

Inheritance study of yield associated traits in F₁ and F₂ generations of bread wheat through half diallel analysis

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Abstract- Current research work was conducted for inheritance study of different morphometric traits in 15 X 15 half diallel cross excluding reciprocals. Fifteen parental lines Morocco, Avocit-YRA, Auqab-2000, Kohistan-97, Pirsabak-08, Margalla-99, Sehar-2006, Chakwal-86, Galaxy-13, Local white, Pak-81, Lasani-2008, Faisalabad-08, BARS-2009 and Mairaj-08 were crossed in half diallel fashion during growing season 2016-17, F₁ evaluated in 2017-18 and F₂ in 2018-19. Analysis of variance indicated significant mean squares for all traits conferring high diversity among parents. Inheritance study revealed additive type of gene action for plant height (F₁), fertile tiller/plant (F₂), harvest index, stay-green trait, 1000 grain weight and peduncle length. Important role of dominance variance for controlling gene expression was found in days to flowering, plant height (F₂), flag leaf area, fertile tiller/plant (F₁) and number of kernels/spikes.

Keyword: Additive, diallel, dominance, genetic components, heritability, Inheritance, wheat

I. INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the most important staple food crops, increasing yield of the crop to meet human requirements of food regarding rapidly growing population is the need of the time. According to a survey conducted by United Nation in 2019 the world population will increase about 9 billion by 2050 and an increase of 60% will be required in wheat production (Khadka *et al.*, 2020). Bread wheat is the third largest staple food crop after maize and rice, rich source of essential nutrients and energy (Igrejas, 2020), providing 20% protein and 18% calories to human (Geren, 2021). Contribution of *Triticum aestivum* to total world wheat production is about 95% (Igrejas, 2020). Wheat is being grown in Europe for centuries, now a days Asian country like China, India and Russia are ranking 1st, 2nd and 3rd respectively in the world for wheat production because it requires less amount of water as compared to other cereal crops (Jarkova, 2019; Geren, 2021). Wheat has major contribution to GDP of Pakistan, provide 72% calories and protein as regular diet and use of wheat per capita is 120 Kg/year. The large-scale cultivation ranks Pakistan in the top 10 wheat producers of world (Iqbal *et al.*, 2022). Two time increase in the current wheat production is

required for Pakistan to fulfil human need (Salim and Raza, 2020).

Diallel designs are cross breeding schemes applicable to both plants and animals using a set of parents with desirable traits. It is a tool associated with genetic understanding of quantitative traits and to identify efficient cross breeding schemes and most productive genetic combinations (Okoro and Mbajiorgu, 2017). Different matting designs are used in diallel where parents, F₁s and reciprocals are analyzed, Griffing (1956) proposed 4 different models widely used in diallel cross now a days, these are aimed to find GCA, SCA, variance components and information of reciprocal and maternal effects. Hayman (1954) proposed analysis to find variance components and genetic ratios for better understanding of genetic inheritance (Makumbi *et al.*, 2018). In current study Hayman analysis was performed to evaluate inheritance.

II. MATERIAL AND METHODS

1. PLANT MATERIAL

Plant material was collected from gene bank at IABGR, NARC Islamabad. A total of 15 homozygous parental lines were used in 15 X 15 half diallel cross shown below.

S. No.	Inbred line	S. No.	Inbred line
i.	Morocco	ii.	Avocit-YRA
iii.	Auqab-2000	iv.	Kohistan-97
v.	Pirsabak-08	vi.	Margalla-99
vii.	Sehar-2006	viii.	Chakwal-86
ix.	Galaxy-13	x.	Local white
xi.	Pak-81	xii.	Lasani-2008
xiii.	Faisalabad-08	xiv.	BARS-2009
xv.	Mairaj-08		

2. BREEDING MODEL

For diallel cross experimental method-II (parents and 1 set of offspring) was used which results in P (P + 1)/2 combination (where P is the number of parents). Crosses were made in a fashion that every parent was crossed with other parent only one time, taking one parent as male and other as female.

3. STATISTICAL ANALYSIS

3.1. Analysis of variance

Analysis of variance in RCBD at 1% and 5% probability level by F test was done using GENES software package (Cruz, 2013; Cruz, 2016).

3.2. Test of adequacy

Additive dominance model was tested to confirm validity of assumptions for diallel through t^2 test and regression analysis test using AGD-R version 5.0 a software package of CIMMYT (Francisco *et al.*, 2015). For validity of additive dominance model t^2 is expected to be insignificant while coefficient of regression is expected to be significantly different from zero ($b=0$) and not from unity ($b=1$). If both the tests are in favor of assumptions the model is fully adequate but if one tests fail, the model is partially adequate and failure of both tests to fulfil assumption completely invalidate the additive dominant model (Mather and Jinks, 1982).

3.3. Hayman analysis

Hayman analysis was also done using AGD-R software introducing with diallel data in AGD-R format diallel method-II (parents and 1 set of offspring). Mathematical detail is as under.

D (additive variance) = $V_{0L0} - E$, where V_{0L0} is Variance between parents and E is environmental component.

H_1 (Dominance variance) = $V_{0L0} + 4 V_{1L1} - 4 W_{0L01} - (3n-2) E/n$. Where V_{1L1} is mean of the variances in the row (V_r), W_{0L01} is Mean of Cov. between parents and descending and n is number of parents.

H_2 (Proportion of +ve/-ve genes) = $4 V_{1L1} - 4 V_{0L1} - 2 E$ Where V_{0L0} is Variance of Mean of Array.

h^2 (Dominance Effect) = $4 (ML_1 - ML_0)^2 - 4 (n-1) E/n^2$. Where $(ML_1 - ML_0)^2$ square of the means difference.

F (Mean Cov. of Add. and Dom. effects) = $2 V_{0L0} - 4 W_{0L01} - 2 (n-2) E/n$.

From above estimates following genetic ratios were determined. For F_2 population the formulas were modified according to Verhalen and Murray (1969) and Verhalen *et al.*, (1971) also followed by Afridi (2016) and Khan *et al.*, (2009). Dominance means degree for $F_1 = (H_1/D)^{1/2}$ and $F_2 = (1/4H_1/D)^{1/2}$

Allele distribution-Symmetry = $(H_2/4H_1)$. If: $H_2/4H_1 = 0.25$ +ve and -ve dominant genes are symmetrical or $H_2/4H_1 \neq 0.25$ +ve and -ve dominant genes are asymmetrical

Relation dominant/recessive (p/q) for $F_1 = ((4DH_1)^{1/2} + F)/(4DH_1)^{1/2} - F$ and for $F_2 = (1/4(4DH_1)^{1/2} + F/2)/(1/4(4DH_1)^{1/2} - F/2)$

If: $p/q = 1$ symmetrical distribution of p and q ($p=q=0.5$)
 $p/q > 1$ then dominant allele are more than recessive
 $p/q < 1$ then recessive allele are more than dominant

Number of genes with dominance = h^2/H_2

Heritability (BS) = $(D/2 + H_1/2 - H_2/4 - F/2)/(D/2 + H_1/2 - H_2/4 - F/2 + E)$

Heritability (ns) for $F_1 = (D/2 + H_1/2 - H_2/2 - F/2)/(D/2 + H_1/2 - H_2/4 - F/2 + E)$ and for $F_2 = (D/4)/(D/4 + H_1/16 - F/8 + E)$

Narrow sense heritability was calculated according to Verhalen and Murray (1969) and Singh and Chaudhary (1985) for F_2 generation. $W_r - V_r$ graph was constructed using GENES software package (Cruz, 2013; Cruz, 2016).

III. RESULTS

1. Analysis of variance (ANOVA)

Analysis of variance revealed significant differences for all the traits under study in both F_1 and F_2 generations by F-test using 1% and 5% significance levels (Table. 1). ANOVA showed high significant value mean high diversity is present among

genotypes and may successfully be used in future breeding programs.

2. Test of adequacy

For validity of additive dominance model t^2 is expected to be insignificant while coefficient of regression is expected to be significantly different from zero ($b=0$) and not from unity ($b=1$). If both the tests are in favor of assumptions the model is fully adequate but if one tests fails, the model is partially adequate and failure of both tests to fulfil assumption completely invalidate the additive dominant model (Mather and Jinks, 1982).

All the traits are adequate for additive dominance model except spike length both in F_1 and F_2 generation. Thus, Spike length wasn't analyzed for Hayman analysis. Days to flowering and Harvest index for F_1 and Plant height, Fertile tiller/plant, 1000-grain weight and Peduncle length for F_2 are fully adequate. Remaining traits in F_1 and F_2 are partially adequate for additive dominance model (Table 2 and 3).

3. Hayman's analysis of inheritance

3.1. Days to flowering

In F_1 significance of 'D' and 'H₁' shows both additive and dominance type of gene action are important in controlling days to flowering. Value of 'H₁' (34.46) is not equal to value of 'H₂' (26.21) presenting asymmetrical distribution of alleles among parents, value of allele distribution-symmetry ($H_2/4H_1 = 0.1902$) is not equal to 0.25 indicating asymmetry among +ve and -ve genes (Table 4). Overall difference between progeny and parents mean $(ML_1 - ML_0)^2 = 3.299$ which is positive value estimating high days to flowering is dominant over low days to flowering. Degree of dominance is established by the value of Y-intercept ($a = -5.815$) where 'a' is less than 0 and negative, on the other hand in $W_r - V_r$ graph regression line is originating below the origin mean both these determine the role of over dominance. Parental order of dominance was determined on basis of inverse relation of $(W_r + V_r)$ to dominance and distribution of array points in $W_r - V_r$ graph. Highest $(W_r + V_r)$ value was found in Galaxy-13 (P9) = 44.124 presenting low frequency of dominant alleles followed by Lasani-2008 (P12) = 32.981, Faisalabad-08 (P13) = 23.256 and BARS-2009 (P14) = 22.470, while lowest $(W_r + V_r)$ value was found in Kohistan-97 (P4) = 4.444 exhibiting high frequency of dominant or low frequency of recessive alleles. Concerning distribution of array points in $W_r - V_r$ graph Avocit-YRA (P2), Kohistan-97 (P4) and Margalla-99 (P6) were falling nearby origin having maximum frequency of dominant alleles while Galaxy-13 (P9) was allocated far away of origin mean containing highest frequency of recessive alleles. Pak-81 (P11), Auqab-2000 (P3), Sehar-2006 (P7) and Local white (P10) are found at intermediate position in graph having nearly equal frequency of 'p' and 'q' alleles. Array points are scattered along the regression line confirming the genetic diversity among parents (Fig. 1.a).

In F_2 population significance of both 'D' and 'H₁' shows the role of both additive and dominant gene actions. Difference of progeny and parents mean $(ML_1 - ML_0)^2 = 3.2989$, this positive value represents high days to flowering is dominant over less days to flowering. Environmental component 'E' is significant, but its value is less than significant values of 'D' and 'H₁'.

Dominant to recessive alleles ratio (6.4772) is greater than 1 indicating that frequency of 'p' alleles is greater than 'q'. Allele distribution symmetry ($H_2/4H_1$) = 0.1729 which is not equal to 0.25 representing asymmetrical distribution of positive and negative alleles (Table 4). Value of Y-intercept ('a' = -0.802) is less than zero and regression line is passing below the origin mean indicating over dominance. Parental order of dominance with respect to (W_r+V_r) value Lasani-2008 (P12) = 9.14, Pirsabak-08 (P5) = 9.70 and Auqab-2000 (P3) (10.47) have lowest value of (W_r+V_r) means contain highest frequency of dominant alleles and Faisalabad-08 (P13) = 30.680, Mairaj-08 (P15) = 29.656 and Local white (P10) = 26.056 have highest (W_r+V_r) value suggesting highest frequency of recessive alleles. Same results are supported by W_r-V_r graph where Lasani-2008 (P12), Pirsabak-08 (P5) and Auqab-2000 (P3) lies near the origin and Faisalabad-08 (P13), Mairaj-08 (P15) and Local white (P10) lies away of origin mean. Array points are scattered along the regression line so genetic diversity among parents is existing (Fig. 1.b).

In both F_1 and F_2 progenies broad sense heritability values 0.4515 and 0.6591 were higher than narrow sense heritability values 0.1359 and 0.2847 respectively suggesting overall dominance (Table 4).

3.2. Plant Height

Significant value of 'D' (45.09) and 'H₁' (35.11), but value of 'D' is greater than 'H₁' indicating important role of additive dominance. value of 'E' (20.6) is significant but less than 'D' and 'H₁' minimizes the role of environmental component in gene expression. Ratio of dominant to recessive alleles (0.2869) is less than unity determining that recessive allele are more frequent than dominant. Asymmetrical distribution of 'p' and 'q' alleles is further established by unequal value of 'H₁' and 'H₂' and $H_2/4H_1 \neq 0.25$ the actual value is 0.3515 which indicate asymmetry of +ve and -ve genes. 'F' (-44.09) is non-significant and negative denoting the presence of recessive allele frequently than dominant (Table 4). Degree of dominance is determined by value of Y-intercept (a = 10.509) which is a positive value and regression line is passing above the origin mean in W_r-V_r graph both these suggests partial dominance. Parental order of dominance was calculated by inverse relation (W_r+V_r) to Avocit-YRA, Kohistan-97 and Margalla-99 have highest (W_r+V_r) values 113.66, 111.43 and 97.72 respectively exhibiting high frequency of recessive alleles and Chakwal-86 and Faisalabad-08 with lowest (W_r+V_r) value 51.80 and 50.36 respectively exhibiting more dominant alleles. Same results are presented by W_r-V_r graph where Avocit-YRA (P2), Kohistan-97 (P4) and Margalla-99 (P6) lies away of origin mean and Chakwal-86 (P8) and Faisalabad-08 (P13) lies near the origin mean (Fig. 2.a).

For value of F_2 'D' (35.93) and 'H₁' (78.18), but value of 'H₁' is greater than 'D' indicating important role of dominance. value of 'E' (19.84) is significant but less than 'D' and 'H₁' reduces the role of environmental component in gene expression. Ratio of dominant to recessive alleles (3.9852) is greater than unity determining that dominant allele are more frequent than recessive. Asymmetrical distribution of 'p' and 'q' alleles is further established by unequal value of 'H₁' and 'H₂' and $H_2/4H_1$ (0.2131) which is not equal to 0.25

representing asymmetry of +ve and -ve genes. 'F' (31.74) is non-significant but possess positive value denoting the higher frequency of dominant allele than recessive (Table 4). Y-intercept (a = -12.504) which is a negative value and in W_r-V_r graph regression line is passing below the origin mean suggesting over dominance. Parental order of dominance shows that Local Kohistan-97 (P4) = 96.39 and Local white (P10) = 95.59 have highest W_r+V_r value and lies away of origin mean exhibiting low frequency of dominant or high frequency of recessive alleles, while Sehar-2006 (P7) = 21.65, Avocit-YRA (P2) = 15.67 and BARS-2009 (P14) = 13.55 have low W_r+V_r value and lies near origin mean so have more dominant or less recessive alleles. Array points are scattered along the regression line which suggests genetic diversity among parents (Fig. 2.b). Both in F_1 and F_2 progenies high broad sense heritability values (0.7074, 0.5528) is greater than narrow sense heritability (0.5321, 0.3020) illustrated dominant proportion is greater to effect overall heritability (Table 4).

3.3. Flag Leaf Area

In F_1 additive component of genetic variance 'D' (41) and dominance variance 'H₁' (77.88) were significant, environmental variance 'E' (9.86) is also significant, but its value is less than 'D' and 'H₁' establishing the role of additive and dominant gene action. Dominance means degree $((H_1/D)^{1/2}) = 1.3781$ the value greater than unity determines the more contribution of dominance variance. Ratio p/q (1.5670) is greater than 1 means dominant allele are more than recessive. Allele distribution symmetry is 0.2296 which slightly differ from 0.25 indicating asymmetrical distribution of +ve and -ve genes. Broad sense heritability (0.7467) is greater than narrow sense heritability (0.2876) endorsing the effect of dominance variance as compared to environmental (Table 5). In W_r-V_r graph regression line passes above the origin mean and value of Y-intercept ('a' = 3.153) is positive indicating role of partial dominance. Parental order of dominance was established with respect to W_r+V_r value, lowest W_r+V_r value was shown by Pirsabak-08 (P5) = 0.98 and BARS-2009 (P14) = 2.70 having high frequency of partial dominant genes and highest W_r+V_r value was shown by Chakwal-86 (P8) = 83.02 and Moroco (P1) = 77.284 having low frequency of partial dominant genes. Same results were represented by W_r-V_r graph where Pirsabak-08 (P5) and BARS-2009 (P14) lies near the origin mean and Chakwal-86 (P8) and Moroco (P1) lie away of origin mean exhibiting maximum and minimum frequencies of partial dominant genes respectively. Genetic diversity among parents was confirmed by distribution of array points which were scattered along the regression line (Fig. 3.a).

In F_2 population value of 'D' is non-significant, H₁ and 'h²' are significant indicating the role of dominance type of gene action. p/q value (2.4383) is greater than 1 suggesting the frequency of dominant alleles is high than recessive alleles. Allele distribution-Symmetry (0.2343) is nearly equal to 0.25 which suggests very little difference between +ve and -ve genes. Environmental variance 'E' is significant, but its value is less than H₁, so dominance is playing its role. Broad sense heritability (0.5218) is greater than narrow sense heritability (0.2672) recommending the effect of dominance variance as compared to environmental (Table 5). Magnitude of Y-

intercept ('a' = 3.677) is a positive value and regression line is originating above the origin mean both these suggest the role of partial dominance. Parental order of dominance is shown as Chakwal-86 (P8) has highest Wr+Vr value 65.325 and Auqab-2000 (P3) and Morocco (P1) have lowest value 2.206 and 3.603 respectively, same results are shown by Wr-Vr graph where Chakwal-86 (P8) lies away of origin mean having minimum frequency of partial dominant genes Auqab-2000 (P3) and Morocco (P1) lies near the origin mean having maximum frequency of partial dominant genes (Fig. 3.b).

3.4. Fertile tiller/plant

In F1 additive component of genetic variance 'D' (12.09) and dominance variance 'H₁' (32.17) were significant, environmental variance 'E' (6.67) is also significant, but its value is less than 'D' and 'H₁' establishing the role of additive and dominant gene action. Dominance means degree ((H₁/D)^{1/2} = 1.6310 the value greater than unity determines the more contribution of dominance variance. Ratio p/q (1.3600) is greater than 1 means dominant allele are more than recessive which is supported by 'F' (6.02), whether it is non-significant but have positive value greater than '0'. Allele distribution symmetry is 0.2258 which slightly differ from 0.25 indicating asymmetrical distribution of +ve and -ve genes. Broad sense heritability (0.64) is greater than narrow sense heritability (0.248) endorsing the effect of dominance variance as compared to environmental (Table 5). In Wr-Vr graph regression line originates below the origin mean and value of Y-intercept ('a' = -2.348) is positive indicating role of over dominance. Parental order of dominance was established with respect to Wr+Vr value, lowest Wr+Vr value was shown by Morocco (P1) = 9.43, Chakwal-86 (P8) = 10.73 and Local white (P10) = 11.28 having high frequency of dominant genes, highest Wr+Vr value was shown by Pirsabak-08 (P5) = 32.46, Faisalabad-08 (P13) = 21.70, Avocit-YRA (P2) = 21.12 and BARS-2009 (P14) = 21.08 having low frequency of dominant genes. Same results were represented by Wr-Vr graph where Morocco (P1), Chakwal-86 (P8) and Local white (P10) lies near the origin mean and Pirsabak-08 (P5), Faisalabad-08 (P13), Avocit-YRA (P2) and BARS-2009 (P14) lie away of origin mean exhibiting maximum and minimum frequencies of dominant genes respectively. Genetic diversity among parents was confirmed by distribution of array points which were scattered along the regression line (Fig. 4.a).

In F2 population value of 'D' (4.45) is significant and 'H₁' (2.9) is non-significant, it recognizes additive gene action for productive tillers / plant. Dominance means degree = 0.4038 with value less than unity indicating the role of additive gene action. Relation dominant to recessive (p/q = -0.0955) is less than 1 suggesting the frequency of recessive alleles is high, it is supported by negative value of 'F' (-4.35) with value less than unity indicating recessive allele are frequent than dominant. Allele distribution-Symmetry (H₂/4H₁ = 0.4436 is not equal to 0.25 means +ve and -ve genes are asymmetrical. As value of 'E' (8.21) is significant and greater than 'D' and 'H₁' but broad sense heritability (0.3574) is greater than narrow sense heritability (0.1107) recommending the effect of dominance variance as compared to environmental variance in gene expression (Table 5). Magnitude of Y-intercept ('a' = -3.327) is

a negative value and regression line is originating below the origin mean both these suggest the role of genes conferring over dominance. Parental order of dominance is shown as Pirsabak-08 (P5) = 20.97, Faisalabad-08 (P13) = 15.81 and Pak-81 (P11) = 14.14 has highest Wr+Vr value and Mairaj-08 (P15) = 4.52, Local white (P10) = 6.06, Morocco (P1) = 6.12 and Chakwal-86 (P8) = 6.95 have lowest value, same results are shown by Wr-Vr graph where Pirsabak-08 (P5), Faisalabad-08 (P13) and Pak-81 (P11) lies away of origin mean having minimum frequency of dominant genes and Mairaj-08 (P15), Local white (P10), Morocco (P1) and Chakwal-86 (P8) lies near the origin mean having maximum frequency of dominant genes (Fig. 4.b).

3.5. Days to Maturity

In F₁ value of 'E' (14.15), 'D' (16.21) and 'H₁' (68.71) are significant. Higher value of 'H₁' than 'D' and 'E' minimize the effect of additive and environmental variance and confirms the role of dominance variance. It is supported by dominance means degree (2.0585) with value greater than unity. Dominant to recessive allele ratio (p/q) is 2.3785 which is greater than 1 showing that presence of dominant allele is frequent than recessive. Unequal value of 'H₁' and 'H₂' represent asymmetry of alleles, positive value of 'F' (27.24) also shows there are more dominant alleles than recessive. H₂/4H₁ ≠ 0.25 and is 0.1844 indicating asymmetry of positive and negative dominant alleles. h²_{bs} (0.5334) is greater than h²_{ns} (0.1157) shows effect of dominant proportion is greater in overall heritability (Table 6). Value of Y-intercept (a = -4.108) is negative and regression line is passing below the origin mean indicating over dominance. Mairaj-08 (P15) has highest (Wr+Vr) value (43.378) and Pak-81 (P11) and Lasani-2008 (P12) have lowest value (11.746 and 13.516) as (Wr+Vr) $\square \frac{1}{\text{Dominance}}$, the inverse proportion of (Wr+Vr) and dominance shows that Pak-81 (P11) and Lasani-2008 (P12) have highest dominant alleles and Mairaj-08 (P15) have lowest frequency of dominant alleles. Same result is from (Wr-Vr) graph that Pak-81 (P11) and Lasani-2008 (P12) fall nearby origin showing maximum frequency of dominant alleles while Mairaj-08 (P15) far away from origin showing maximum frequency of recessive alleles. Array points are scattered along the regression line that means genetic diversity is present among the parents (Fig. 5.a).

In F₂ non-significant value of 'D' (5.51) and significant 'H₁' (112.66) suggests that dominance is operative, it is supported by dominance means degree (2.2602) with value greater than unity. 'E' (21.99) is significant, but its value is less than 'H₁' abating the role of environmental variance. Relation dominant / recessive (p/q = 0.7203) is less than 1 demonstrating recessive allele frequency is frequent. Allele distribution-Symmetry is 0.2413 which is nearly equal to 0.25 gives approximate indication of symmetrical positive and negative genes distribution among parents. Heritability estimates in F₂ h²_{bs} (0.6067) is greater than h²_{ns} (0.0446) means effect of dominant proportion is greater to overall heritability (Table 6). The value of Y-intercept is positive value (0.087) approaching to zero indicating relatively complete dominance same results are derived from Wr, Vr graph where regression line is passing through origin mean confirming the complete dominance. Mairaj-08 (P15) = 66.503, Auqab-2000 (P3) = 66.417 and Pirsabak-08 (P5) = 62.058 have highest (Wr+Vr) value and

Pak-81 (P11) = 19.123, Local white (P10) = 28.757 and Lasani-2008 (P12) = 35.615 have lowest indicating lowest and highest frequency of dominant alleles in parents respectively based on inverse proportion of (W_r+V_r) to dominance. Same results are derived from variance, covariance graph Mairaj-08 (P15), Auqab-2000 (P3) and Pirsabak-08 (P5) lies away and Pak-81 (P11), Local white (P10) and Lasani-2008 (P12) near to origin mean presenting lowest and highest frequency of dominant alleles respectively. Array points are scattered along the regression line that means genetic diversity is present among the parents (Fig. 5.b).

3.6. Harvest index

In F_1 additive component of genetic variance 'D' (21.84) is significant and dominance variance ' H_1 ' (1.35) is non-significant, environmental variance 'E' (12.68) is also significant, but its value is less than 'D' establishing the role of additive gene action. Dominance means degree $((H_1/D)^{1/2}) = 0.2486$ the value less than unity. Ratio p/q (-0.2986) is less than 1 means recessive allele are more than dominant which is supported by value of 'F' (-20.11), with negative value. Allele distribution symmetry is 2.0577 which differ from 0.25 indicating asymmetrical distribution of +ve and -ve genes. Broad sense heritability (0.5982) is greater than narrow sense heritability (0.5102) endorsing the effect of dominance variance as compared to environmental (Table 6). In W_r-V_r graph array points cluster near the tangent of parabola indicating additive gene action. Parental order of dominance was established with respect to W_r+V_r value, lowest W_r+V_r value was shown by Kohistan-97 (P4) = 20.259, Faisalabad-08 (P13) = 25.070, Pirsabak-08 (P5) = 27.034 and Pak-81 (P11) = 28.163 having high frequency of dominant genes, highest W_r+V_r value was shown by Sehar-2006 (P7) = 50.81, Moroco (P1) = 43.18, Chakwal-86 (P8) = 41.80, Local white (P10) = 40.58 and BARS-2009 (P14) = 40.51 having low frequency of dominant genes. Same results were represented by W_r-V_r graph where Kohistan-97 (P4), Faisalabad-08 (P13), Pirsabak-08 (P5) and Pak-81 (P11) lies near the origin mean and Sehar-2006 (P7), Moroco (P1), Chakwal-86 (P8), Local white (P10) and BARS-2009 (P14) lies away of origin mean (Fig. 6.a).

Similarly, in F_2 population In F_1 additive component of genetic variance 'D' (36.25) is significant and dominance variance ' H_1 ' (13.93) is non-significant establishing the role of additive gene action. Environmental variance (E = 10.04) is significant, but its value is less than 'D' minimizing the role of environmental variance. Dominance means degree $((H_1/D)^{1/2}) = 0.31$ the value less than unity. Ratio p/q (-0.0655) is less than 1 means recessive allele are more than dominant which is supported by 'F' (-25.62), having negative value. Allele distribution symmetry is 0.3631 which differ from 0.25 indicating asymmetrical distribution of +ve and -ve genes. Broad sense heritability (0.7659) is greater than narrow sense heritability (0.3911) recommending the effect of dominance variance as compared to environmental (Table 6). Array points are clustering near the tangent of parabola indicating additive gene action. Margalla-99 /P6 (30.421) have lowest W_r+V_r value and lie near the origin mean, while BARS-2009 /P14 (90.482) have highest W_r+V_r values and lie away of origin mean (Fig. 6.b).

3.7. Number of kernels /spike

In F_1 'D' (67.83) and ' H_1 ' (332.15) significant and value of ' H_1 ' is much greater than 'D' suggests that dominant gene action operative. The value of 'E' (19.85) is significant but less than ' H_1 ' curtailing the role of environmental variance in gene expression. Dominance means degree (2.2129) is greater than unity. Ratio of dominant to recessive alleles (1.6222) is greater than unity determining that dominant allele are more frequent than recessive. Asymmetrical distribution of 'p' and 'q' alleles is also shown by unequal value of ' H_1 ' (332.15) and ' H_2 ' (251.99) and $H_2/4H_1 \neq 0.25$, the actual value is 0.1897 which indicate that +ve and -ve genes distribution is asymmetrical. 'F' (71.24) is non-significant but its value is greater than zero denotes recessive allele occurrence is frequent than dominant (Table 7). Y-intercept (a = -0.493) has negative value and regression line is passing below the origin mean in W_r-V_r graph both these suggests over dominance. Highest W_r+V_r value was observed for Margalla-99 (181.42), Local white (153.65) and Kohistan-97 (153.25) having low frequency of dominant allele, whereas low W_r+V_r noted for Faisalabad-08 (28.80), Pirsabak-08 (61.87) and BARS-2009 (68.60) possessing high frequency of dominant alleles. In W_r-V_r graph where Margalla-99 (P6), Local white (P10) and Kohistan-97 (P4) lies away of origin mean and Faisalabad-08 (P13), Pirsabak-08 (P5) and BARS-2009 (P14) lies near the origin mean. Array points are found scattered along the regression line confirming genetic diversity among parents (Fig. 7.a).

In F_2 'D' (7.25) is non-significant ' H_1 ' (210.15) is significant suggesting the presence of dominant and absence of additive action. The value of 'E' (44.13) is significant but less than ' H_1 ' minimizing the role of environmental variance in gene expression. Dominance means degree (2.6927) is greater than unity. Ratio of dominant to recessive alleles (8.0456) is greater than one and 'F' (30.39) is a positive value greater than 1 determining that dominant allele are more frequent than recessive. Allele distribution-Symmetry (0.2054) is determining asymmetrical distribution of +ve and -ve genes. (Table 7). Y-intercept (a = -19.315) is a negative value and regression line is passing below the origin mean in W_r-V_r graph both these suggests over dominance. Highest W_r+V_r value was observed for Local white (121.67), Sehar-2006 (93.74) and Mairaj-08 (91.95) having low frequency of dominant allele, whereas low W_r+V_r noted for Kohistan-97 (31.81), Auqab-2000 (31.91), Chakwal-86 (33.26) possessing high frequency of dominant alleles. In W_r-V_r graph where Local White (P10), Sehar-2006 (P7) and Mairaj-08 (P15) lies away of origin mean and Kohistan-97 (P4), Auqab-2000 (P3) and Chakwal-86 (P8) lies near the origin mean. Array points are found scattered along the regression line indicating genetic diversity among parents (Fig. 7.b).

In both F_1 and F_2 high broad sense heritability value (0.8363, 0.5328) is greater than narrow sense heritability (0.3166, 0.0328) illustrated dominant proportion is greater to effect overall heritability (Table 7).

3.8. Stay-green trait

In F_1 'D' (17.44) is significant ' H_1 ' (15.79) is non-significant showing additive gene action is operative and dominance is absent. 'E' (11.05) is significant, but its value is less than 'D' minimizing the role of environmental component. Dominance

means degree (0.9514) is less than unity. Relation dominant / recessive (1.4129) is greater than unity determining that dominant allele are more frequent than recessive which is supported by 'F' (5.68) with positive value greater than 1. Value of 'H₁' (15.79) and H₂' (16.38) have less difference and H₂/4H₁ (0.2594) is approximately equal to 0.25 which indicate that +ve and -ve genes differ slightly or nearly equal (Table 7). Value of Y-intercept (a = 4.986) which is a positive value and regression line is passing above the origin mean in Wr-Vr graph indicating partial dominance. Highest Wr+Vr value was observed for Auqab-2000 (P3) = 39.35, Mairaj-08 (P15) = 34.25 and Avocit-YRA (P2) = 32.95, lying away of origin mean and have low frequency of dominant allele, whereas low Wr+Vr noted for BARS-2009 (P14) = 8.66 and Faisalabad-08 (P13) = 12.05 lying near origin mean and possess high frequency of dominant alleles (Fig. 8.a).

In F₂ both 'D' (23.79) and 'H₁' (20.16) are significant, but value of 'H₁' is less than 'D' and 'D' is highly significant suggesting the important role of additive gene action. The value of 'E' (8.54) is significant but less than 'H₁' and 'D' lessening the role of environmental variance in gene expression. Ratio of dominant to recessive alleles (1.9271) is greater than one determining that dominant allele are more frequent than recessive. Allele distribution-Symmetry (0.2706) determining asymmetrical distribution of +ve and -ve genes (Table 7). Y-intercept (a = 5.993) is a positive value and regression line is passing above the origin mean in Wr-Vr graph which suggests partial dominance. Highest Wr+Vr value was observed for Avocit-YRA (P2) = 37.25, Mairaj-08 (P15) = 35.70 and Galaxy-13 (P9) = 34.13, lying away of origin mean and have low frequency of dominant allele, whereas low Wr+Vr recorded for BARS-2009 (P14) = 9.63 and Pak-81 (P11) = 14.41 lying near origin mean and possess high frequency of dominant alleles. Array points are found scattered along the regression line indicating genetic diversity among parents (Fig. 8.b).

In both F₁ and F₂ high broad sense heritability value (0.4670, 0.6045) is greater than narrow sense heritability (0.2694, 0.3997) illustrated dominant proportion is greater to effect overall heritability (Table 7).

3.9. 1000-grain weight

In F₁ significance of 'D' (22.79) and non-significance of 'H₁' specifies additive type of gene action supported by dominance means degree (0.77) with value less than unity. 'E' (17.8) is significant, but its value is less than 'D' abating the role of environmental component. Value of allele distribution-symmetry (0.2989) is not equal to 0.25 indicating asymmetry among +ve and -ve genes. Relation dominant / recessive (1.1694) is greater than and 'F' (2.74) has positive value both these suggest dominant allele are frequent than recessive. In F₂ value of 'D' (22.37) and 'E' (18.99) are significant with greater value of 'D' and H₁ (2.11) is non-significant indicating additive gene action supported by dominance means degree (0.1535) with value less than unit. Allele distribution-symmetry (1.2208) is not equal to 0.25 indicating asymmetry among +ve and -ve genes. Relation dominant / recessive (-0.2941) is less than 1 and 'F' (-12.6) possess negative value both showing more frequency of recessive allele than dominant (Table 8). In both

F₁ and F₂ value of Y-intercept (a = 4.411 and 0.575) is positive value, on the other hand in Wr-Vr graph regression line is originating above the origin mean both these determine the role of partial dominance. Parental order of dominance was determined on basis of inverse relation of (Wr+Vr) to dominance and distribution of array points in Wr-Vr graph. In F₁ highest (Wr+Vr) value was found in Kohistan-97 (P4) = 62.38, Margalla-99 (P6) = 43.86 and Pak-81 (P11) = 42.27 lying away of origin mean in Wr-Vr graph exhibit low frequency of dominant and allele than recessive, while lowest (Wr+Vr) value was found in Galaxy-13 (P9) = 11.08, Pirsabak-08 (P5) = 14.54 and Faisalabad-08 (P13) = 16.04 lying near origin mean in graph possess high frequency of dominant or low frequency of recessive alleles. Array points are scattered along the regression line confirming the genetic diversity among parents (Fig. 9.a). In F₂ high Wr+Vr value was found Kohistan-97 (P4) = 62.37, Pak-81 (P11) = 55.46 and Mairaj-08 (P15) = 54.87, located away of origin on graph, have more recessive allele than dominant, in contrast Avocit-YRA (P2) = 13.61, Chakwal-86 (P8) = 14.65 and Galaxy-13 (P9) = 17.75 are found with low Wr+Vr value, lies near origin mean and exhibit high frequency of dominant allele than recessive (Fig. 9.b).

In both F₁ and F₂ progenies broad sense heritability value 0.4173 and 0.4567 were higher than narrow sense heritability value 0.2850 and 0.2128 respectively suggesting overall dominance effect (8).

3.10. Peduncle length

F₁ showed significant 'D' (14.68), 'H₁' (13) and 'E' (10.37) where 'D' is highly significant and have greater value than 'E' and 'H₁' suggesting additive gene action is operative, dominance means degree (0.9411) is less than one. Allele distribution-Symmetry is 0.3313 which confirms asymmetry of -ve and +ve allele. Relation dominant / recessive (0.7464) is less than 1 and F (-4.01) has negative value indicating the presence of recessive allele frequently than dominant (Table 8). Value of Y-intercept (a = 0.501) is positive value and regression line is passing above the origin mean indicating partial dominance. Highest (Wr+Vr) value was recorded for Morocco (P1) = 34.22 and Local white (P10) = 32.36 possessing low frequency of dominant allele and lying away of origin in graph. Low Wr+Vr value was found in Margalla-99 (P6) = 9.75 and Pirsabak-08 (P5) = 14.87 present at location near origin in Wr-Vr graph, exhibit high frequency of dominant allele (Fig. 10.a). For F₂ value of 'D' (16.89) and 'E' (12.92) are significant while 'H₁' (8.02) is non-significant which indicate additive gene action. Dominance means degree (0.3445) is less than unity. Dominant to recessive allele ratio (p/q) is 4.3831 which is greater than 1 and 'F' (7.31) has positive value showing that presence of dominant allele is frequent than recessive. Unequal value of 'H₁' (8.02) and 'H₂' (10.55) and H₂/4H₁ (0.3290) ≠ 0.25 and indicate asymmetry of positive and negative dominant allele (Table 8). Value of Y-intercept (a = -0.341) is negative value and regression line is originating below the origin mean indicating over dominance. Highest (Wr+Vr) value was recorded for BARS-2009 (P14) = 39.02 and Margalla-99 (P6) = 37.76 possessing low frequency of dominant allele and lying away of origin in graph. Low Wr+Vr value was found in

Moroco (P1) = 4.26 and Chakwal-86 (P8) = 5.31 present at location near origin in Wr-Vr graph, exhibit high frequency of dominant allele (Fig. 10.b).

Both in F₁ and F₂ BS heritability (0.5268 and 0.3228) estimates are greater than NS heritability (0.3301 and 0.2524) means effect of dominant proportion is greater to overall heritability (Table 8).

IV. DISCUSSION

In current study days to flowering found with higher value of H₁ than D (dominance gene action), non-significant value for F component, allele distribution symmetry less than 1 (over dominance), mean degree of dominance greater than 1, broad sense heritability greater than narrow sense, Y-intercept (a) with negative value and regression line passing below origin mean (over dominance) was also observed by Farshadfar *et al.*, (2013).

For plant height additive component D is greater than H₁ (additive gene action) in F₁ and less than H₁ (dominance action) in F₂ with partial dominance for plant height was also observed by Afridi, (2016). E component is significant but lower than D and H₁ and h²_{ns} less than h²_{bs} similar demonstration were made by Mohammadi, *et al.*, (2021); Farshadfar, *et al.*, (2013) and Afridi, (2016).

Ahmad, *et al.*, (2016) observed dominance type of gene action controlling the flag leaf area, with positive and non-significant value of F, allele distribution symmetry value less than 0.25, p/q value greater than 1 (dominant allele are frequent) and broad sense heritability less than narrow sense, identical to observations of current study. Similarly, Salmi, *et al.*, (2021) studied partial dominance for flag leaf area.

As in current study both additive and dominance type gene actions were recorded for productive tillers/plant, previous studies related to current study are conducted by Ahmad *et al.*, (2016) revealing additive gene action and dominance gene action was reported by Kumar, *et al.*, (2019) with over dominance, non-significant value of F component and asymmetry of gene distribution among parents. Greater broad sense heritability than narrow sense was also reported by Ul-Allah, *et al.*, (2021).

Dominant type gene action for days to maturity with dominance mean degree greater than 1 (over dominance), asymmetrical gene distribution among parents, access of dominant allele and lower value of narrow sense heritability was also recorded by Akram, *et al.*, (2008) and Afridi *et al.*, (2018). Ismail, *et al.*, (2003) observed more frequency of recessive allele for F₂ population.

Inamullah *et al.*, (2006) and Afridi *et al.*, (2018) described additive type of gene action controlling harvest index. Mean degree of dominance less than 1 and positive value of Y-intercept (a), regression line passing above the origin mean (partial dominance), asymmetrical distribution of genes among parents and h²_{bs} greater than h²_{ns} also reported by Afridi *et al.*, (2018).

El-Said, (2018) also observed H₁ significant and greater than D (dominance gene action) for number of kernels/spike with dominance mean degree greater than 1 (over dominance), F non-significant but positive, relation p/q greater than 1 (dominant allele are in access), allele distribution symmetry not

equal to 0.25 (asymmetrical gene distribution) and h²_{bs} greater than h²_{ns}.

Agbowuro and Salami, (2021) also reported additive type of gene action for stay-green trait where value of additive variance (0.064) was greater than the value of dominance variance (0.035). He also measured dominance mean degree (0.546) less than 1 (partial dominance) and low estimate of narrow sense heritability (0.36).

Ahmad, *et al.*, (2020) and Afridi *et al.*, (2018) observed additive gene action in controlling inheritance of 1000 grains weight. Afridi *et al.*, (2018) also estimated asymmetry of gene distribution among parents, dominance mean degree less than one (partial dominance), access of dominant allele in one and access of recessive allele in other generation and broad sense heritability value greater than narrow sense heritability value.

Afridi *et al.*, (2018) studied the inheritance of peduncle length for F₁ and F₂ he reported additive type of gene action with partial and over dominance. Mohammadi, *et al.*, (2022) also reported additive type of gene action and broad sense heritability value greater than narrow sense heritability. Mohammadi, *et al.*, (2021) studied asymmetrical gene distribution among parents.

V. CONCLUSION AND RECOMMENDATIONS

Analysis of variance showed high significant value mean high diversity is present among genotypes and may be used in future breeding programs successfully. Faisalabad-08 have highest harvest index and lowest plant height, it should be modified for fertile tiller/plant and grain yield. Mairaj-08 exhibit stay-green trait, highest fertile tiller/ plant and grain yield also show higher number of kernels/ spike lower peduncle and relatively larger spike length, it may be modified for grain weight. Chakwal-86 have highest 1000 grain weight and fertile tiller/ plant thus, recommended for future breeding programs.

High value of broad sense heritability than narrow sense heritability and higher value of dominance (H₁) than additive component (D) in both F₁ and F₂ progenies shows importance of dominance for days to flowering, flag leaf area, and number of kernels/ spike, it is recommended that selection should be delayed to latter generations to overcome segregation and to maintain stable variety, especially for fertile tiller/ plant, days to maturity and number of kernel/ spike where in Wr-Vr graph regression line also originates below origin mean acquiring over dominance.

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Table 1. Mean squares for morphometric traits in half diallel cross (15 X 15).

Traits	Mean squares (F ₁)			Mean squares (F ₂)		
	Genotypes	Error	CV%	Genotypes	Error	CV%
Df	119	238		119	238	
Days to flowering	47.8196**	11.3902	3.37	52.8336**	7.3486	2.62
Plant height	174.3674**	20.6021	5.23	105.79**	19.8405	5.21
Flag leaf area	101.3681**	9.8618	8.45	49.7062**	9.9146	12.05
Fertile tiller / Plant	44.8918**	6.6688	26.52	26.6297**	8.2084	30.59
Days to maturity	77.2851**	14.148	2.26	128.844**	21.9915	2.83
Spike length	15.3964**	1.6389	10.23	21.1659**	5.7465	19.88
Harvest index	87.9909**	12.6769	8.82	110.51**	10.0362	11.61
No. of kernel /spike	313.7769**	19.8498	8.08	213.615**	44.1267	13.06
Stay-green trait	47.9705**	11.048	2.11	53.8375**	8.5391	1.87
1000 grain weight	67.5908**	17.7951	8.53	78.0482**	18.988	9.07
Peduncle length	50.5708**	10.3687	9.68	41.0528**	12.9185	10.53

NS, ** and * non-significant, significant at 1% and 5% probability levels respectively by F test.

Table 2. Test of adequacy for various traits in 15 X 15 F₁ half diallel cross of *Triticum aestivum*

Traits	Test of adequacy for F ₁			
	t ² test	Regression analysis		Conclusion
		b ₁	b ₀	
Days to flowering	0.289ns	2.16NS	3.286*	Fully adequate
Plant height	3.048ns	3.264*	4.524*	Partially adequate
Flag leaf area	0.68ns	2.991*	2.074NS	Partially adequate
Fertile tiller/plant	1.537ns	1.28NS	1.624NS	Partially adequate
Days to maturity	0.002ns	2.714*	1.103NS	Partially adequate
Spike length	52.784*	14.987*	0.399NS	Inadequate
Harvest index	0.721ns	0.407NS	4.833*	Fully adequate
No. of kernels/spike	0.381ns	3.527*	0.845NS	Partially adequate
Stay-green trait	3.241ns	4.631*	1.453NS	Partially adequate
1000-grain weight	2.335ns	3.624*	2.61*	Partially adequate
Peduncle length	0.798ns	1.244NS	2.159NS	Partially adequate

Table 3. Test of adequacy for various traits in 15 X 15 F₂ half diallel cross of *Triticum aestivum*

Traits	Test of adequacy for F ₂			
	t ² test	Regression analysis		Conclusion
		b ₁	b ₀	
Days to flowering	0.0003ns	2.947*	0.71NS	Partially adequate
Plant height	0.636ns	0.939NS	3.059*	Fully adequate
Flag leaf area	3.02ns	4.817*	1.061NS	Partially adequate
Fertile tiller/plant	1.85ns	0.073NS	4.466*	Fully adequate
Days to maturity	2.591ns	4.933*	0.684NS	Partially adequate
Spike length	7.486*	1.052NS	0.809NS	Inadequate
Harvest index	4.563ns	3.458*	5.981*	Partially adequate
No. of kernels/spike	0.388ns	2.312*	0.813NS	Partially adequate
Stay-green trait	0.318ns	2.977*	1.554NS	Partially adequate
1000-grain weight	0.011ns	1.344NS	4.622*	Fully adequate
Peduncle length	0.315ns	1.24NS	2.795*	Fully adequate

Table 4. Estimates of genetic components of variation in 15 X 15 F₁ and F₂ half diallel cross of *Triticum aestivum* for days to flowering and plant height.

Components of genetic variance	Days to flowering			Plant height		
	F ₁	F ₂	F ₂	F ₁	F ₂	F ₂
	Estimates	SE	Estimates	SE	Estimates	SE
E	11.39** ± 0.89	7.35** ± 1.08	20.6** ± 1.48	19.84** ± 1.48	19.84** ± 2.23	2.23
D	10.19* ± 3.57	13.12** ± 4.32	45.09** ± 5.91	35.93** ± 5.91	35.93** ± 8.9	8.9
F	12.79ns ± 7.93	19.3ns ± 9.59	-44.09** ± 13.13	31.74ns ± 13.13	31.74ns ± 19.78	19.78
H1	34.46** ± 6.63	52.88** ± 8.02	35.11** ± 10.98	78.18** ± 10.98	78.18** ± 16.54	16.54
H2	26.21** ± 5.36	36.57** ± 6.48	49.37** ± 8.86	66.63** ± 8.86	66.63** ± 13.35	13.35
h2	44.83** ± 3.58	11.37* ± 4.33	-4.34ns ± 5.92	23.38* ± 5.92	23.38* ± 8.92	8.92
Dominance means degree	1.839	1.0037	0.8824	0.7376	0.7376	0.7376
Allele distribution-Symmetry	0.1902	0.1729	0.3515	0.2131	0.2131	0.2131
Relation dominant / recessive	2.0363	6.4772	0.2869	3.9852	3.9852	3.9852
Number of dominant genes	1.7101	0.3108	-0.0879	0.3509	0.3509	0.3509
Heritability (BS)	0.4515	0.6591	0.7074	0.5528	0.5528	0.5528
Heritability (ns)	0.1359	0.2847	0.5321	0.302	0.302	0.302

Table 5. Estimates of genetic components of variation in 15 X 15 F₁ and F₂ half diallel cross of *Triticum aestivum* for flag leaf area and fertile tillers/plant.

Components of genetic variance	Flag leaf area			Fertile tillers/plant		
	F ₁	F ₂	F ₂	F ₁	F ₂	F ₂
	Estimates	SE	Estimates	SE	Estimates	SE
E	9.86** ± 2.45	9.91* ± 2.13	6.67** ± 0.7	8.21** ± 0.7	8.21** ± 0.29	0.29
D	41** ± 9.82	15.43 ± 8.52	12.09* ± 2.8	4.45** ± 2.8	4.45** ± 1.17	1.17
F	24.96ns ± 21.82	8.7ns ± 18.94	6.02ns ± 6.22	-4.35ns ± 6.22	-4.35ns ± 2.6	2.6
H1	77.88** ± 18.24	28.05 ± 15.84	32.17* ± 5.2	2.9ns ± 5.2	2.9ns ± 2.18	2.18
H2	71.52** ± 14.73	26.29 ± 12.79	29.05* ± 4.2	5.15* ± 4.2	5.15* ± 1.76	1.76
h2	11.67ns ± 9.84	36.54 ± 8.54	2.64ns ± 2.8	-2.03ns ± 2.8	-2.03ns ± 1.17	1.17
Dominance means degree	1.3781	0.6741	1.631	0.4038	0.4038	0.4038
Allele distribution-Symmetry	0.2296	0.2343	0.2258	0.4436	0.4436	0.4436
Relation dominant / recessive	1.567	2.4383	1.36	-0.0955	-0.0955	-0.0955
Number of dominant genes	0.1632	1.3898	0.0909	-0.3941	-0.3941	-0.3941
Heritability (BS)	0.7467	0.5218	0.64	0.3574	0.3574	0.3574
Heritability (ns)	0.2876	0.2672	0.248	0.1107	0.1107	0.1107

Table 6. Estimates of genetic components of variation in 15 X 15 F₁ and F₂ half diallel cross of *Triticum aestivum* for days to maturity and harvest index.

Components of genetic variance	Days to maturity			Harvest index		
	F ₁		F ₂	F ₁		F ₂
	Estimates	SE	Estimates	SE	Estimates	SE
E	14.15** ± 1.06	1.06	21.99** ± 2.18	2.18	12.68** ± 0.5	0.5
D	16.21** ± 4.26	4.26	5.51ns ± 8.73	8.73	21.84** ± 2	2
F	27.24* ± 9.46	9.46	-4.05ns ± 19.39	19.39	-20.11** ± 4.45	4.45
H1	68.71** ± 7.91	7.91	112.66* ± 16.21	16.21	1.35ns ± 3.72	3.72
H2	50.67** ± 6.39	6.39	108.73* ± 13.09	13.09	11.11** ± 3.01	3.01
h2	174.41* ± 4.27	4.27	21.29* ± 8.74	8.74	288.61** ± 2.01	2.01
Dominance means degree	2.0585		2.2602		0.2486	0.31
Allele distribution-Symmetry	0.1844		0.2413		2.0577	0.3631
Relation dominant / recessive	2.3785		0.7203		-0.2986	-0.0655
Number of dominant genes	3.4423		0.1958		25.9733	0.2717
Heritability (BS)	0.5334		0.6067		0.5982	0.7659
Heritability (ns)	0.1157		0.0446		0.5102	0.3911

Table 7. Estimates of genetic components of variation in 15 X 15 F₁ and F₂ half diallel cross of *Triticum aestivum* for number of kernels/spike and stay-green trait.

Components of genetic variance	Number of kernels/spike			Stay-green trait		
	F ₁		F ₂	F ₁		F ₂
	Estimates	SE	Estimates	SE	Estimates	SE
E	19.85** ± 5.92	5.92	44.13** ± 3.56	3.56	11.05** ± 1.21	1.21
D	67.83* ± 23.68	23.68	7.25ns ± 14.23	14.23	17.44** ± 4.86	4.86
F	71.24ns ± 52.62	52.62	30.39ns ± 31.63	31.63	5.68ns ± 10.8	10.8
H1	332.15** ± 43.99	43.99	210.15* ± 26.44	26.44	15.79ns ± 9.03	9.03
H2	251.99** ± 35.52	35.52	172.68* ± 21.35	21.35	16.38* ± 7.29	7.29
h2	-0.83ns ± 23.72	23.72	104.7** ± 14.26	14.26	14.07* ± 4.87	4.87
Dominance means degree	2.2129		2.6927		0.9514	0.4604
Allele distribution-Symmetry	0.1897		0.2054		0.2594	0.2706
Relation dominant / recessive	1.6222		8.0456		1.4129	1.9271
Number of dominant genes	-0.0033		0.6063		0.8585	0.7069
Heritability (BS)	0.8363		0.5328		0.467	0.6045
Heritability (ns)	0.3166		0.0328		0.2694	0.3997

Table 8. Estimates of genetic components of variation in 15 X 15 F₁ and F₂ half diallel cross of *Triticum aestivum* for 1000 grain weight and peduncle length.

Components of genetic variance	1000 Grain weight			Peduncle length		
	F ₁	F ₂	F ₂	F ₁	F ₂	F ₂
	Estimates	SE	Estimates	SE	Estimates	SE
E	17.8** ± 1.31	18.99** ± 1.02	10.37** ± 0.75	12.92** ± 0.93		
D	22.79** ± 5.23	22.37** ± 4.09	14.68** ± 3.01	16.89** ± 3.71		
F	2.74ns ± 11.62	-12.6ns ± 9.08	-4.01ns ± 6.7	7.31ns ± 8.25		
H1	13.51ns ± 9.71	2.11ns ± 7.6	13* ± 5.6	8.02ns ± 6.9		
H2	16.16ns ± 7.84	10.3ns ± 6.13	17.23** ± 4.52	10.55ns ± 5.57		
h ²	-4.39ns ± 5.24	-4.54ns ± 4.1	-1.58ns ± 3.02	-0.69ns ± 3.72		
Dominance means degree	0.77	0.1535	0.9411	0.3445		
Allele distribution-Symmetry	0.2989	1.2208	0.3313	0.329		
Relation dominant / recessive	1.1694	-0.2941	0.7464	4.3831		
Number of dominant genes	-0.2717	-0.4411	-0.0916	-0.0657		
Heritability (BS)	0.4173	0.4567	0.5268	0.3228		
Heritability (ns)	0.285	0.2128	0.3301	0.2524		

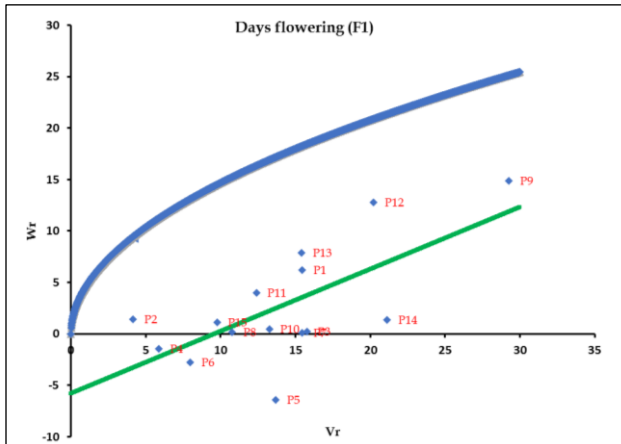


Figure 1.a Wr Vr graph for days to flowering F_1 generation

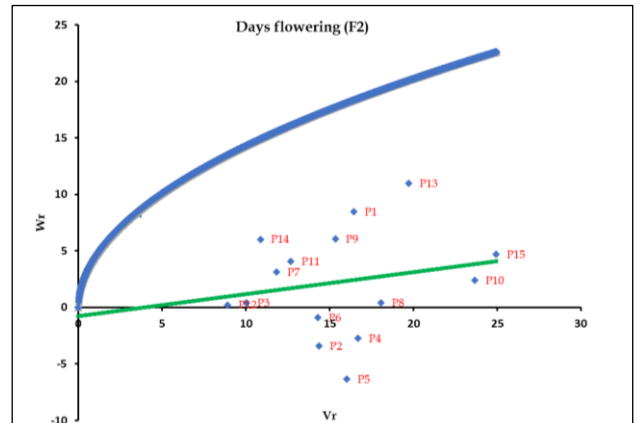


Figure 1.b Wr Vr graph for days to flowering F_2 generation

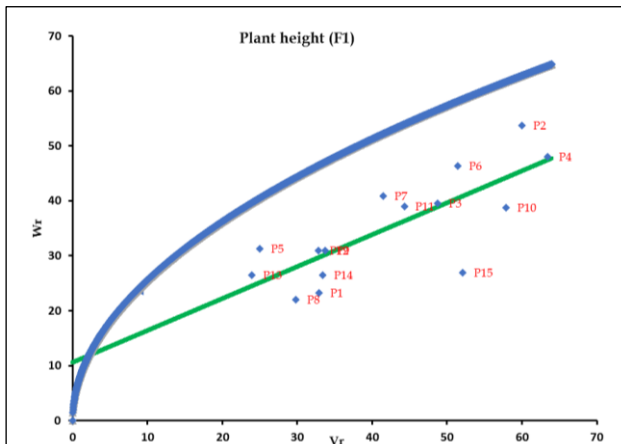


Figure 2.a Wr Vr graph for plant height F_1 generation

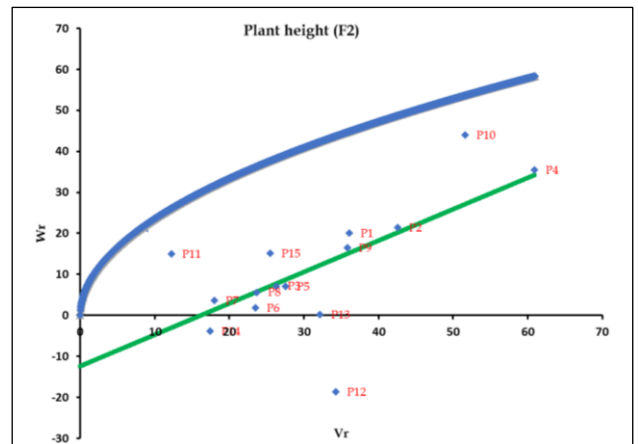


Figure 2.b Wr Vr graph for plant height F_2 generation

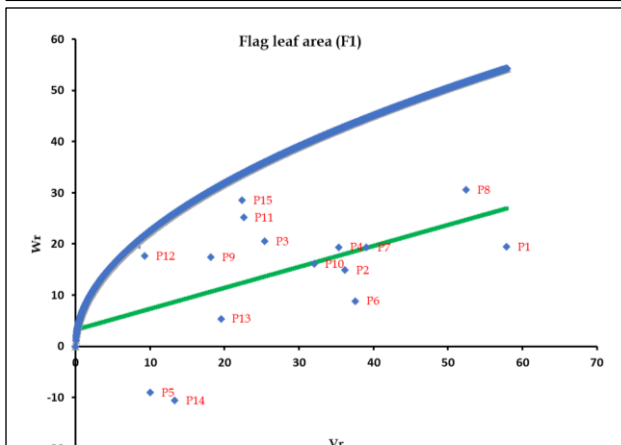


Figure 3.a Wr Vr graph for flag leaf area F_1 generation

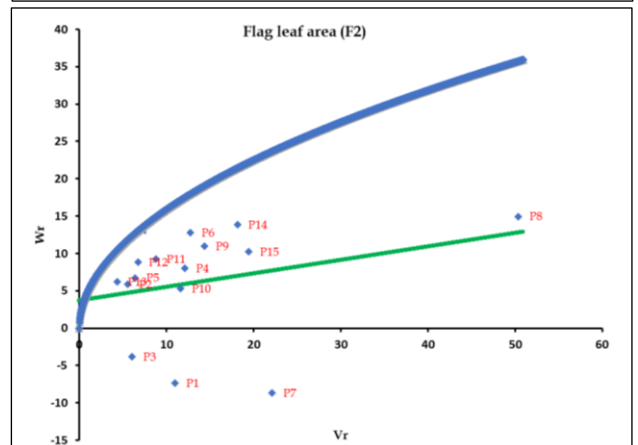


Figure 3.b Wr Vr graph for flag leaf area F_2 generation

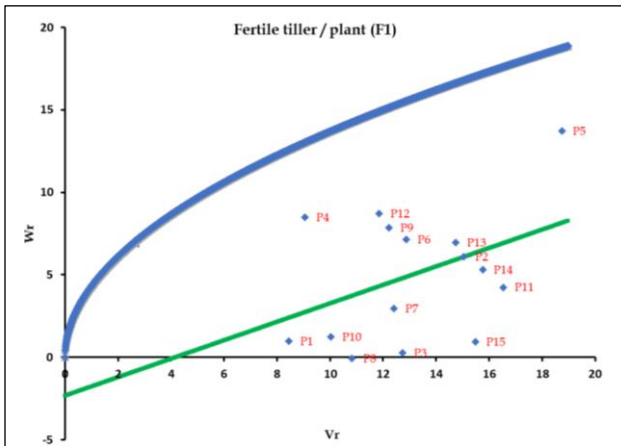


Figure 4.a W_r V_r graph for fertile tillers/plant F_1 generation

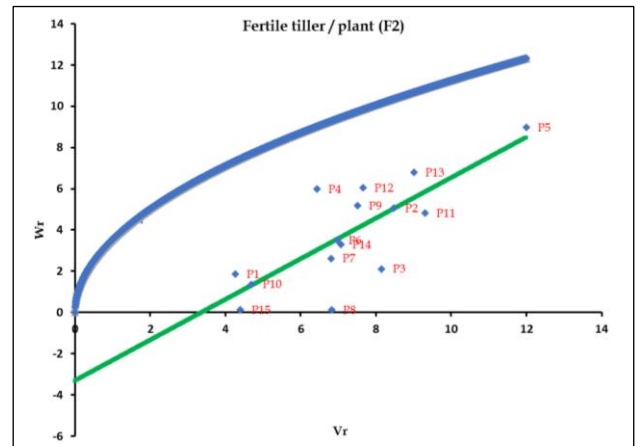


Figure 4.b W_r V_r graph for fertile tillers/plant F_2 generation

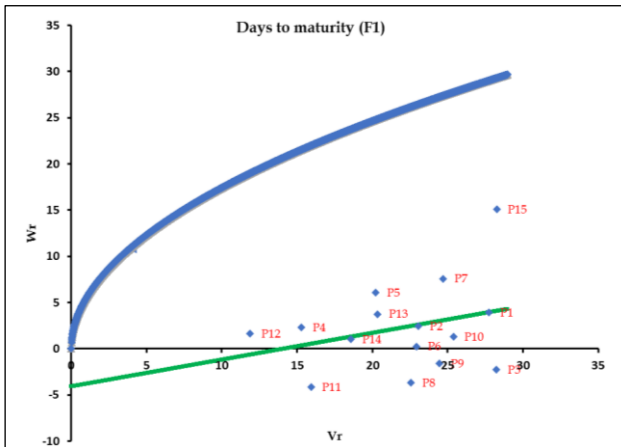


Figure 5.a W_r V_r graph for days to maturity F_1 generation

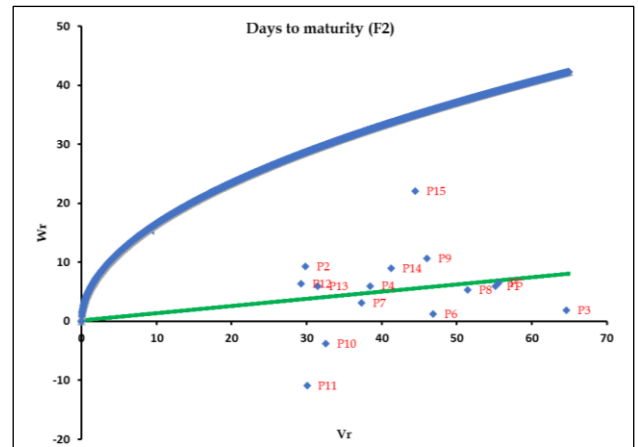


Figure 5.b W_r V_r graph for days to maturity F_1 generation

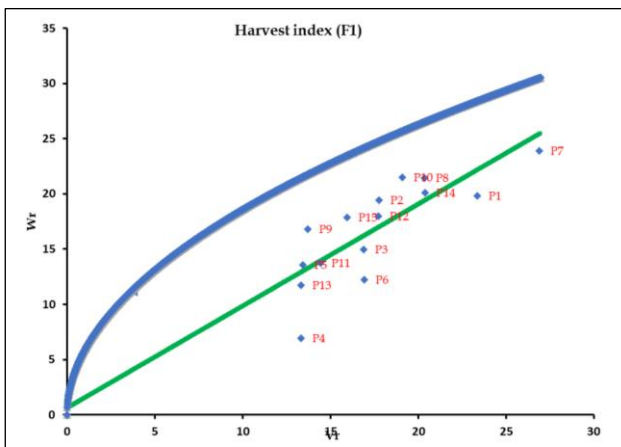


Figure 6.a W_r V_r graph for harvest index F_1 generation

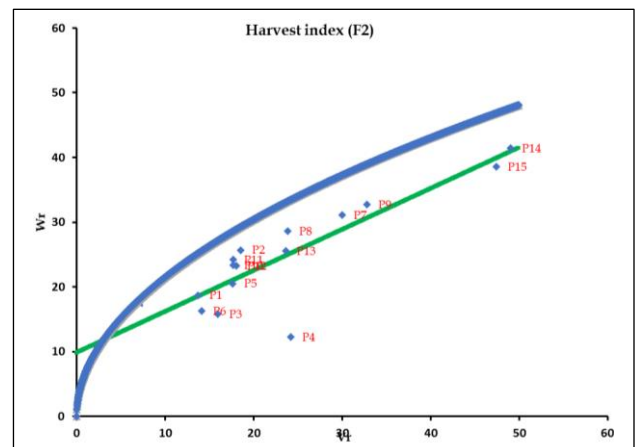
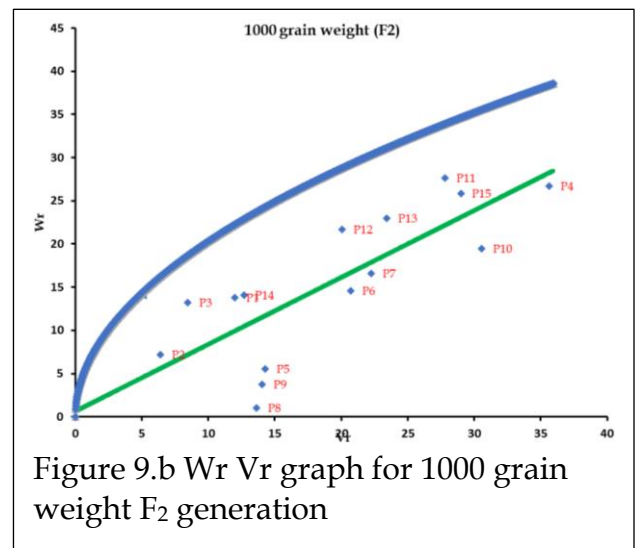
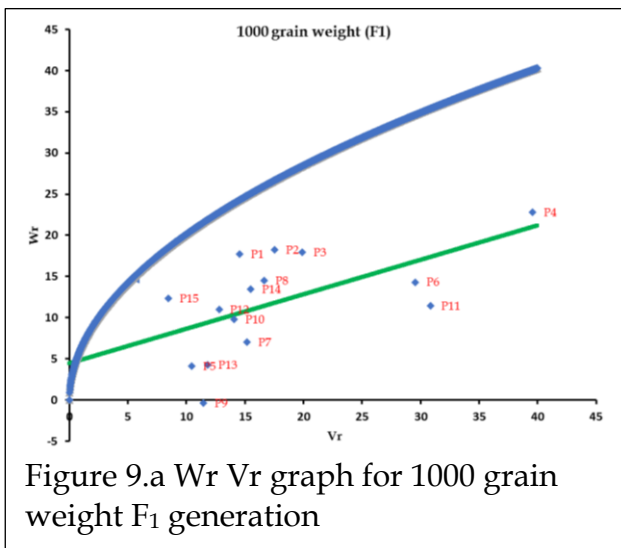
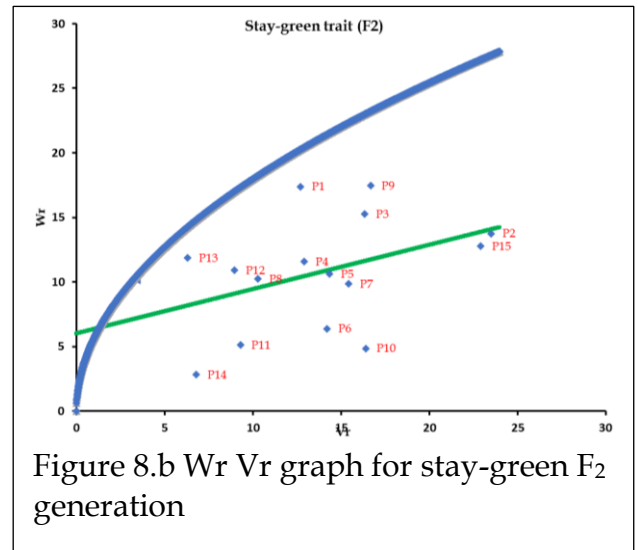
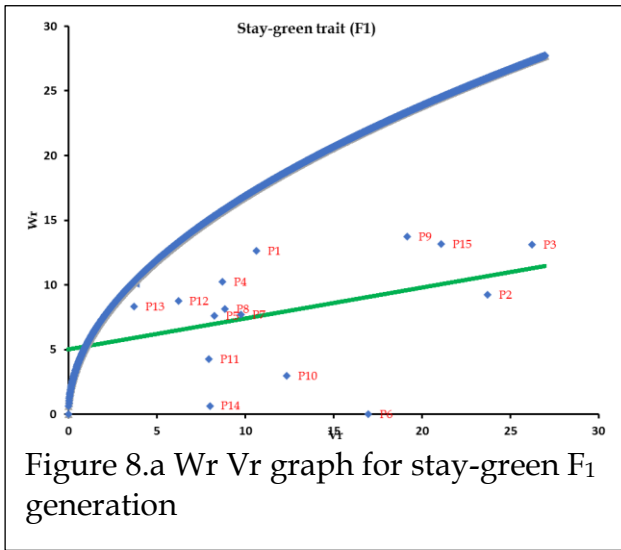
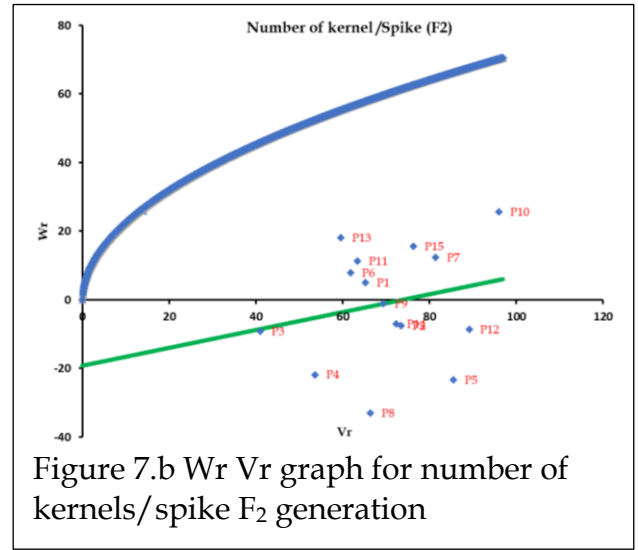
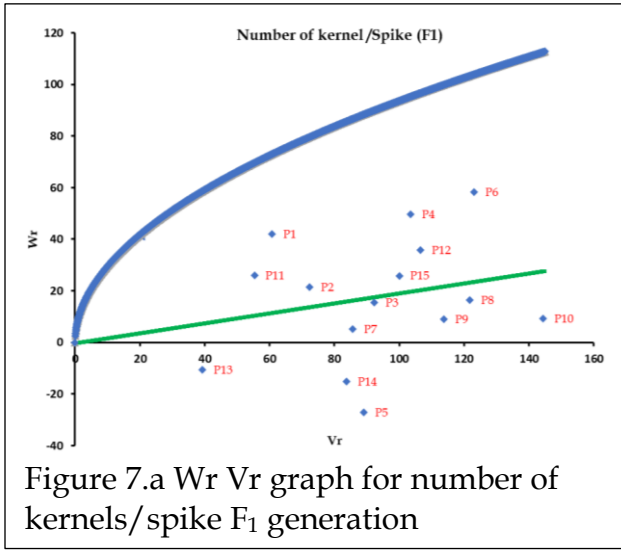


Figure 6.b W_r V_r graph for harvest index F_1 generation



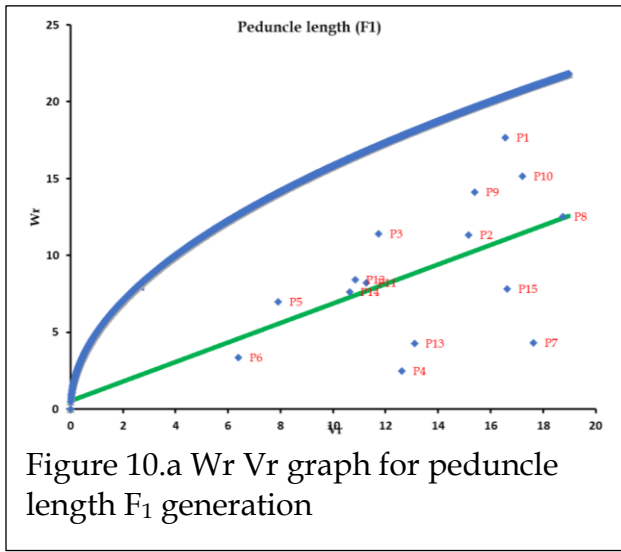


Figure 10.a W_r V_r graph for peduncle length F_1 generation

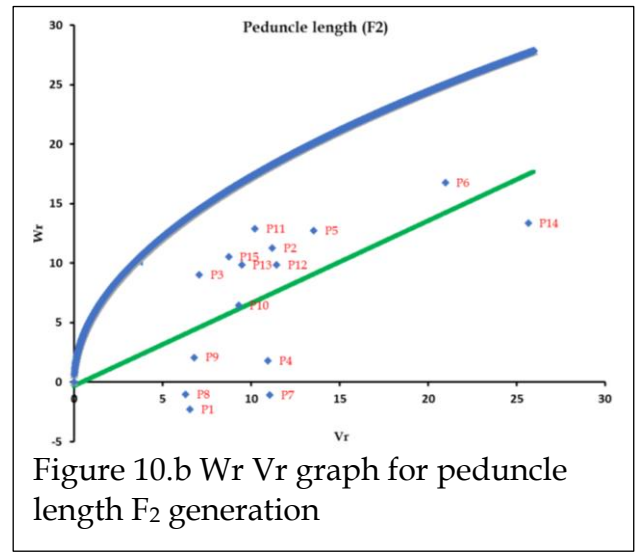


Figure 10.b W_r V_r graph for peduncle length F_2 generation