest index is the ratio of economic yield to total biological yield (Donald, 1965) or

$$HI = (Y/TDM) \times 100$$

Where Y is grain yield and TDM is total plant dry matter.

Genetic components of variation were estimated following Mather and Jinks (1982) and Singh and Chaudhary (1985).

RESULTS AND DISCUSSION

Analysis of variance for harvest index presented in Table 1 exhibited highly significant differences for female and male parents along with the interaction between male and female in F_1 and F_2 generations. This signified the importance of additive as well as

Table 1. Analysis of variance for harvest index

S.O.V.	Df	F_1 Generation		F_2 Generation	
		Mean squares	F Ratio	Mean squares	F Ratio
Blocks	2	2.52	0.60^{NS}	102.32	2.55^{NS}
Female (F)	7	267.32	53.51**	463.47	11.56**
Male (M)	7	229.61	48.96**	344.48	8.59**
FxM	49	40.94	8.20**	138.20	3.45**
Error	126	4.99		40.11	
Total	191				
Reciprocal	28	12.26	2.45**	157.64	3.80**

NS = Non significant, ** = P<0.01

Table 2. Regression analysis of Wr and Vr for harvest index

Item	F_1 Generation	F_2 Generation
Regression coefficient (b)	1.07 ± 0.18	0.41 ± 0.13
Difference of b from zero (b_0)	5.72*	2.96*
Difference of b from unity (b_1)	-0.40^{NS}	4.24*

NS = Non significant, * = P<0.05

Table 3. Analysis of variance of Wr and Vr for harvest index

S.O.V.	Df	F_1 Generation		F_2 Generation	
		Mean squares	F Ratio	Mean squares	F Ratio
Wr + Vr					
Between arrays	7	3078.1	6.37**	5771.0	3.50*
Within arrays	16	483.2		1649.0	
Wr-Vr					
Between arrays	7	132.91	3.51*	1955.0	0.92^{NS}
Within arrays	16	37.87		2133.0	

NS = Non significant, * = P<0.05, ** = P<0.01

non-additive components of genetic variation for this character. Reciprocal effects were significant in both the generations.

When subjected to adequacy tests the data for each generation were found partially adequate. The F_1 data qualified the joint regression analysis of variance test (Table 2) as the value of b differed significantly from zero but not from unity. The F_2 data did not qualify on the basis of this test as the value of b differed significantly from zero as well as unity. The analysis of variance for Wr + Vr and Wr-Vr presented in Table 3 showed that Wr+Vr and Wr-Vr values varied significantly from array to array for F_1 data hence it could not qualify this test. The F_2 data qualified this test as the values for Wr+Vr differed between arrays however differences between arrays for Wr-Vr values were non significant. Hence the data for each generation were partially adequate.

Formal analysis of variance is presented in Table 4 which revealed that for F_1 the items a (additive), b dominance and its components b_2, asymmetrical gene distribution and b_3, specific gene effects are significant and b_1 was non significant showing absence of directional dominance when tested against pooled block interaction because χ^2 (10.50) value was less than tabulated when Bartlett's test was applied. Reciprocal effects c and d were significant, therefore "a" was retested against c and its significance was reduced to non significant. When b and its components were retested against d only b and b_2 representing overall dominance and asymmetrical gene distribution maintained their significance and b_2 was reduced to non-significant. For F_2 the components a, b, b_2, b_3 and

Table 4. Formal analysis of variance for harvest index according to Mather and Jinsk (1982)

Item	Df	F_1 Generation			F_2 Generation		
		Mean squares	F Ratio	F Ratio c&d	Mean squares	F Ratio	F Ratio c&d
a	7	211.01	21.12*	1.59 ^{NS}	304.69	3.79*	0.81 ^{NS}
b_1	1	29.43	2.94 ^{NS}	0.66 ^{NS}	126.76	1.58*	
b_2	7	138.15	13.82*	3.11*	193.10	2.40*	
b_3	20	57.68	5.77*	1.30 ^{NS}	188.56	2.35*	
b	28	76.79	7.68*	1.73*	187.48	2.33*	
c	7	132.37	13.25*		374.28	4.66*	
d	21	44.33	4.43*		115.48	1.43 ^{NS}	
a x blocks	14						
b_1 x blocks	2						
b_2 x blocks	14						
b_3 x blocks	40						
b x blocks	56						
c x blocks	14						
d x blocks	42						
Block interactions	63	9.99			80.21		

NS = Non significant, * = P<0.05

Table 5. Estimates of genetic components of variation for harvest index

Components	F_1 Generation	F_2 Generation
E	1.652 ± 1.618	13.692 ± 4.925
D	75.153 ± 4.833	64.025 ± 14.709
F	56.288 ± 11.472	37.25 ± 34.912
H_1	59.778 ± 11.161	89.257 ± 33.96
H_2	39.00 ± 9.710	72.163 ± 29.551
h^2	0.601 ± 6.49	- 5.610 ± 19.769
$\sqrt{H_1/D}$	0.89	1.18
$H_2/4H_1$ (□v)	0.16	0.20
$\sqrt{4DH_1 + F}$	2.44	1.65
$\sqrt{4\ DH_1 - F}$		
Heritability (Narrow sense)	0.63	0.40
Heritability (Broad sense)	0.94	0.77

c were significant while, b_1 and d were non significant. This necessitated the retesting of a against c. Retesting of "a" against c reduced it to non-significant. Table 5 revealed that genetic component of variation E representing the environmental effects was significant for F_2 generation and non significant for F_1. The value of D, additive component was significant for both the generations. Component due to dominance H_1 and H_2 were also significant. The degree of dominance with value less than 1 for F_1 showing prevalence of additive gene action and more than 1 for F_2 showing the prevalence of over dominance type of gene action in F_2. The value of F was positive and significant showing that dominance genes were more frequent among the parents and the proportionate ratio had value more than 1 for each generation indicating that dominant genes were frequent in the parents. The value of *uv* was less than 0.25 in both generation showing asymmetrical gene frequencies. The value of dominance effect h^2 was non significant for F_1 but

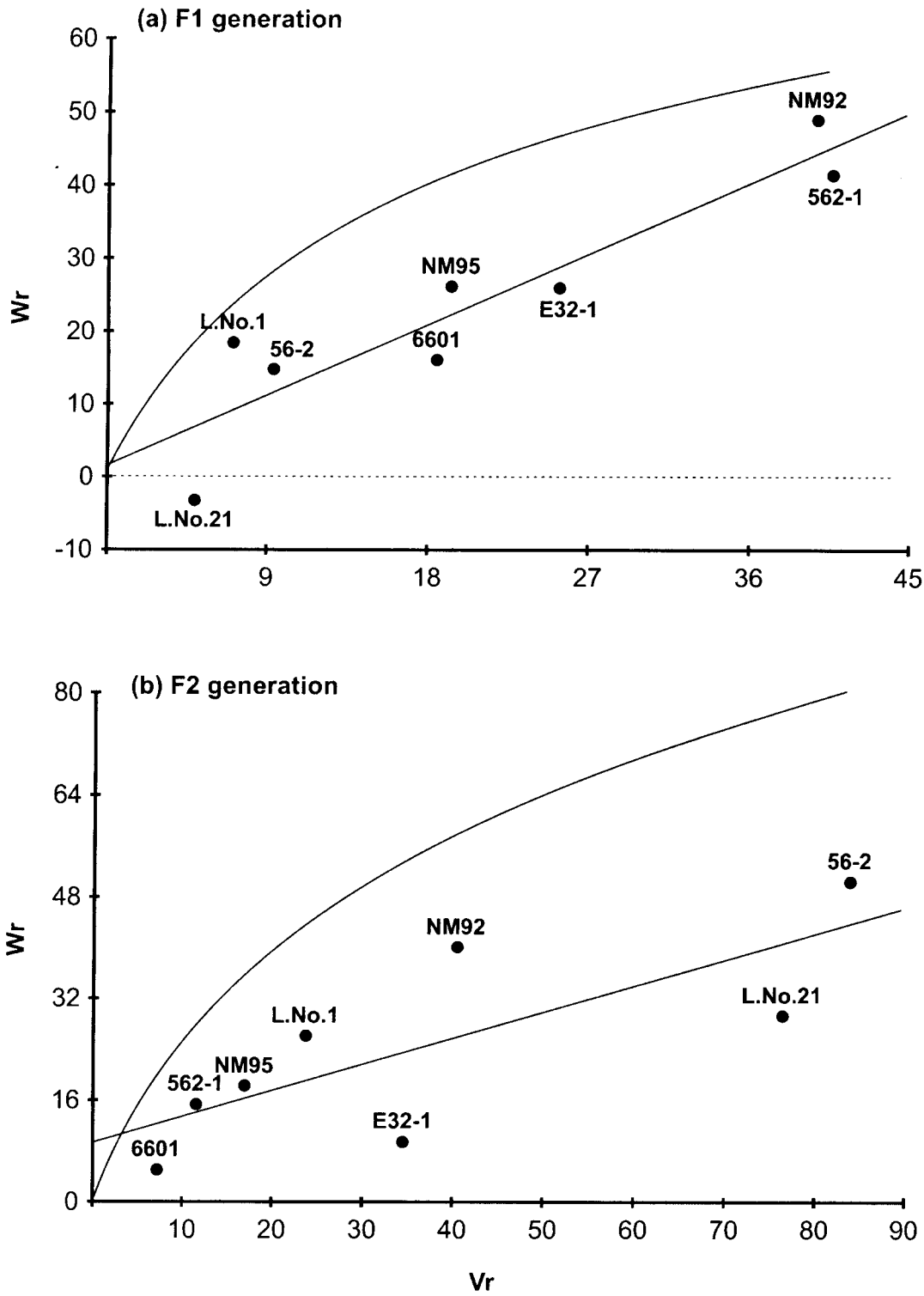

Fig. a, b : Vr/Wr graph for harvest index (%)

negative and significant for F_2 showing that recessive genes have increasing value. The value of r was positive for F_1 showing that dominant genes have increasing value while this was negative for F_2 showing recessive genes have dominant values. Fig a. showed that partial dominance type of gene action prevailed as the regression line cuts the Wr axis above the origin. L. No. 21 possessed maximum dominant gene while NM-92 and 6601 possessed maximum recessive genes. Fig b revealed that line intercepted the Wr axis above the origin hence partial dominance type of gene action prevailed. Variety 6601 contained maximum dominant genes while line 56-2 had maximum recessive genes as evident by the position of arrays on the regression line.

Ahuja and Chowdhary (1981) in mungbean, Chand *et al.* (1996) in wheat reported the presence of additive type of gene action. Dijee *et al.* (2000) reported non-additive gene action in cowpea whereas Khattak *et al.* (2002) elucidated the significance of both additive and non additive components for mungbean.

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