

Genetic Analysis of Yield and Related Characters of Lablab Bean

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Received 1 Jan 2019, Revised 17 Feb 2019, Accepted 15 March 2019,
Published 28 April 2019

Scientific Editors: Puspita Raj Paudel, Shambhu Khatriwada, Jiban Shrestha
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ABSTRACT

An experiment was conducted with a view to determine the nature and extent of gene action of yield and yield related characters of lablab bean. Five parents and their 10 F₁s synthesized from 5 x 5 half diallel cross were evaluated in a Randomized Complete Block Design with three replications. The analysis of variance showed that the difference among the genotypes (parents and F₁s) were highly significant for all the characters which revealed the presence of wide variability among the genotypes under this study. Hayman's ANOVA (modified by Jones) suggested that the presence of additive and dominance gene actions for all the characters. The 'Vr-Wr' graph indicated partial dominance for the characters viz. days to first inflorescence appearance, days to first flowering, days to pod maturity, days to seed maturity, number of nodes per inflorescence, edible pod length, edible pod breadth, edible pod weight and pod yield per plant. Over dominance was observed for number of inflorescences per plant, number of pods per inflorescence and hundred seed weight. Complete dominance was observed only for number of pods per plant in lablab bean. As the development of hybrid variety is not possible in lablab bean, diallel selective mating system may be adopted for improvement of yield traits by using knowledge of gene actions. The hybrids with predominant additive gene action for yield related traits may be advanced to obtain transgressive segregants and pure lines for higher pod yield per plant.

Keywords: Country bean, diallel, dominance, gene action, earliness, pod yield

INTRODUCTION

Lablab bean (*Lablab purpureus* L.) is a popular winter vegetable crop in Bangladesh. It is a species of bean in the family of Fabaceae. This is popularly known as country bean or *Deshi seem* in Bangladesh. It is a self-pollinated crop that has a set of diploid chromosome ($2n = 2x = 20, 22, 24$) (Philip, 1982). Lablab bean is cultivated to wide areas under diverse climatic conditions. It is grown well where daily temperature range from 17°- 30°C and can widely be cultivated from sand to clay soil, in a pH range of 4.5–7.5 (Cook et al 2005). The commercial cultivation of lablab bean relates also in poor sandy to medium loam soil. It has been reported that lablab bean does not grow well in saline or poorly-drained soils, but it grows better than most legumes under acidic condition (Valenzuela and Smith, 2002). Being a drought tolerant crop, it grows well in dry lands with limited rainfall. It can continue to grow in drought or shady conditions, and well grow in areas with an average annual rainfall is 25–120 cm (Cook et al 2005). It is well suited to arid and warm climates where rainfall is around 600 mm during the growing season (Cobley and Steele, 1976). Lablab bean is more drought resistant than other similar legumes (Maass et al 2010), and can access soil water 180 cm deep (Cook et al 2005). It prefers relatively cool seasons (temperature ranging from 14-28°C with the sowing done in July-August. The crop starts flowering in short days (11-11.5 hour's day length) and continues indeterminately in spring. It was found that lablab bean flowers throughout the growing season (Kumar et al 2013).

Different cultivars of bean are used for different purpose. It has been estimated that, lablab bean seed contain 19-31% protein, 2% fat, 61% carbohydrate (includes 5% fibers) as well as adequate levels of vitamins and minerals (Kumar et al 2014). Maass et al (2010) found protein isolate from the bean can

be used as a food additive for improving cake quality. Edible pods of lablab bean provide substantial amount of protein in addition to vitamin A, vitamin C, riboflavin, potassium, sulphur iron, and sodium (Deka and Sarker 1990, Newaz 1992). The flavonoid overlaid in lablab bean play a role in the prevention of cancer (Kobayashi et al 2002) and as a chemotherapeutic and/or chemo preventive agent for head and neck cancer (Alhasan et al 2001). Polyphenol oxidase like tryrosinase is present in plant tissue of lablab bean has potential for the treatment of hypertension in humans (Naeem et al 2009). Thus mature seed provide a cheaper source of protein that consume at both as cooking and frying. Apart from consuming as vegetable or pulse in Asia, lablab bean is widely grown as a forage or green manure crop in the tropics and subtropics (Purseglove 1977). Being a legume, it can also fix atmospheric nitrogen to the extent of 170 kg/ha besides leaving enough crop residues to enrich the soils with organic matter.

According to the latest statistics, the total lablab bean production was 93055, 94356 and 94756 metric ton in the year of 2012-2013, 2011-2012 and 2010-2011, respectively in Bangladesh from 42129, 42300 42760 acres of land (BBS, 2014). Thus production is decreased proportionally with decreasing area. The average yield of lablab bean was 5.45 metric ton per hectare during the year 2012-2013 (BBS 2014). Maass et al. (2010) also observed that lablab bean may suffer from low yields when grown as a main cash crop. This poor figure is a matter of lackadaisical for bean production in Bangladesh. However, this low yield status is attributed due to the lack of high yielding varieties and prescribed production practices. Besides this low productivity, crop has others problem in the people in Bangladesh. Most of the farmers of Bangladesh are very poor. They want to get good profit early in the season. The cultivars photosensitivity and longer duration is a great problem in this regard. Again, consumer preferences also vary with pod size, shape, color and aroma. The efforts of improving the crop by utilizing indigenous and exotic germplasm have been useful in breaking the yield barriers (Shivashankar and Kulkarni 1989, Shivashankar et al 1993) resulting in compact plant type, reduced duration and photo-insensitive types.

Hybridization among different genotypes and genetic analysis of different yield and related characters of lablab bean measures the potential of breeding program. Thus it is important to assess breeding potential of parents and select good combiners in lablab bean. Success of any breeding program is relied on choice of parents. This study depicts the nature and magnitude of gene action regarding evolving related characters of parents and their offspring. Gene actions may show heterosis in F_1 or linkage in other generation. Thus crop improvement programs are created by this necessary information of fixable genes and exploitation of heterosis. Being a self-pollinated crop, it is estimated theoretically less degree of heterosis. But this study provides higher heterosis in relation to yield trait that helps for increasing the higher production.

Little information has been obtained on the various types of gene action and their relative importance in the inheritance of important traits in lablab bean. Plant breeders are primarily concerned with the improvement of those traits which are directly or indirectly related to the economic values (Wynne and Coffelt 1973). Such traits are generally quantitative in nature and governed by several numbers of genes each having small effect and acting in a cumulative manner called polygenes (Srivastaba and Bajpai 1977). Among the various biometrical tools, diallel analyses furnish fruitful result for identification of genetic parameters regarding combining ability as well as dominance relationship of the parents with their gene effects by studying the F_1 hybrids. It is also provides information on the nature and magnitude of genetic variance on which success of plant breeding depends. Based on above facts present research was conducted with the objective to estimate the nature and extent of gene action of yield and related characters in lablab bean.

MATERIALS AND METHODS

Vr-Wr Analysis (Hayman's Approach)

Diallel analysis has been widely used in genetic analysis of quantitative characters in many crop plants. Diallel cross was analyzed with statistical techniques first by Sprague and Tatum (1942).

Hayman analysis of variance : The Hayman analysis of variance was carried out following Morley Jones modifications for diallel without reciprocals (Jones, 1965) using mean value of diallel fashion.

Where,

a = additive effects

b₁ = mean dominance

b₂ = additional dominance effects that can be accounted for by genes having one allele present in only one line the remaining n-1 lines being assumed to carry same alternative allele (= dominance deviation due to arrays)

b₃ = residual dominance effects

dev² = sum of square of deviations from the mean

ur = Y_i + Y_{ii}

tr = 2 (Y_i + Y_{ii}) - (p + 2) Y_{ii}

Vr-Wr analysis and graphical presentation: The Vr-Wr analysis facilitates study of major genetic features of quantitative characters (Hayman, 1954). The array variance (Vr) and parent offspring covariance (Wr) and regression Wr on Vr was calculated to test the adequacy of the simple additive dominance genetic model, to discern the relative proportion of dominant to recessive genes present in the common parents of the arrays and to find average level of dominance.

The parabola $Wr = \sqrt{V_p \cdot V_r}$ in the Vr-Wr graph delimits the area in which the coordinate (Vr, Wr) array data occur and the Wr intercepts is an indicator of the average degree of dominance, being positive with partial dominance and negative with over dominance. If there is no dominance all the points on the Vr, Wr graph are estimates of single point (Wr, Vr) with $Wr = 2Vr$, there is no regression and the line is tangent to the limiting parabola, with complete dominance, the regression line is of unit slope and passes through the origin.

The variance (Vr) and covariance (Wr) of array whose common parent bears most of the dominant genes will be relatively smaller in magnitude than the array whose common parent carries most of the recessive genes. Parents with dominant allele will have low Vr and Wr and will be near the origin while highly recessive parents have large Vr and Wr and will be furthest from the origin.

Standard deviation graph was plotted from the standardized values of parental mean (Yr_i) and (Wr + Vr) _i values from n arrays, using suitable scale. The intersecting points will locate the relative distribution of array points (parents) in the standardized graphs having four quarter specified by predominance of dominant/recessive alleles with positive/negative effects.

Genetic Components of Variation: The genetic components of variation in F₁ diallel population were calculated according to Jinks (1956) as follows:

$D = V_0L_0 - E$ = Variation due to additive effect

$F = 2V_0L_0 - 4W_0L_{01} - 2(p-2) E/p$ = Mean co-variance of additive and dominance effects.

$H_1 = V_0L_0 + 4V_1L_1 - 4W_0L_{01} - (3p-2) E/p$ = component of variation due to the dominance effect of the genes.

$H_2 = 4V_1L_1 - 4V_0L_1 - 2E = H_1 [1 - (u - v)^2]$ = proportion of positive genes U and proportion of negative V in the parents.

$h_2 = 4(ML_1 - ML_0)^2 - 4(p-1) E/p^2$ = dominance effect (as the algebraic sum over all loci in heterozygous phase in all crosses).

$E = [(Error\ SS + Rep.\ SS)/df.] / \text{no. of reps.}$ = the expected environmental component of variation.

Where,

V_0L_0 = variance of parents

V_1L_1 = mean variance of the arrays

W_0L_{01} = the mean covariance between the parent and the arrays

V_0L_1 = Variance of the mean of arrays

$(ML_1 - ML_0)^2$ = the difference between the mean of the parents and the mean of their P₂ progeny.

The significance of the estimates of various components were tested by calculated their corresponding standard errors.

The standard error is the under root of the products of common multiplier and specific multipliers calculated from the formula as follows:

Common multiplier or variance (S^2) was calculated with the formula –
 $S^2 = \frac{1}{2} [\text{var} (Wr - Vr)]$

Specific multipliers of various components are calculated from the formula as follows:

$$D = (p^5 + p^4)/p^5$$

$$F = (4p^5 + 20p^4 - 16p^3 + 16p^2)/p^5$$

$$H_1 = (p^5 + 41p^4 - 12p^3 + 4p^2)/p^5$$

$$H_2 = 36p^4/p^5$$

$$h_2 = (16p^4 + 16p^2 - 32p + 16)/p^5$$

$$E = p^4/p^5$$

Thus, the components of variation with their standard errors are as:

$$D \pm SE (D)$$

$$F \pm SE (F)$$

$$H_1 \pm SE (H_1)$$

$$H_2 \pm SE (H_2)$$

$$h_2 \pm SE (h_2)$$

$$E \pm SE (E)$$

The parameters were tested for their significance by t-test; the t-value which exceeded 1.96 was marked significant. The following parameters were also calculated:

$$[\sqrt{(4DH_1) + F}] / [\sqrt{(4DH_1) - F}] = \text{the relative proportion of dominant and recessive gene in the parents}$$

h_2/H_2 = the number of genes which control the character and exhibit dominance.

$\sqrt{(H_1/D)}$ = mean degree of dominance

$H_2/4H_1$ = Proportion of dominant genes with positive/negative effects.

Heritability in both narrow and broad, sense were estimated using D, H₁, F and E components of genetic variation as outlined by Verhalen and Murray (1969) for F₂ population:

$$\text{Narrow sense heritability } (h_n^2) = \frac{1/4D}{1/4 D + 1/4 H_1 - 1/4 F + E}$$

RESULTS

A 5 x 5 half diallel population developed from five morphologically diverse parents was studied in the present investigation. Mean squares from simple analysis of variance, Hayman's ANOVA (modified by Jones 1965), genetic components variations are presented in **Table 1** to 3. Analysis of variance showed highly significant values for all the characters studied in case of parents, F₁'s and parents vs F₁'s except days to first flowering, days to edible pod maturity, days to seed maturity, number of pods per inflorescence and edible pod length in parent's vs F₁'s (**Table 1**).

Hayman's Analysis (Graphical and Numerical Approach)

Days to first inflorescence appearance : It was found highly significant value for analysis of variance to determine days to first inflorescence appearance for all the item suggested by Hayman's and followed by Jones (1965) (**Table 2**). The regression line was merged 'Wr' axis above the point of origin in 'Vr-Wr' graph that indicated presence of partial dominance for controlling the character days to first inflorescence appearance (**Figure 1a**). Array point of five parents scattered all along the regression line in 'Vr-Wr' graph.

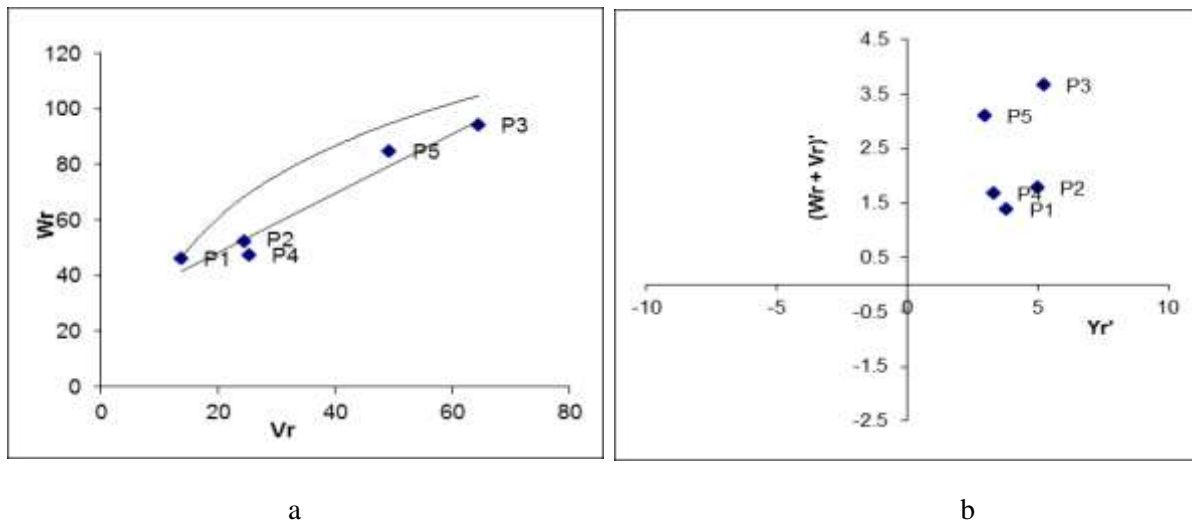


Figure 1. 'Vr-Wr' (a) and parental mean (b) graph for days to first inflorescence appearance in 5 x 5 half diallel population in lablab bean.

The consistency of dominance or recessive with positive or negative effects in opposition to parental mean score was determined in the $Yr-(Wr+Vr)'$ graph (Figure 1b). Early inflorescence appearance was negatively associated with the direction of higher Yr' value. It was found that P₅ possessed the early appearance inflorescence among the parents. The highly significant value was observed for components D, H₁, H₂ and F for days to first inflorescence appearance (Table 3). H₂ and h₂ indicated dominance with asymmetry and higher degree of dominance with negative effects, respectively.

Table 1. Analysis of variance for 13 different characters in a five parental half diallel population in lablab bean

Sources of Variation	df	DFI	DFF	DPM	DSM	NIP	NNI	NPI	NPP	EPL	EPB	EPW	HSW	PYP
Rep.	2	4.48 ^{NS}	8.99 ^{NS}	30.63 ^{NS}	40.49 ^{NS}	54.24 ^{NS}	0.96 ^{NS}	0.11 ^{NS}	3220.47 ^{NS}	1.09 ^{NS}	0.01 ^{NS}	0.01 ^{NS}	0.07 ^{NS}	0.57 ^{NS}
Genotype	14	207.60**	680.24**	1017.98**	1316.06**	4402.79**	15.73**	5.99**	325508.72**	12.34**	1.25**	16.83**	163.37**	34.89**
P	4	534.23**	1512.35**	2012.39**	2687.65**	947.65**	35.07**	11.76**	263617.77**	24.25**	2.31**	33.05**	137.54**	7.11**
F ₁ 's	9	84.17**	379.36**	685.14**	852.47**	4737.14**	5.43**	4.08**	333332.74**	8.38**	0.71**	10.13**	150.29**	37.89**
P vs F ₁ 's	1	11.99**	59.62 ^{NS}	35.97 ^{NS}	2.01 ^{NS}	15106.18**	31.06**	0.10 ^{NS}	502656.40**	0.26 ^{NS}	1.83**	12.19**	384.44**	118.99**
Error	28	1.52	23.68	15.63	16.63	56.23	0.62	0.41	14156.78	1.51	0.01	0.36	0.19	1.74

* $P > 0.05$; ** $P > 0.01$; NS = non-significant

DFA= Days to first inflorescence, DFF= Days to first flowering, DPM= Days to Pod Maturity, DSM= Days to Seed Maturity, NIP= Number of inflorescence per plant, NNI= Number of node per inflorescence, NPI= Number of pods per inflorescence, NPP= Number of pods per plant, EPL= Edible pod length (cm), EPB= Edible pod breadth (cm), EPW= Edible pod weight (g), HSW= Hundred seed weight (g), PYP= Pod yield per plant (kg).

Table 2. Hayman's ANOVA (modified by Morley Jones) for 13 different characters in a five parental half diallel population in lablab bean

Sources of Variation	df	DFI	DFF	DPM	DSM	NIP	NNI	NPI	NPP	EPL	EPB	EPW	HSW	PYP
A	4	209.69**	684.04**	826.44**	1351.02**	1803.77**	12.57**	3.76**	203452.53**	12.70**	1.22**	16.43**	56.09**	14.39**
B	10	107.59**	358.69**	561.99**	665.78**	3267.51**	9.50**	3.45**	204661.64**	6.36**	0.65**	8.56**	106.57**	23.54**
b ₁	1	4.00**	19.87 ^{NS}	11.99 ^{NS}	0.67 ^{NS}	5035.39**	10.35**	0.03 ^{NS}	167552.13**	0.09 ^{NS}	0.61**	4.06**	128.15**	39.66**
b ₂	4	25.78**	98.15**	214.33**	128.88**	1773.33**	2.81**	1.63**	90005.88**	1.49*	0.03**	0.83**	43.79**	8.22**
b ₃	5	193.76**	634.89**	950.12**	1228.32**	4109.27**	14.68**	5.59**	303808.14**	11.51**	1.16**	15.71**	152.48**	32.56**
Error	28	0.51	7.89	5.21	5.54	18.74	0.21	0.14	4718.93	0.50	0.0036	0.12	0.06	0.58

* $P > 0.05$; ** $P > 0.01$; NS = non-significant

DFA= Days to first inflorescence, DFF= Days to first flowering, DPM= Days to Pod Maturity, DSM= Days to Seed Maturity, NIP= Number of inflorescence per plant, NNI= Number of node per inflorescence, NPI= Number of pods per inflorescence, NPP= Number of pods per plant, EPL= Edible pod length (cm), EPB= Edible pod breadth (cm), EPW= Edible pod weight (g), HSW= Hundred seed weight (g), PYP= Pod yield per plant (kg).

As dominance gene action was predominant for this trait which may helps to get transgressive segregant to develop pureline variety. The significant value of component E (0.29^{**}) also revealed the essential contribution of environment for this character. Similar result also reported by Sen et al (2018).

Days to first flowering: The analysis of variance showed eminent significant value for all the items except 'b₁' for days to first flowering (Table 2). The value 'b₁' was found non-significant for this trait. The item 'b₂' and dominance deviation was also observed significant value of item 'b₃' for expressing this character. The presence of partial dominance was reported for controlling the character days to first flowering as the regression line intersected the 'Wr' axis above the point of origin (Figure 2a). It was clearly visible that P₄ located near the point of origin and in contrast, the parent P₃ located far from the origin. The array points for this character were scattered all along the 'Vr-Wr' graph.

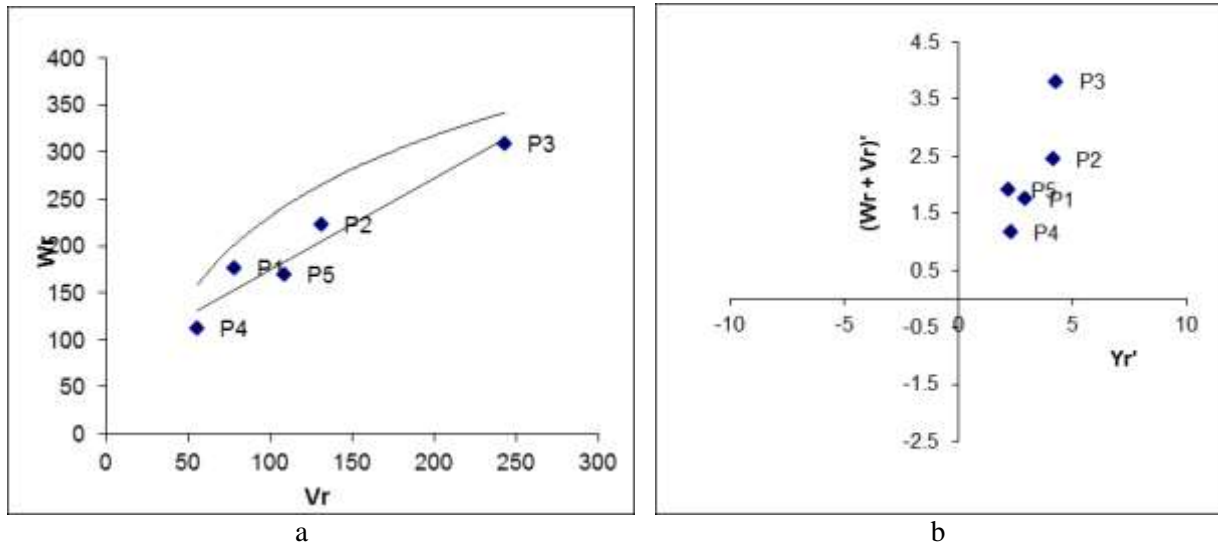


Figure 2. 'Vr-Wr' (a) and parental mean (b) graph for days to first flowering in 5 x 5 half diallel populations in lablab bean.

The Yr'-(Wr+Vr)' graph showed relative distribution of five parental score that indicated predominance of recessive alleles with positive effect (Figure 2b). The parent P₂ and P₃ showed higher Yr' values and parent P₅ has lower values for this character.

Table 3. Estimation of different genetic components of variation and ratios for 13 different characters in a five parental half diallel population in lablab bean

Sources of Variation	DFI	DFF	DPM	DSM	NIP	NNI	NPI	NPP	EPL	EPB	EPW	HSW	PYP
D	117.79**	500.33**	668.03**	892.85**	315.53**	11.58**	3.85**	85634.64**	7.84**	0.77**	10.96**	45.82**	2.09**
F	96.68**	212.88**	403.23**	247.10**	64.59 ^{NS}	7.87**	3.38**	11577.59*	1.76**	0.11**	2.71**	45.55**	-3.59**
H ₁	488.05**	1316.64**	1875.11**	2213.79**	766.25**	33.43**	11.91**	201764.16**	19.20**	1.80**	26.87**	146.37**	1.24 ^{NS}
H ₂	-428.71**	-1126.59**	-1234.69**	-1886.47**	4355.98**	-25.33**	-6.47**	75627.29**	-17.10**	-1.53**	-22.35**	63.97**	36.21**
h ₂	-3.69**	-10.23**	4.30 ^{NS}	-3.38 ^{NS}	118.39*	5.57**	-0.37**	-714.85 ^{NS}	0.35**	1.37**	3.50**	19.82**	10.86**
E	0.29**	3.78**	2.77 ^{NS}	3.04*	9.35 ^{NS}	0.11**	0.07**	2237.95*	0.25**	0.002**	0.06**	0.03 ^{NS}	0.28*
(H ₁ /D) ^{0.5}	1.66	1.62	1.68	1.57	1.56	1.70	1.76	1.53	1.57	1.53	1.57	1.79	0.77
H ₂ /4 H ₁	-0.22	-0.21	-0.16	-0.21	1.42	-0.19	-0.14	0.09	-0.22	-0.21	-0.21	0.11	7.31
KD/KR	-1.65	-4.94	-2.11	-4.95	2.23	-2.87	-3.19	1.75	2.36	157.74	-19.01	-1.20	-0.51
h ₂ /H ₂	0.01	0.01	-0.003	0.002	0.03	-0.22	0.06	-0.01	-0.02	-0.89	-0.16	0.31	0.30
h ² _n	0.31	0.30	0.31	0.31	0.29	0.30	0.30	0.30	0.29	0.31	0.31	0.31	0.26

* $P > 0.05$; ** $P > 0.01$; NS > non-significant

DFA= Days to first inflorescence, DFF= Days to first flowering, DPM= Days to Pod Maturity, DSM= Days to Seed Maturity, NIP= Number of inflorescence per plant, NNI= Number of node per inflorescence, NPI= Number of pods per inflorescence, NPP= Number of pods per plant, EPL= Edible pod length (cm), EPB= Edible pod breadth (cm), EPW= Edible pod weight (g), HSW= Hundred seed weight (g), PYP= Pod yield per plant (kg).

Positive and significant measures were found for components D, H_1 , F and E for days to first flowering in lablab bean (Table 3). On the other hand, negative significant measure was found for components H_2 (-1126.59**) and h_2 (-3.69**).

Days to first edible pod maturity: The significant value was found for item 'a', 'b', 'b₂' and 'b₃' for the character of days to first edible pod maturity (Table 2). The non-significant value was found for the item 'b₁'. The regression line in 'Vr-Wr' graph touches 'Wr' axis far above the point of origin (Figure 3a) for days to edible pod maturity. The array points P₃ and P₁ situated far from the origin. The 'Vr-Wr' graph also showed scattered array points along the regression line.

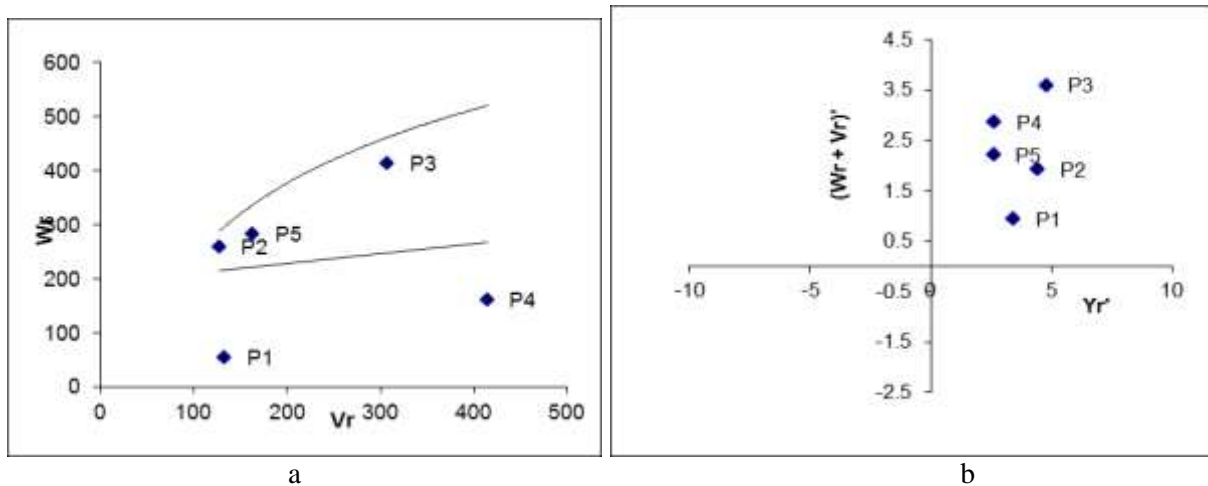


Figure 3. 'Vr-Wr' (a) and parental mean (b) graph for days to edible pod maturity in 5 x 5 half diallel populations in lablab bean.

The predominance of recessive alleles with positive effect was found for all the five parental score for controlling days to edible pod maturity in $Yr'-(Wr + Vr)'$ graph (Figure 3b). It was found that both P₄ and P₅ were closely located having lower 'Yr' value than rest of the parental (P₁, P₂ and P₃) for edible pod maturity in lablab bean. The significant value was found for the components D, H_1 and F for days to edible pod maturity (Table 3). The components h_2 and E found non-significant value. The negative value for $H_2/4H_1$ (0.16) was far from 0.25.

Days to seed maturity: The analysis of variance showed significant value for all the items except 'b₁' for days to seed maturity (Table 2). Again, item 'b₂' and 'b₃' conveyed asymmetrical dominance and part of dominance deviation (which were not related to item 'b₁' and 'b₂'), respectively. The item 'b₁' was found non-significant for days to seed maturity. The regression line touches 'Wr' axis above the point of origin in 'Vr-Wr' graph that indicated presence of partial dominance for controlling days to seed maturity (Figure 4a). The parent P₂ situated near to origin whereas P₃ situated far away from origin. The $Yr'-(Wr+Vr)'$ graph showed relative distribution of five parental score that indicated predominance of recessive alleles with positive effect (Figure 4b). It was found that the parent P₂ had the lowest value in $(Wr+Vr)'$ axis and P₃ had higher value. It was observed that both P₄ and P₅ were closely located with lower Yr' value and the parents P₄ and P₅ had higher value for days to seed maturity.

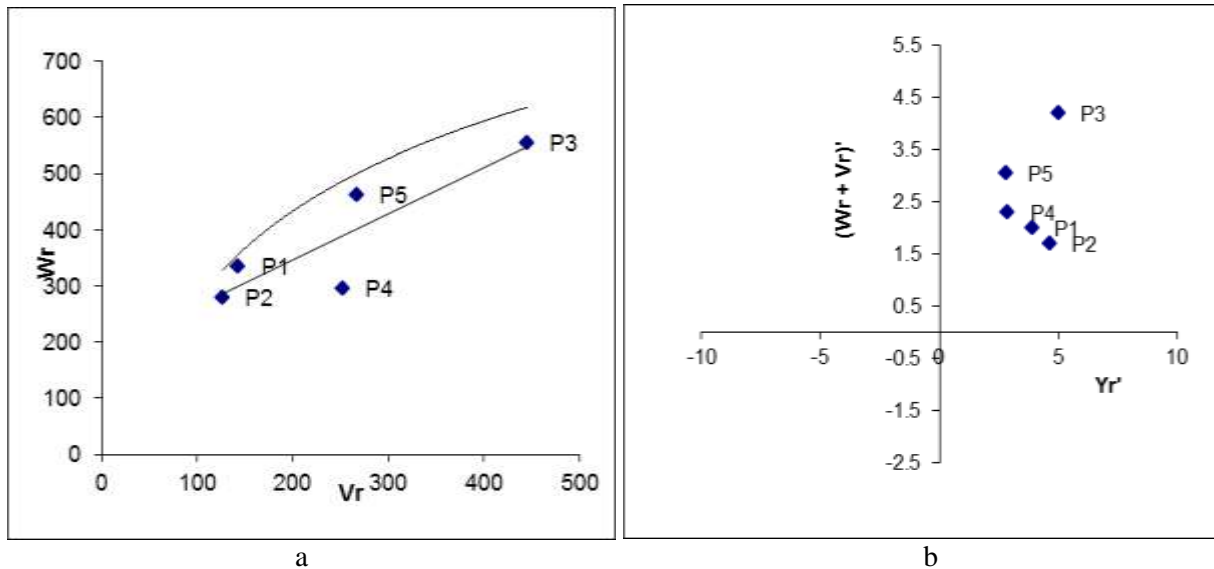


Figure 4. 'Vr-Wr' (a) and parental mean (b) graph for days to seed maturity in 5 x 5 half diallel populations in lablab bean.

Significant positive value was found for the components D, H₁, F and E for days to seed maturity (Table 3). In contrast negative significant measure was found for components H₂.

Number of inflorescences per plant: The significant value of item 'a' and 'b' ensured the presence of both additive and dominance components (Table 2). The item 'b₁', 'b₂' and 'b₃' was found significant for number of inflorescence per plant. It was found that the regression line intersected the 'Wr' axis below the point of origin in 'Vr-Wr' graph (Figure 5a). The scattered distribution was observed for the parental arrays all along the regression line.

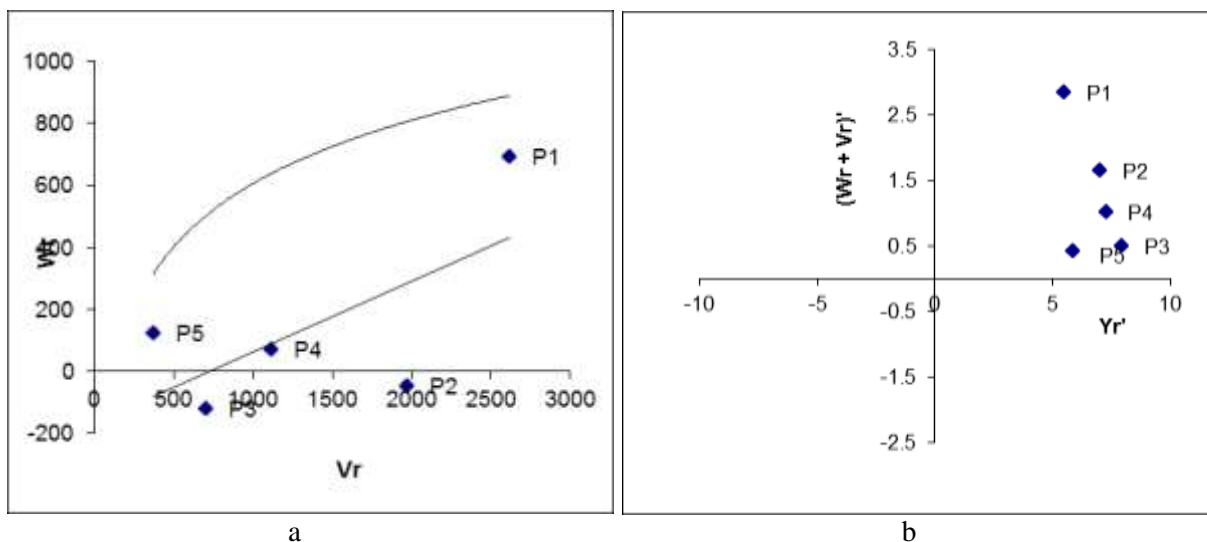


Figure 5. 'Vr-Wr' (a) and parental mean (b) graph for number of inflorescences per plant in 5 x 5 half diallel populations in lablab bean.

The parental graph clearly showed that all the five parents had predominance of recessive alleles with positive effects for number of inflorescences per plant (Figure 5b). The parent P₃ gave the highest 'Yr' value for number of inflorescences per plant. The positive significant value was observed for components D, H₁ and H₂ for number of inflorescence per plant (Table 3). The non-significant value was observed for the component E.

Number of nodes per inflorescence: The significant value of item 'a' and 'b' revealed the presence of both additive and dominance components, respectively (Table 2). The V_r - W_r graph for number of nodes per inflorescence showed that the regression line intersected the ' W_r ' axis slightly above the point of origin (Figure 6a). The array points P_4 and P_5 located near the point of origin and in contrast, P_1 located far from the origin. Array points were found distributed all along the regression line in the graph (Figure 6a).

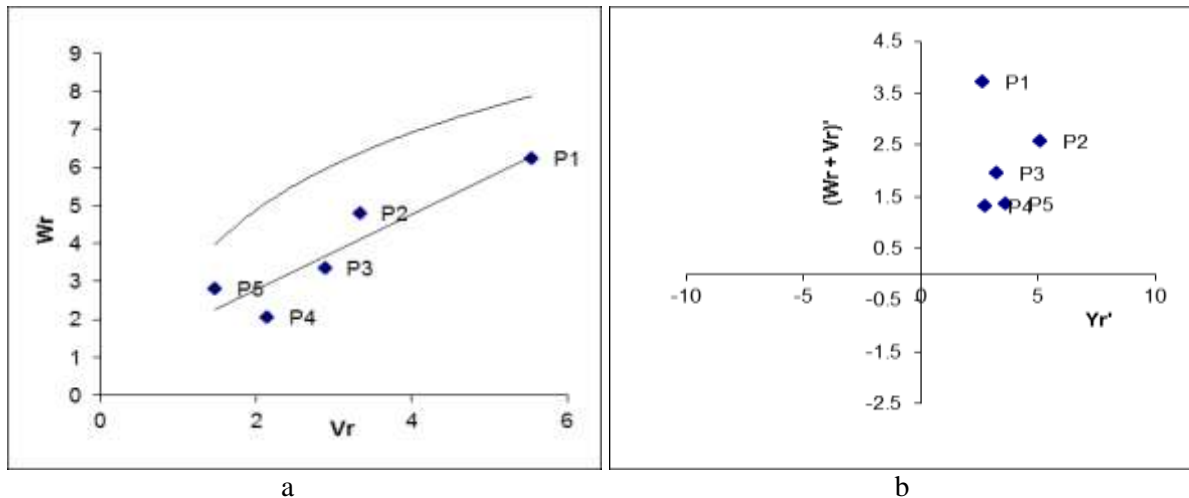


Figure 6. ' V_r - W_r ' (a) and parental mean (b) graph for number of nodes per inflorescence in 5 x 5 half diallel populations in lablab bean.

The Yr' - $(W_r + Vr')$ graph indicated predominance of recessive alleles with positive effect. The parent P_2 showed the highest Yr' value and the parent P_5 gave the minimum Yr' value for number of nodes per inflorescence. The positive significant measure was found for the components D, H_1 , F and E (Table 3). In contrast, negative significant measure was found for components H_2 (-25.33**). Again, positive significant value was observed for component h_2 .

Number of pods per inflorescence: The analysis of variance showed significant value for all the items except ' b_1 ' for number of pods per inflorescence (Table 2). Non-significant value was found for the item ' b_1 ' for number of pods per inflorescence. The regression line intersected the W_r axis below the point of origin in the V_r - W_r graph for the character of number of pods per inflorescence as (Figure 7a). Scattered distribution of array points was found all along the regression line. It was noticed that P_1 having lower ' Yr' ' value whether P_2 had higher ' Yr' ' measure. The highly significant value was observed for components D, H_1 and for number of pods per inflorescence (Table 3). The components H_2 and h_2 was found significant for this trait. The significant of component E also observed for this character.

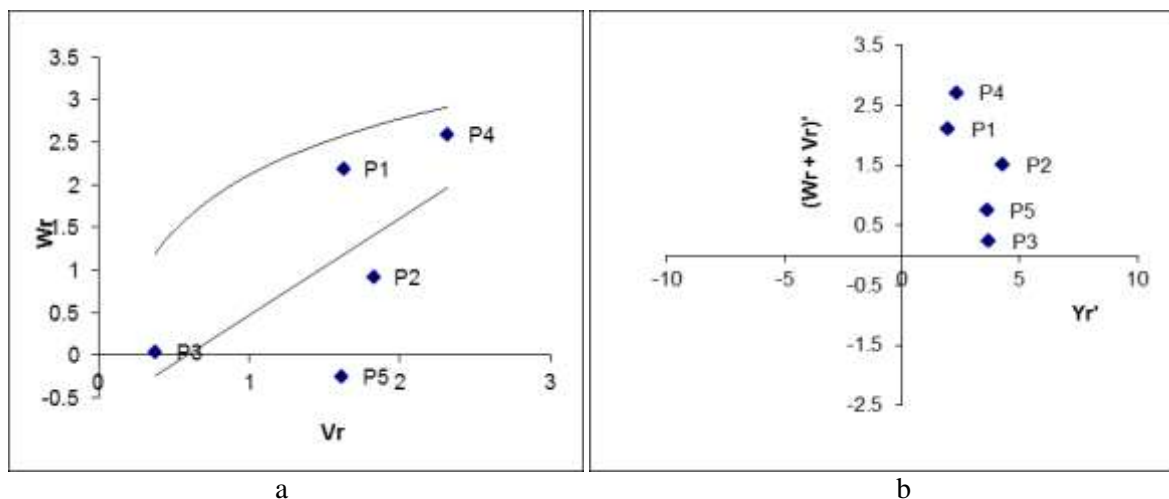


Figure 7. ' V_r - W_r ' (a) and parental mean (b) graph for number of pods per inflorescence in 5 x 5 half diallel populations in lablab bean.

Number of pods per plant: Highly significant value was found for mean sum square of number of pods per plant for all the items in Table 2. The item 'b₁', 'b₂' and 'b₃' was found significant. The regression line passed in 'Wr' axis through the point of origin in 'Vr-Wr' graph for number of pods per plant (Figure 8a). The distribution of array point showed that parent P₅ situated nearby the origin and on the other hand array point of P₁ situated far away from origin. Array point of five parents scattered all along the regression line in 'Vr-Wr' graph. The Yr'-(Wr+Vr)' graph showed relative distribution of five parental score (Figure 8b). It was observed that both P₂ and P₃ were closely located having higher Yr' value for number of pods per plant than rest of the parental score. Significant positive value was observed for components D, H₁, H₂ and F. The component E was found significant for this character.

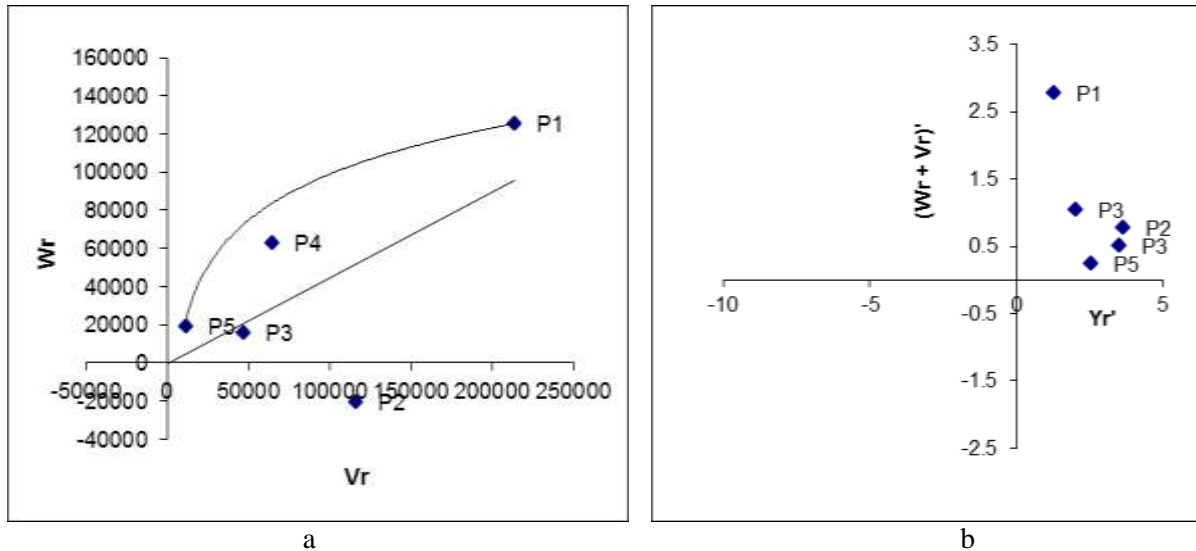


Figure 8. 'Vr-Wr' (a) and parental mean (b) graph for number of pods per plant in 5 x 5 half-diallel populations in lablab bean.

Edible pod length (cm): The significant value was found for item 'a', 'b', 'b₂' and 'b₃' for the character edible pod length (Table 2). The non-significant value was observed for item 'b₁'. The regression line intersected the 'Wr' axis far above the point of origin in 'Vr-Wr' graph (Figure 9a). Scattered distribution was observed for the array points all along the regression line. The parental graph clearly showed that all the five parents had predominance of recessive alleles with positive effects for edible pod length (Figure 9b). Edible pod length was positively associated with the direction of higher Yr' value. The parent P₂ possessed the highest Yr' value for edible pod length. It was found positive significant measure for components D, H₁, F and E for edible pod length in lablab bean (Table 3). In contrast, negative significant measure was found for components H₂. Again, positive and significant value was observed for component h₂.

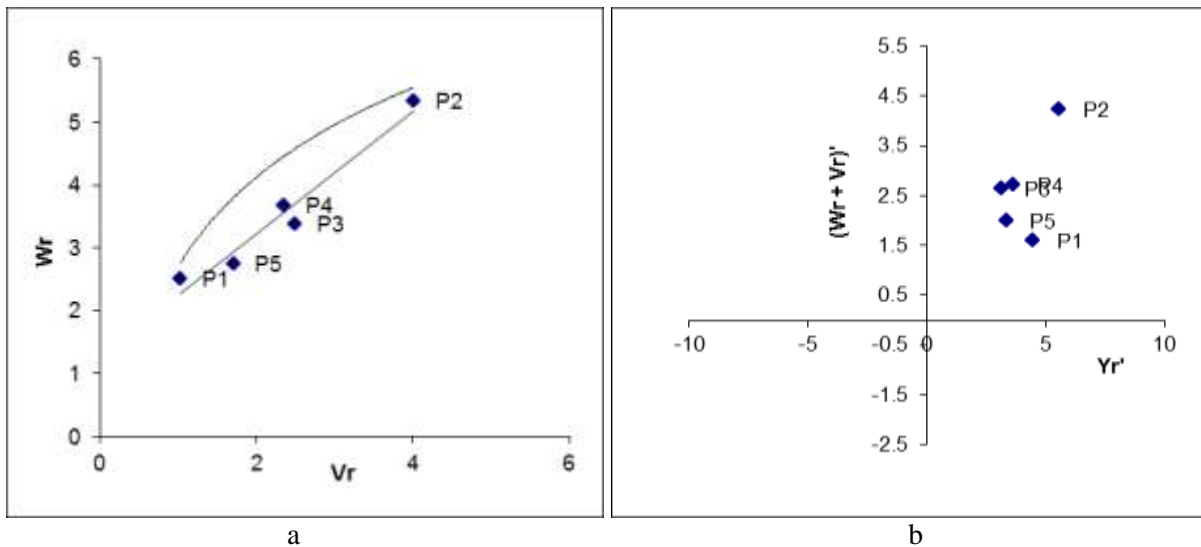


Figure 9. 'Vr-Wr' (a) and parental mean (b) graph for edible pod length in 5 x 5 half diallel populations in lablab bean.

Edible pod breadth (cm): The significant value of item 'a' and 'b' revealed the presence of both additive and dominance components, respectively for the expression of edible pod breadth (Table 2). The significant value was found for the item 'b₁', 'b₂' and 'b₃' for this character.

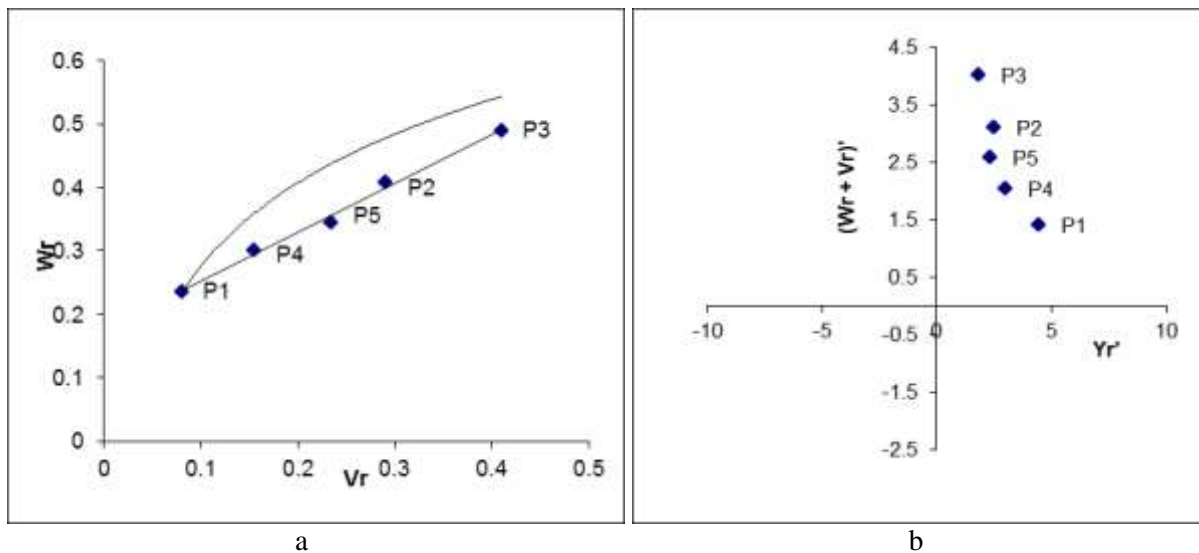


Figure 10. 'Vr-Wr' (a) and parental mean (b) graph for edible pod breadth in 5 x 5 half diallel populations in lablab bean.

VR-Wr graph for edible pod breadth showed that the regression line intersected the 'Wr' axis above the point of origin (Figure 10a). The array point of parent, P₃ located far away from the origin and P₁ located near the origin. The Yr'-(Wr+Vr)' graph showed relative distribution of five parental score (Figure 11b). It was easily notified the presence of higher Yr' measure for P₁ parental score for edible pod breadth. The positive significant measure was identified for components D, H₁, F and E (Table 3). The negative significant measure was found for components H₂. The value of KD/KR (157.74) was very high for edible pod breadth.

Edible pod weight (g): Edible pod weight showed the significant value for all the items found in Table 2. It was revealed the meaningful presence of additive, dominance, asymmetrical distribution of dominance, unidirectional distribution of dominance and part of dominance deviation for expressing this character in positive direction.

From the V_r - W_r graph, it was revealed the presence of partial dominance for expressing the character edible pod weight as the regression line touched the ' W_r ' axis above the point of origin (Figure 11a). Here, it could be easily identified that none of the parents located near the origin. Thus parents possessed negligible amount of dominant alleles. Majority of the array points situated at the middle part of the ' V_r - W_r ' graph that suggested the parents contain equal proportion of dominant and recessive alleles. The parent P_5 possessed maximum frequency of recessive alleles among the parent as it located far away from the origin.

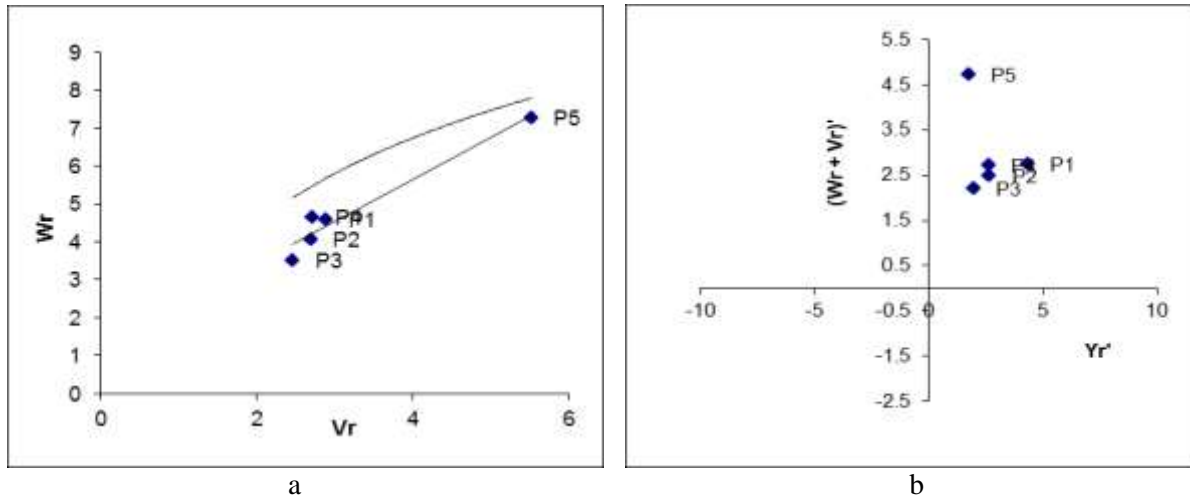


Figure 11. ' V_r - W_r ' (a) and parental mean (b) graph for edible pod weight in 5 x 5 half diallel populations in lablab bean.

Edible pod weight (g): Edible pod weight showed the significant value for all the items found in **Table 2**. It was revealed the meaningful presence of additive, dominance, asymmetrical distribution of dominance, unidirectional distribution of dominance and part of dominance deviation for expressing this character in positive direction.

From the V_r - W_r graph, it was revealed the presence of partial dominance for expressing the character edible pod weight as the regression line touched the ' W_r ' axis above the point of origin (Figure 11a). Here, it could be easily identified that none of the parents located near the origin. Thus parents possessed negligible amount of dominant alleles. Majority of the array points situated at the middle part of the ' V_r - W_r ' graph that suggested the parents contain equal proportion of dominant and recessive alleles. The parent P_5 possessed maximum frequency of recessive alleles among the parent as it located far away from the origin. The preponderance of recessive alleles with positive effect was found for all the five parental score for controlling this character in $Y_r'-(W_r + V_r)$ graph (Figure 11b). It was clearly presented that P_1 located having higher Y_r' score that indicated the possibility of obtaining maximum pod weight from P_1 .

It was found positive significant measure for components D , H_1 , F and E that indicated the importance of additive, dominance, interaction of additive and dominance and environment for expressing pod weight in lablab bean (**Table 3**). Again, negative significant measure was found for components H_2 that suggested the dominance with asymmetry in negative direction. The positive significant value was observed for component h_2 that indicated higher degree of dominance in positive effects.

Hundreds seed weight (g): It was found highly significant value for analysis of variance for expressing hundred seed weight for all the items (**Table 2**). The significant value of item 'a' and 'b' was found significant. Item 'b₁' was also found significant. Asymmetric distribution of dominance and part of dominance deviation were suggested from item 'b₂' and 'b₃', respectively. In V_r - W_r graph the regression line intersected the ' W_r ' axis below the point of origin for hundred seed weight (Figure 12a). The array point of the parent P_2 located far away from the origin and P_1 located in near the origin. Array point of five parents was scattered all along the regression line in ' V_r - W_r ' graph for hundred seed weight.

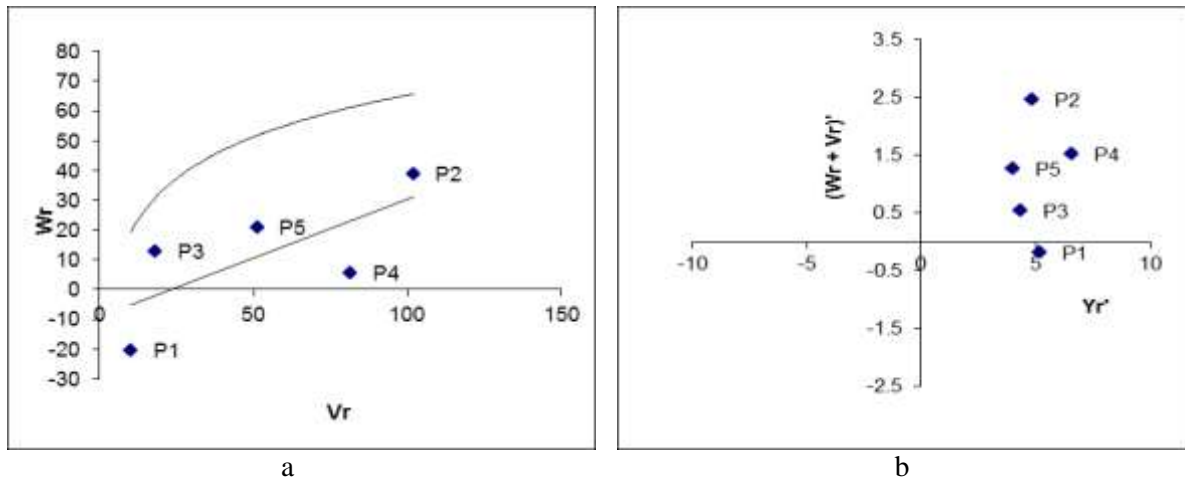


Figure 12. 'Vr-Wr' (a) and parental mean (b) graph for hundred seed weight in 5 x 5 half diallel populations in lablab bean.

The $Yr'-(Wr+Vr)'$ graph showed the distribution of P_1 parent had the negative $(Wr+Vr)'$ and positive Yr' score (Figure 12b). In contrast, relative distribution was observed for the rest of the parental score. The positive significant value was observed for all components except E in Table 3. The non-significant value was observed for the component E.

Pod yield per plant (kg): Analysis of variance showed higher significant value for pod yield per plant for all the items suggested by Hayman's and followed by Morley Jones (Table 2). The item 'a' and 'b' was reported to be significant for pod yield per plant. Significant value of item 'b₁', 'b₂' and 'b₃' was also found significant. The regression line passed through 'Wr' axis slightly above the point of origin in 'Vr-Wr' graph for expressing the eminent character pod yield per plant (Figure 13a). The distribution of array point of P_5 located nearby the origin and array point of P_1 parent situated far away from origin. The scattered distribution of array points of five parents was observed all along the regression line in 'Vr-Wr' graph.

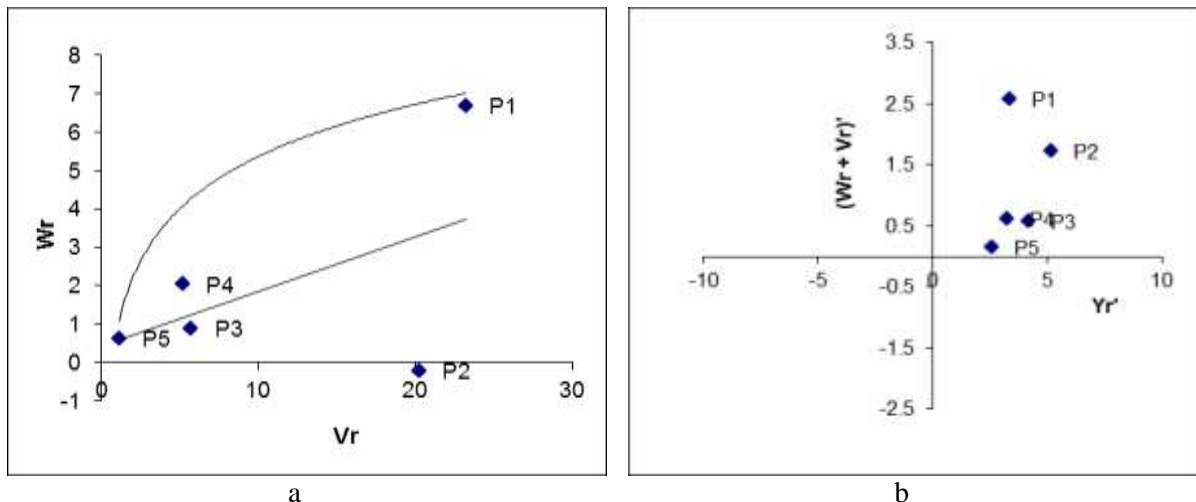


Figure 13. 'Vr-Wr' (a) and parental mean (b) graph for pod yield per plant in 5 x 5 half diallel populations in lablab bean.

The $Yr'-(Wr+Vr)'$ graph showed the distribution of parent had both the negative $(Wr+Vr)'$ and positive Yr' score (Figure 13b). The parent P_2 possessed the highest Yr' value for pod yield per plant. The significant value was found for components D, H_2 and h_2 (Table 3). The negative value for component F was observed for the character pod yield per plant in lablab bean. It was notified KD/KR (-0.59) value was lower than 1.0 with the heritability in narrow sense was 26%.

DISCUSSION

The result presented here provides information on gene action, combining ability and heterosis for plant and fruit characteristics of lablab bean genotypes. The significant test of item 'a' and 'b' reported that both additive and dominance gene action played a vital role for different genotype regulating days to first inflorescence appearance. Significant difference for item 'b₁' and 'b₂' indicated presence of unidirectional dominance (i.e. between parent and hybrid) and asymmetrical distribution of dominant gene for this character, respectively. The item 'b₃' was also highly significant that depicted the residual dominance deviations for this trait. The distribution of array point of P₁ nearby the origin was supposed to contain maximum frequency of dominant alleles; array point of P₃ parent situated far away from origin suggested presence of maximum frequency of recessive alleles among the five parents. Array point of five parents scattered all along the regression line in 'V_r-W_r' graph suggested genetic diversity among the parents for days to first inflorescence appearance. It was clearly observed that all the five parents had predominance of recessive alleles with positive effects for days to first inflorescence appearance. The parent P₃ contained maximum amount of recessive alleles whereas P₁ contained minimum number of recessive alleles. Parent P₂ and P₃ gave the higher Y_r' values which indicated delayed appearance of first inflorescence in plant. Thus early inflorescence appearance was negatively associated with the direction of higher Y_r' value. It was found that P₅ possessed the early appearance inflorescence among the parents. The highly significant value was observed for components D, H₁, H₂ and F suggested the importance of both additive and dominance effects and their interaction in the expression of days to first inflorescence appearance. H₂ and h₂ indicated dominance with asymmetry and higher degree of dominance with negative effects, respectively.

The presence of partial dominance was reported for controlling the character days to first flowering as the regression line intersected the 'W_r' axis above the point of origin. The array point of P₄ located near the point of origin which revealed the presence of maximum frequency of dominant alleles and in contrast the parent P₃ possessed maximum frequency of recessive alleles. V_r-W_r graph also revealed genetic diversity among the parents for this character. The Y_r'-(W_r+V_r)' graph indicated predominance of recessive alleles with positive effect. The higher Y_r' values indicated that the parents P₂ and P₃ require maximum days for first flowering related with preponderance of recessive alleles in direction to higher positive effect. Thus it indicated that early days to first flowering was co-operated in the direction of lower values where parent P₅ was depicted the earliness for this character. Positive significant measure for components D, H₁, F and E indicated the essential role of additive, dominance, their interaction and environment for expression of days to first flowering in lablab bean. On the other hand, negative significant measure for the components H₂ and h₂ suggested that the dominance with asymmetry and higher degree of dominance in negative direction. As non-additive gene action was predominant for this trait and due to nonfeasibility of hybrid variety in lablab bean, diallel selective mating system may be adopted followed by biparental mating and recurrent selection for improvement of this trait.

The significant value of item 'a', 'b', 'b₂' and 'b₃' for the character of days to first edible pod maturity revealed the meaningful presence of additive, dominance, asymmetrical distribution of dominance and also dominance deviation for expressing this character in positive direction. The non-significant value for the item 'b₁' indicated the absence of unidirectional dominance. The regression line in 'V_r-W_r' graph revealed partial dominance for controlling the character days to edible pod maturity. Considering the distribution of array points, P₃ and P₁ contained higher amount of recessive and dominant alleles among the parent, respectively. The scattered array points along the regression line proved the higher genetic diversity among parents for this trait. The predominance of recessive alleles with positive effect was found for all the five parental score for controlling days to edible pod maturity in Y_r'-(W_r+V_r)' graph. The lower 'Y_r' value for parent P₄ and P₅ revealed that they required less time whereas P₁, P₂ and P₃ parent needed higher time for edible pod maturity in lablab bean. The significant value of D, H₁ and F components revealed that the additive, dominance and their interaction effects played a key role for controlling days to edible pod maturity. The negative value for H₂/4H₁ was far from 0.25 which ensured unequal distribution of negative and positive alleles.

The item 'a' and 'b' referred the presence of both additive and dominance components for controlling this character. Again, item 'b₂' and 'b₃' conveyed asymmetrical dominance and part of dominance deviation (which were not related to item 'b₁' and 'b₂'), respectively. The non-significant value of item 'b₁' suggested the absence of unidirectional dominance for controlling days to seed maturity. The 'Vr-Wr' graph indicated presence of partial dominance for controlling days to seed maturity. The parent P₂ was supposed to contain maximum frequency of dominant alleles whereas P₃ contain maximum frequency of recessive alleles. The relative distribution of five parental score indicated the predominance of recessive alleles with positive effect. It was found from the (Wr+Vr)' axis that the parent P₂ contain minimum recessive alleles and P₃ contained higher frequency of recessive alleles among the parents. Lower Yr' value indicated that the parents P₄ and P₅ required less time for days to seed maturity. Significant positive measure for the components D, H₁, F and E indicated the essential role of additive, dominance, their interaction and also environment for expressing the character days to seed maturity in lablab bean.

The significant value of item 'a' and 'b' ensured the presence of both additive and dominance components and unidirectional dominance was proved by item 'b₁'. Asymmetric distribution of dominance and part of dominance deviation were suggested from item 'b₂' and 'b₃', respectively. It was revealed the presence of over dominance for controlling number of inflorescence per plant as the regression line intersected the 'Wr' axis below the point of origin in 'Vr-Wr' graph. This figure also showed genetic diversity among the parents in relation to this character. The parental graph clearly showed that all the five parents had predominance of recessive alleles with positive effects for number of inflorescences per plant. The highest 'Yr' value for the parent P₃ indicated higher number of positive alleles for expression of inflorescences per plant. The positive significant value for components D, H₁ and H₂ suggested the importance of both additive and dominance effects with asymmetrical distribution in positive direction for the expression of number of inflorescence per plant.

The significant value of item 'a' and 'b' revealed the presence of both additive and dominance components, respectively. Significant 'b₁' value suggests unidirectional dominance. Asymmetric distribution of dominance and part of dominance deviation were suggested from item 'b₂' and 'b₃' for controlling number of nodes per inflorescence, respectively. Partial dominance was reported for controlling this character from the 'Vr-Wr' graph. It was further visible that P₄ and P₅ contain maximum frequency of dominant alleles and P₁ possessed maximum frequency of recessive alleles among the parent. Distribution of array points revealed the presence of genetic diversity among the parents this character. The Yr'-(Wr+Vr)' graph indicated the predominance of recessive alleles with positive effect. The components D, H₁, F and E indicated that the essential role of additive, dominance, their interaction and also environment for expressing the character number of nodes per inflorescence in lablab bean. Negative significant measure of H₂ suggests the dominance with asymmetry in negative direction and positive significant value of h₂ indicates the higher degree of dominance with positive effects.

The items 'a' and 'b' referred the presence of both additive and dominance components for controlling this character. Non-significant value of item 'b₁' suggested the absence of unidirectional dominance for controlling number of pods per inflorescence and pods per plant. The Vr-Wr graph confirmed the presence of over dominance for controlling the character of number of pods per inflorescence and complete dominance for pods per plant. This figure also showed genetic diversity among the parents in relation to these characters. High proportion of recessive alleles with positive effect was found for all the five parents for controlling number of pods per inflorescence in Yr'-(Wr+Vr)' graph. It was notified that the parent P₁ and P₂ had the lower and higher number of pods per inflorescence, respectively. The highly significant value of the components D, H₁ and F for both the characters suggested the importance of both additive and dominance effects and their interaction in the expression of these characters. The components H₂ and h₂ indicated dominance with asymmetry and higher degree of dominance with negative effects, respectively. The significant of component E revealed the essential contribution of environment for both characters.

The significant value for the item 'a', 'b', 'b₂' and 'b₃' revealed the meaningful presence of additive, dominance, asymmetrical distribution of dominance and also dominance deviation for expressing the traits edible pod length and pod breadth in positive direction. The non-significant value of item 'b₁' indicated the absence of unidirectional dominance. It was revealed the presence of partial dominance for expressing the character edible pod length and pod breadth from the 'V_r-W_r' graph. This figure also showed genetic diversity among the parents in relation to this character. The parental graph clearly showed that all the five parents had predominance of recessive alleles with positive effects for edible pod length. The graph (W_r+V_r)' showed that P₂ contained maximum amount of recessive alleles whereas P₁ contained minimum number of recessive alleles among the five parents. The highest Y_r' value for parent P₂ suggests higher edible pod length. Positive and significant measure of components D, H₁, F and E indicated that the importance of additive, dominance, interaction of additive and dominance and environment for expressing edible pod length and pod breadth in lablab bean. In contrast, negative significant measure of components H₂ suggests the dominance with asymmetry in negative direction. Again, positive significant value of h₂ indicated that higher degree of dominance in positive effects.

Edible pod weight was revealed the meaningful presence of additive, dominance, asymmetrical distribution of dominance, unidirectional distribution of dominance and part of dominance deviation for expressing this character in positive direction. It was revealed the presence of partial dominance for expressing the character edible pod weight from the V_r-W_r graph. The standardized graph showed that parents possessed negligible amount of dominant alleles. Majority of the array points situated at the middle part of the 'V_r-W_r' graph that suggested the parents contain equal proportion of dominant and recessive alleles. The parent P₅ possessed maximum frequency of recessive alleles among the parent. The preponderance of recessive alleles with positive effect was found for all the five parental score for controlling this character in Y_r'-(W_r +V_r)' graph. The higher Y_r' score indicated that there was possibility of obtaining maximum pod weight from P₁.

It was found positive significant measure for components D, H₁, F and E that indicated the importance of additive, dominance, interaction of additive and dominance and environment for expressing pod weight in lablab bean (Table 3). Again, negative significant measure was found for components H₂ that suggested the dominance with asymmetry in negative direction. The positive significant value was observed for component h₂ that indicated higher degree of dominance in positive effects.

The significant test of item 'a' and 'b' reported that both additive and dominance components played a vital role for regulating this eminent character. Significant value of item 'b₁' and 'b₂' indicated that the presence of unidirectional dominance and asymmetrical distribution of dominant gene for this character, respectively. Significant value of 'b₃' was depicted the part of dominance deviations which were not related to item 'b₁' and 'b₂' for expressing pod yield per plant. The regression line indicated presence of partial dominance for expressing the eminent character pod yield per plant. The distribution of array point of P₅ revealed that this parent supposed to contain maximum frequency of dominant alleles; on the other hand array point of P₁ suggested the presence of maximum frequency of recessive alleles. Genetic diversity among the parents in relation this character suggested by the scattered distribution of array points all along the regression line in 'V_r-W_r' graph. The consistency of dominance or recessive alleles with positive or negative effects in opposition to parental mean score was determined in the Y_r'-(W_r+V_r)' graph. It was clearly observed that all the five parents had predominance of recessive alleles with positive effects for this character. P₂ possessed the highest Y_r' value which indicated the highest pod yield per plant. The significant value of the components D, H₂ and h₂ indicated the importance of additive gene effect, dominance effect with asymmetry and higher degree of dominance in positive effect. The negative value for component F suggested the eminent role of interaction of additive and dominance effect in negative direction for controlling pod yield per plant in lablab bean. Lowed KD/KR (-0.59) value than 1.0 indicated higher frequency of recessive alleles with the narrow sense heritability of pod yield per plant. As non-additive gene action was predominant for most of the traits and due to nonfeasibility of hybrid variety in lablab bean, diallel selective mating system may be adopted followed by biparental mating and recurrent selection for improvement of these traits.

ACKNOWLEDGMENTS

The authors would like to acknowledge their gratitude towards university authority for the support from Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur 1706, Bangladesh through research program of Department of Genetics and Plant Breeding.

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