agriculture

MDPI

Article

Use of Graphical and Numerical Approaches for Diallel Analysis of Grain Yield and Its Attributes in Bread Wheat (*Triticum aestivum* L.) under Varying Environmental Conditions

Gita R. Chaudhari [1,*], D. A. Patel [1], A. D. Kalola [2] and Sushil Kumar [3]

[1] Department of Genetic & Plant Breeding, BACA, Anand Agricultural University, Anand 388110, Gujarat, India
[2] Department of Statistics, BACA, Anand Agricultural University, Anand 388110, Gujarat, India
[3] Department of Agricultural Biotechnology, Anand Agricultural University, Anand 388110, Gujarat, India
* Correspondence: geetchaudhary89@gmail.com or geetchaudhari89@aau.in

Abstract: Improving yield is the main aim of plant breeders. In the case of bread wheat (*Triticum aestivum*), a major challenge in this regard is genotype–environment interactions, and a knowledge of these is required to successfully select high-yielding genotypes. In this study, graphical and numerical approaches of diallel analysis have been used to reveal such interactions. Ten different wheat genotypes were crossed using a half-diallel approach. The parents, hybrids, and standard checks were evaluated at the Regional Research Station, Anand Agricultural University, Gujarat, Anand, India under both standard and late-sown conditions in two separate years (E_1 and E_2 (normal-18 November 2018 and late sown-10 December 2018, respectively, *Rabi* 2018–2019), E_3 and E_4 (normal-18 November 2019 and late sown-10 December 2019, respectively, *Rabi* 2019–2020)). For each sowing, 't^{2}' values were calculated for eleven phenotypic characteristics: days to 50% heading, days to maturity, plant height, number of effective tillers per plant, length of main stem, number of spikelets per main spike, number of grains per main spike, grain yield per main spike, grain yield per plant, 1000-grain weight, and harvest index. Components of the gene effect revealed that the number of spikelets per main spike in E_2 and E_4, and the number of grains per main spike in E_2 were governed by both additive and dominance gene action across the environments. Other characteristics were the greater influence of the dominance gene effect, except for days to 50% heading in E_1, E_2, E_3, and E_4; days to maturity in E_2, E_3, and E_4; grain yield per main spike in E_4. Many characteristics exhibited overdominance, an asymmetrical distribution of positive–negative, dominance–recessive genes, and narrow-sense heritability in all environments. In graphical analysis, regression value 'b' was unity for days to 50% heading (E_1 and E_4) and 1000-grain weight (E_3 and E_4), which revealed an absence of digenic interactions for these characteristics in the respective environments. Therefore, a given population may be improved to isolate superior recombinants for the development of desired parents in future breeding programs.

Keywords: bread wheat; environments; half diallel; graphical and numerical approach; yield

check for updates

Citation: Chaudhari, G.R.; Patel, D.A.; Kalola, A.D.; Kumar, S. Use of Graphical and Numerical Approaches for Diallel Analysis of Grain Yield and Its Attributes in Bread Wheat (*Triticum aestivum* L.) under Varying Environmental Conditions. *Agriculture* **2023**, *13*, 171. https://doi.org/10.3390/agriculture13010171

Academic Editor: Aimin Zhang

Received: 15 November 2022
Revised: 26 December 2022
Accepted: 5 January 2023
Published: 9 January 2023

Copyright: © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https://creativecommons.org/licenses/by/4.0/).

1. Introduction

Wheat (*Triticum aestivum* L.) is the world's most consumed cereal, serving as the main source of food for approximately one third of the world's population [1]. The growing population has necessitated the enhancement of cereal crop production worldwide. It is essential to enhance the production of cereal crops accordingly. The yield and attributes have been improved and fully exploited using breeding-based methods in various cereal crops including bread wheat [2]. An estimate of gene action is crucial in a successful breeding program. For plant breeders, parent selection is exceedingly important during the breeding of high-yielding varieties of crop plants. Information on the genetic architecture of yield and its attributes is essential for the removal of undesirable crosses based on

the performance of the early generations and the improvement of crosses effectively [3]. Studies have suggested that diallel analysis is a viable method for understanding the genetic background of quantitative characteristics and to determine the parent potential [4,5]. A plant breeder has to perform effective selection in the segregating populations using diallel analysis, in order to understand the genetic basis of the characteristics.

There are various approaches available for the analysis of diallel crosses such as Griffing's and Hayman's approaches [6,7]. These two are often used in the data interpretation in breeding programs, such as in crop improvement, to elucidate the inheritance of characteristics and the nature of gene action [8].

The gene interaction and their effects can be determined using a numerical and graphical approach (Wr-Vr graph). The Wr-Vr approach estimates the ratio of the number of dominant genes to that of recessive genes existing in the common arrays of the parents, and is calculated from diallel tables. This is subsequently subjected to graphical representation and interpretation. The area under the regression line in the graph indicates the degree of dominance. Additionally, we can create parabola limits in this graph. This method is simple and facilitates easy data analysis and interpretation if the main assumptions of the diallel analysis are fulfilled [8]. He [9] noted that diallel analysis delivers more conformation than other methods, but has more crucial assumptions [10]. Diallel analysis facilitates the detection of an epistasis or linkage [10]; however, Griffing's diallel approach does not [6]. When using Griffing's analysis to estimate variance components, it has been suggested that simple tests, such as the Wr-Vr evaluation found in Hayman's model [7], may be used to confirm the presence of an epistasis and/or linkage disequilibrium [11,12]. The validity of the hypothesis of the additive-dominance model can be verified by a unit slope of the regressions of Wr and Vr and non-significance of t^2, as prescribed by [7].

Constraints reduce the production potential due to climate changes that occur throughout the growth season. One of the main factors affecting the yield and productivity of the wheat crop is heat stress. For wheat crop enhancement, it is necessary to comprehend how genes interact with their environment. In light of the aforementioned information, in this work, we employed the diallel analysis described in [10,13] to clarify the genetic makeup of the parents with regard to various characteristics and to estimate the gene action for various quantitative characteristics in bread wheat. Our findings can be used in particular breeding programs to produce the desired outcomes.

2. Materials and Methods

2.1. Plant Material and Field Performance Evaluation

The experimental material comprised 10 parents, their 45 hybrids, and 2 check varieties. Here, Figure 1 represents the plant stature of parents and checks.

The genotypes represented cultivated (commercial varieties and checks) in Table 1 and this material was obtained from the Centre of Excellence for Research on Wheat, Sardarkrushinagar Dantiwada Agricultural University (SDAU), Vijapur, Gujarat. All the experiments were performed in accordance with the relevant guidelines and regulations. All plant materials were available within the institute and are available in the public domain, eliminating the need to obtain permissions. The details of the parental genotypes, Checks, and Hybrid crosses are given in Table 1 and Supplementary Table S1. The characteristics of the selected parental lines are given Figure 2. The crosses were made during *Rabi* (winter) 2017–2018 and 2018–2019 as per 10 × 10 diallel mating, excluding reciprocals.).

The numerical analysis was performed as per procedures outlined by [7,13–17] described in detail by [18,19] and the graphical approach as per [7,10]. The analysis was based on the following assumptions of diallel analysis: 1. diploid segregation; 2. no differences in reciprocal crosses, i.e., absence of maternal effect; 3. independent action of non-allelic genes in the diallel cross, i.e., absence of epistasis; 4. homozygous parents; 5. genes independently distributed between the parents, i.e., absence of linkages; 6. absence of multiple allelism. These assumptions were verified using the 't2' test [13]. The 't2' test evaluates the adequacy of the basic assumption of the additive dominance model. The

material used in this experiment was examined in terms of the treaty with assumptions basic to Hayman diallel analysis. The parents used in this study were homozygous and diverse in their origin, while the maternal effects were presumed to be absent in the studied material. Two general tests, namely, the t2 test and regression of Wr on Vr, were used to test other assumptions. Therefore, a non-significant 't2'value would indicate the uniformity of the Wr-Vr, and confirm the validity of the postulated hypothesis, particularly the adequacy of the additive dominance model [20].

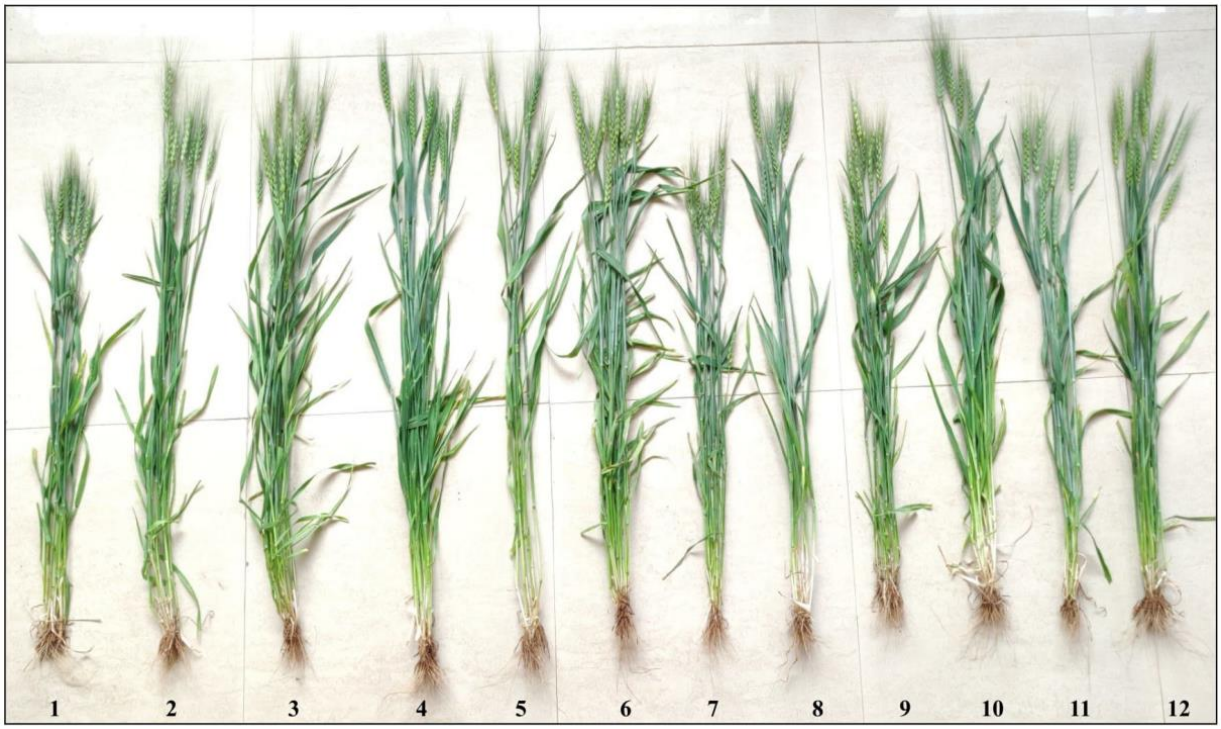

Figure 1. Plant stature of parents and checks (**1**: GW 451; **2**: GW 496; **3**: LOK 1; **4**: GW 322; **5**: GW 366; **6**: HI 1544; **7**: GW 173; **8**: GW 11; **9**: HD 2864; **10**: UAS 385; **11**: MASC 6222; **12**: HD 2932).

Table 1. List of varieties and their pedigree information.

Sr. No.	Released Varieties	Pedigree	Source
1	GW 451	GW324/4/CROC_1/AE.SQUARROSA (205)/JUP/JY/3/SKAUZ/4/KAUZ/5/GW 339	Centre of Excellence for Research on Wheat, SDAU, Vijapur, Gujarat
2	GW 496	HD 2285/CPAN 1861	
3	LOK 1	S 308/S 311	
4	GW 322	PBW 173/GW 196	
5	GW 366	DL 802-3/GW 232	
6	HI 1544	HIND162/BOBWHITE/CPAN 2099	
7	GW 173	TW 275 -7-6-10/LOK1	
8	GW 11	LOK 1/HW 1042//LOK 1	
9	HD 2864	DL509-2/DL377-8	
10	UAS 385	GW344/UAS239/DWR162	
Standard check varieties			
1	MASC 6222–TS	HD 2189*2//MASC 2496	
2	HD 2932–LS	KAUZ/STAR//HD 2643	

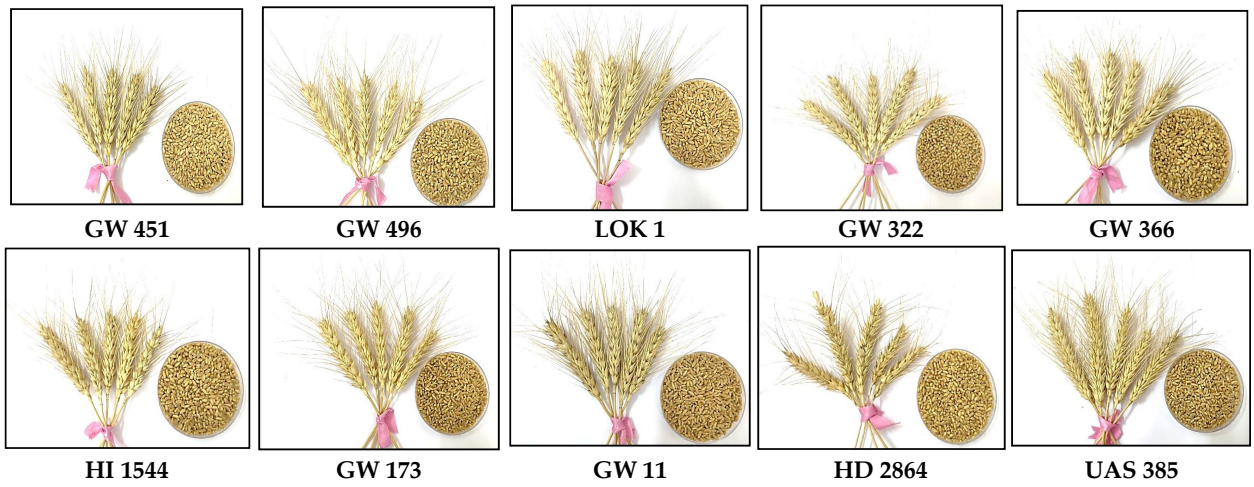

Figure 2. Spikes and grain of parental genotypes.

The parents, hybrids, and standard checks were evaluated in a complete randomized block design with three replications at the Regional Research Station, Anand Agricultural University, Anand, Gujarat, India (22°35′ N, 72°55′ E) during normal and late-sown conditions in four environments: E_1 and E_2 (normal and late sown, respectively, *Rabi* 2018–2019), and E_3 and E_4 (normal and late sown, respectively, *Rabi* 2019–2020). Each treatment consisted of 3 m long female lines with 20 × 10 cm (normal) and 18 × 10 cm (late) inter- and intra-row spacings, respectively. Two different spacings were used as the recommended agronomic practices. Likewise, the recommended nutrient management was deployed to grow a healthy plant stand and raise the crop (Supplementary Table S2). Immediately after sowing, need-based supplementary surface irrigation was provided (Supplementary Table S2). Observations for different quantitative characteristics under study excluding phenological traits, viz., days to 50% heading and days to maturity, were recorded on five randomly selected competitive plants in each experimental unit; however, border plants were excluded while selecting and tagging the plants for recording observations. The phenological characteristics were recorded on a population of an experimental unit.

The recorded observations included yield and its component traits: number of effective tillers per plant, length of main spike, number of spikelets per main spike, number of grains per main spike, 1000-grain weight, grain yield per main spike, grain yield per plant, and harvest index, and morphological traits: days to 50% flowering, days to maturity, and plant height. The replicated mean data were analyzed using Statistical Package for Agricultural Research data analysis (SPAR version 2.0). The Information on statistical tools is used in this study [14].

However, 't^2' also tests the adequacy of the basic assumption of the additive dominance model.

The 't^2' test for the uniformity test of $W_r - V_r$ is

$$t^2 = \frac{n-2}{4}\left[\frac{[\text{Var.Vr} - \text{Var.Wr}]^2}{\{(\text{Var.Vr})\,(\text{Var.Wr.})\} - \text{Cov}^2(\text{Vr.Wr})}\right]$$

It would be compared with table value of 't' at 4 and $n - 2$ degrees of freedom.

2.2. Estimation of Genetic Parameters

Subsequently, the components of genetic variation, viz., additive effects (D), dominance components (H_1 and H_2), environmental variance (*E*), covariance of additive and dominance effects (*F*), and dominance effects of all loci in the heterozygous phase (h^2), were estimated. Component analysis was performed only for the data that fit the additive dominance model. These genetic components of variation were calculated from the diallel table as per [9].

The model used to estimate the genetic parameters with consideration of the above equations different genetic parameters were estimated as:

$$\hat{D} = V_P - E$$
$$\hat{H}_1 = 4\overline{V}r + Vp - 4\overline{W}r - (3P-2)E/p$$
$$\hat{H}_2 = 4\overline{V}r - 4V\overline{r} - 2E$$
$$\hat{h}^2 = 4(ML_i - ML_0)^2 - 4(P-1)\hat{E}/p^2$$
$$\hat{F} = 2V_0L_0 - 4W_0L_{0i} - 2(P-2)\hat{E}/P \quad \text{i.e., } 2\,Vp - 4\,\overline{W}r - 2\,(P-2)\hat{E}/p$$
$$\hat{E} = \frac{VE}{r} = M^1e$$

For pooled analysis, E-pooled was used instead of *E*.

where:

P = Number of parents.

$\hat{D}$ = Component of genetic variation due to additive gene effect.

$\hat{H}_1$ = Component of genetic variation attributable to dominant effects of genes.

$\hat{H}_2$ = Component of genetic variation due to dominant effect corrected for genes distribution.

$\hat{F}$ = Relative frequency of dominance to recessive alleles in the parental population and variation in the dominance level over loci.

$\hat{h}^2$ = Net dominance variable effect expressed as the algebraic sum over all the loci in heterozygous condition in all the crosses.

$\hat{E}$ = Component of variation due to environmental effect.

3. Results

3.1. Numerical Approach

We estimated the 't^2' values for different characteristics in each environment, presented in Table 2. Among the twelve characteristics studied, the estimated 't^2' values were found to be significant for the three characteristics: plant height, grain yield per plant, and biological yield per plant in all the environments; however, the t^2 for days to 50% heading was non-significant in all the environments. The 't^2' value of the remaining characteristics was significant in either E_1, E_2, E_3, E_4, or a combination of the environments. The significance of 't^2' suggested the failure of certain assumptions (diploid segregation, no differences in reciprocal crosses, independent action of non-allelic genes in the diallel cross, i.e., absence of epistasis, homozygous parents, genes independently distributed between the parents, i.e., no linkages and no multiple allelism) of diallel analysis. Therefore, estimates of the uniformity of the Wr-Vr value are shown in Tables 3 and 4.

3.1.1. Days to 50% Heading

The 't^2' value was non-significant in all environments. The significance of additive (D) and dominance (H_1 and H_2) components of the gene effect revealed that the characteristic was governed by both additive as well as dominant gene actions in all the environments. The estimates of the average degree of dominance suggested the presence of overdominance in all environments (E_1:1.69%, E_2:1.20%, E_3:1.50%, and E_4:1.23%). An asymmetrical distribution of positive and negative alleles among the parents was observed in all environments as the $H_2/4H_1$ was <0.25. The positive values of F and KD/KR > 1 indicated an excess of dominant genes in all environments, except E_1. At least one dominant gene or group of genes appeared to govern the characteristic as the h^2/H_2 was <1 across all environments. The dominant gene or group of genes was not computed, as h^2 values were positive or non-significant. The estimates of narrow-sense heritability were low to medium in all analyses (E_1: 24.58%, E_2: 48.33%, E_3: 30.33%, and E_4: 49.69%) (Table 3).

Table 2. 't^{2}' value and regression coefficient for different metric characteristics of Wr on Vr.

SN	Characteristics	t^2 Test				b (Regression)			
		E_1	E_2	E_3	E_4	E_1	E_2	E_3	E_4
1	Days to 50% heading	1.96	0.20	0.60	0.04	0.18 ++	0.87 $$	0.15 +	0.69 $
2	Days to maturity	11.63 **	2.58	0.09	0.07	0.29 $++	0.27 ++	0.51	0.44
3	Plant height	6.21 **	9.56 **	10.18 **	19.17 **	0.19 ++	0.20 ++	0.06 ++	0.17 ++
4	No. effective tillers per plant	1.34	13.53 **	0.45	18.10 **	0.20 ++	−0.13 ++	0.36+	−0.11 ++
5	Length of main spike	3.96 **	1.31	0.93	21.47 **	0.13 ++	0.16 ++	0.37 +	0.22 $++
6	Number of spikelets/main spike	7.07 **	0.20	3.28	2.04	0.24 ++	0.60	0.31 ++	0.59
7	Number of grains per main spike	3.01	0.208	6.68 **	0.24	−0.07 ++	0.57	0.04 ++	0.65
8	Grain yield per main spike	34.90 **	0.004	21.91 **	0.04	0.10 ++	0.14 +	0.08 ++	0.20
9	Grain yield per plant	29.21 **	7.32 **	43.61 **	7.99 **	0.22 $++	0.01 ++	0.21 $++	0.13 ++
10	1000-grain weight	1.81	0.04	0.97	0.006	0.67 $$+	0.46 $$++	0.71 $$	0.66 $
11	Biological yield per plant	476.05 **	7.14 **	88.27 **	8.41 **	−0.04 ++	0.04 ++	−0.06 ++	0.20 ++
12	Harvest index	0.97	11.22 **	3.94 *	9.71 **	−0.20 ++	0.55 $$++	−0.29 ++	0.35 $++

*, ** Significant at 5% and 1% levels, respectively; $, $$ Significant at 5% and 1% levels, respectively, when Ho: b = 0; +, ++ Significant at 5% and 1% levels, respectively, when Ho: b = 1; E_1: Normal Sowing, E_2: Late Sowing (*Rabi* 2018–2019); E_3: Normal Sowing, E_4: Late Sowing (*Rabi* 2019–2020).

Table 3. Non-significant genetic components for days to 50% heading, days to maturity, no. of effective tillers per plant, and length of main spike.

	Days to 50% Heading				Days to Maturity [$]			No. of Effective Tillers Per Plant [&]		Length of Main Spike [&]	
Genetic Components	**E_1**	**E_2**	**E_3**	**E_4**	**E_2**	**E_3**	**E_4**	**E_1**	**E_3**	**E_2**	**E_3**
$\hat{E}$	0.44	0.60 *	0.64	0.54	0.91	0.54	0.82	0.28	0.30	0.14 **	0.13 **
$\hat{D}$	17.32 **	7.37 **	19.04 **	7.09 **	5.11 **	10.15 **	2.93 **	0.87	0.74	0.13	0.13
$\hat{F}$	−2.16	5.22 **	1.58	5.73 **	2.04	1.19	0.82 **	−0.08	−1.04	−0.19	0.13
$\hat{H}_1$	49.19 **	10.69 **	42.75 **	10.74 **	19.88 **	24.31 **	10.56 **	11.18 **	9.58 **	1.82 **	2.11 **
$\hat{H}_2$	41.79 **	9.36 **	36.90 **	8.75 **	13.80 **	17.58 **	8.21 **	8.25 **	7.89 **	1.45 **	1.55 **
$\hat{h}^2$	10.64	0.01	11.33	0.23	3.41	4.76	4.25	0.08	0.04	0.88 **	1.22 **
$(\hat{H}1/\hat{D})^{0.5}$	1.69	1.20	1.50	1.23	1.97	1.55	1.90	3.59	3.59	3.79	4.01
$\hat{H}_2/4\hat{H}_1$	0.21	0.22	0.22	0.20	0.17	0.18	0.19	0.18	0.21	0.20	0.18
KD/KR	0.93	1.83	1.06	1.98	1.23	1.08	1.16	0.97	0.67	0.67	1.28
$\hat{h}^2/\hat{H}_2$	0.25	0.00	0.31	0.03	0.25	0.27	0.52	0.01	0.01	0.61	0.79
% Heritability (narrow sense)	24.58	48.33	30.33	49.69	19.21	28.64	18.35	6.53	5.91	4.69	5.01

[$]: only three environments sowing; [&]: only two environments sowing. KD/KR = $\{(4\hat{D}\hat{H}_1)^{0.5} + \hat{F}\}/\{(4\hat{D}\hat{H}_1)^{0.5} - \hat{F}\}$; *, ** Significant at 5 and 1 percent levels, respectively; E_1: Normal Sowing, E_2: Late Sowing (*Rabi* 2018–2019); E_3: Normal Sowing, E_4: Late Sowing (*Rabi* 2019–2020).

Table 4. Non-significant genetic components for no. of spikelets per main spike, no. of grains per main spike, grain yield per main spike, 1000-grain weight, and harvest index.

	No. of Spikelets per Main Spike [$]			**No. of Grains per Main Spike** [$]			**Grain Yield per Main Spike** [&]		**1000-Grain Weight**				**Harvest Index** [#]
Genetic Components	**E_2**	**E_3**	**E_4**	**E_1**	**E_2**	**E_4**	**E_2**	**E_4**	**E_1**	**E_2**	**E_3**	**E_4**	**E_1**
$\hat{E}$	0.49 **	0.39 **	0.36 **	1.53	6.85 **	3.14	0.02	0.01	0.63	0.64	1.01	0.79	9.34
$\hat{D}$	2.01 **	0.82	2.19 **	17.21	23.12 **	21.02 **	0.09 **	0.10 **	12.46 **	30.12 **	13.82 **	30.78 **	66.93
$\hat{F}$	−0.31	−0.28	0.53	12.26	2.40	4.56	0.19	0.23 **	−4.71	12.56	−0.54	14.22	115.29
$\hat{H}_1$	5.26 **	5.04 **	4.47 **	98.85 **	109.88 **	121.19 **	0.49 **	0.45 **	41.62 **	68.97 **	37.71 **	62.35 **	357.26 **
$\hat{H}_2$	4.81 **	3.87 **	3.86 **	79.04 **	78.17 **	85.93 **	0.35 **	0.29 **	32.99 **	52.25 **	30.82 **	47.28 **	290.10 **
$\hat{h}^2$	11.25 **	−0.13	5.63 **	13.29	33.53 **	35.67 **	0.15 **	0.07	77.41 **	85.02 **	76.95 **	90.71 **	59.62
$(\hat{H}1/\hat{D})^{0.5}$	1.62	2.48	1.43	2.40	2.18	2.40	2.38	2.07	1.83	1.51	1.65	1.42	2.31
$\hat{H}_2/4\hat{H}_1$	0.23	0.19	0.22	0.20	0.18	0.18	0.18	0.16	0.20	0.19	0.20	0.19	0.20
KD/KR	0.91	0.87	1.19	1.35	1.05	1.09	2.65	3.37	0.81	1.32	0.98	1.39	2.19
$\hat{h}^2/\hat{H}_2$	2.34	−0.03	1.46	0.17	0.43	0.42	0.43	0.24	2.35	1.63	2.50	1.92	0.21
% Heritability (narrow sense)	21.06	10.58	28.99	15.65	14.62	13.99	18.27	29.12	20.31	33.80	24.63	37.49	19.32

[$]: only three environments sowing; [&]: only two environments sowing; [#]: only one environments sowing. KD/KR = $\{(4\hat{D}\hat{H}_1)^{0.5} + \hat{F}\}/\{(4\hat{D}\hat{H}_1)^{0.5} - \hat{F}\}$; ** Significant at 5 and 1 percent levels, respectively. E_1: Normal Sowing, E_2: Late Sowing (*Rabi* 2018–2019); E_3: Normal Sowing, E_4: Late Sowing (*Rabi* 2019–2020).

3.1.2. Days to Maturity

The 't^2' value was found to be significant in E_1, whereas it was non-significant in the other environments. The significance of additive (D) and dominance (H_1 and H_2) components of the gene effect revealed that the characteristic was governed by both additive as well as dominance gene effects in all environments; however, preponderance gene effects were noticed through the magnitude of the component of gene effects.

The estimates of the average degree of dominance suggested the existence of overdominance gene action in all environments (E_2:1.97%, E_3:1.55%, and E_4:1.90%). An asymmetrical distribution of positive and negative alleles among the parents was observed in all environments as the value of the $H_2/4H_1$ ratio was less than 0.25. Positive values of F and KD/KR > 1 in all the analyses indicated an excess of dominant genes among the parents. At least one dominant gene or group of genes appeared to govern the character as the h^2/H_2 was <1 across the environments. The dominant gene or group of genes was not computed, as the h^2 values were positive or non-significant. The estimates of narrow-sense heritability were low in all the environments (E_1: 19.21%, E_2: 28.64%, and E_3: 18.35%), which also confirmed that the characteristic was under the control of dominance gene effects (Table 3).

3.1.3. Number of Effective Tillers per Plant

The 't^2' value was significant in E_2 and E_4, which suggested a non-adherence to failure of certain assumptions of diallel analysis. The significance of both dominance components (H_1 and H_2) of the gene effect in E_1 and E_3 indicated that the characteristic was mainly governed by dominance gene effect. The estimate of the average degree of dominance (3.59) suggested the presence of overdominance. The asymmetrical distribution of positive and negative alleles among the parents was observed as the $H_2/4H_1$ was less than the expected value (0.25). The negative value of F and KD/KR < 1 indicated that the characteristic was controlled by several recessive genes. $h^2/H_2 < 1$ suggested that at least one dominant group of genes governed this trait. The dominant gene or group of genes was not computed, as the h^2 values were positive or non-significant. The estimate of narrow-sense heritability was extremely low in E_1 (6.53%) and E_2 (5.91%), which also confirmed that this characteristic was under control of the dominance gene effect (Table 3).

3.1.4. Length of Main Spike

The 't^2' value was significant in E_1 and E_4, which suggested failure of certain assumptions of diallel analysis. The significance of only dominance components (H_1 and H_2) of the gene effect in E_2 and E_3 revealed that the characteristic was solely governed by dominance gene action. The estimates of the average degree of dominance $((H1/D)^{0.5})$ suggested the presence of overdominance. $H_2/4H_1 < 0.25$ indicated the asymmetrical distribution of positive and negative alleles among the parental genotypes. The negative F value and KD/KR < 1 observed in E_2 indicated that the characteristic was controlled by several recessive genes; however, in E_3, the characteristic was mainly governed by several dominant genes as the values of F were positive and KD/KR was <1. The estimates of h^2/H_2 ratio indicated that at least one dominant group of genes appeared to govern this trait in E_2 and E_3. Significant and positive estimates of h^2 in both environments indicated a net dominance gene effect sum over loci. The estimates of narrow-sense heritability were low in both E_2 (4.69%) and E_3 (5.01%) (Table 3).

3.1.5. Number of Spikelets per Main Spike

The 't^2' value was significant in E_1, whereas it was non-significant in the rest of the environments. However, additive components of the gene effect had a greater influence in E_2 and E_4, and dominance components (H_1 and H_2) of the gene effect were significant in E_2 and E_4 with the prevalence of the dominant gene effect, whereas only the dominance gene effect governed the characteristic in E_3. The values of the average degree of dominance indicated the presence of over-dominance in all the three environments. $H_2/4H_1 < 0.25$ indicated an asymmetrical distribution of positive and negative alleles among the parental

genotypes. The negative F value and KD/KR < 1 indicated that the characteristic was mainly controlled by several predominant recessive genes in E_2 and E_3. The positive value of F and KD/KR > 1 indicated that the characteristic was controlled by several dominant genes in E_4. The estimate of h^2/H_2 ratio was >2 in E_2 and >1 in E_4 and one dominant group of genes appeared to govern this characteristic. The estimate of narrow-sense heritability was low in E_2 (21.06%), E_3 (10.58%), and E_4 (28.99%), which also confirmed that this characteristic was mainly under the control of the dominance gene effect (Table 4).

3.1.6. Number of Grains per Main Spike

The 't_2' value was significant in E_3, whereas it was non-significant in the rest of the environments. Additive (D) and dominance components (H_1 and H_2) of the gene effect were significant with the preponderance of the dominant gene effect in E_2 and E_4, whereas only the dominance gene effect was involved in E_1. The values of the average degree of dominance indicated the presence of overdominance. $H_2/4H_1 < 0.25$ indicated the asymmetrical distribution of positive and negative alleles among the parental lines in E_1, E_2, and E_4. The positive values of F and KD/KR > 1 indicated a symmetrical distribution of dominant and recessive genes among the parental genotypes, and the action of several dominant genes across the environments. $h^2/H_2 < 1$ suggested that at least one dominant group of genes governed this trait. Significant and positive estimates of h^2 in E_2 and E_4 indicated the net dominance gene effect sum over loci. The estimates of narrow-sense heritability were low in E_1 (15.65%), E_2 (14.62%), and E_3 (13.99%) (Table 4).

3.1.7. Grain Yield per Main Spike

The 't^2' value was significant in E_1 and E_3, which suggested failure of certain assumptions of diallel analysis. The significance of additive (D) and dominance components (H_1 and H_2) of the gene effect in E_2 and E_4 revealed that the characteristic was governed by both additive and dominance gene action. The estimate of the average degree of dominance (E_2: 2.38 and E_4: 2.07) suggested the presence of overdominance. An asymmetrical distribution of positive and negative alleles among the parents was observed as the value of $H_2/4H_1$ was less than the expected value (0.25). The positive value of F and KD/KR > 1 indicated that the characteristic was controlled by several dominant genes. $h^2/H_2 < 1$ suggested that at least one dominant group of genes governed this trait. A significant and positive estimate of h^2 observed in E_2 indicated the net dominance gene effect sum over loci. The estimate of narrow-sense heritability was low in E_2 (18.27%) and E_4 (29.12%), which also confirmed that this characteristic was under control of the dominance gene effect (Table 4).

3.1.8. 1000-Grain Weight

The 't^2' value was non-significant in all the analyses. The significance of additive (D) and dominance components (H_1 and H_2) of the gene effect revealed that the characteristic was governed by both additive and dominance gene actions in all environments. The estimates of the average degree of dominance suggested the presence of overdominance in all the environments. $H_2/4H_1 < 0.25$ indicated an asymmetrical distribution of positive and negative alleles among the parental genotypes in all the environments. The positive value of F and KD/KR > 1 in E_2 and E_4 indicated that the characteristic was controlled by several dominant genes, while a negative value of F and KD/KR < 1 in E_1 and E_3 indicated that the characteristic was controlled by several recessive genes. $h^2/H_2 > 1$ indicated that more than two to three dominant groups of genes appeared to govern this characteristic. Significant and positive estimates of h^2 in all the environments indicated the net dominance gene effect sum over loci. The estimates of narrow-sense heritability were low or medium in all the analysis (E_1: 20.31%, E_2: 33.80%, E_3: 24.63%, and E_4: 37.49%) (Table 4).

3.1.9. Harvest Index

The 't^2' value test was significant in E_2, E_3, and E_4, which suggested failure of certain assumptions of diallel analysis. The significance of only dominance components (H_1 and H_2) of the gene effect in E_1 revealed that the characteristic was solely governed by dominance gene action. The estimate of the average degree of dominance (2.31) suggested the existence of overdominance. An asymmetrical distribution of positive and negative alleles among the parents was observed as the value of $H_2/4H_1$ was less than the expected value (0.25). The positive value of F and KD/KR > 1 indicated that the characteristic was controlled by several dominant genes. $h^2/H_2 < 1$ suggested that at least one dominant group of genes governed this trait. The estimate of narrow-sense heritability was low (19.32%), which also confirmed that this characteristic was mainly controlled by the dominance gene effect (Table 4).

3.2. Graphical Analysis

To test the validity of the basic assumptions postulated for diallel analysis [5], the Wr-Vr homogeneity 't^2' test was performed. The 't^2' value was significant for most of the characteristics either in E_1, E_2, E_3, and E_4, or in their different combinations, indicating failure of any of the basic assumptions of diallel analysis. However, further verification of the validity of the assumption in respect of the presence or absence of epistatic gene effects could be made more precisely from the Wr-Vr graph. The array points on the Wr-Vr graph are expected to fall on the line of unity (45°) and, therefore, the value of regression 'b' should significantly deviate from zero, but not from one, suggesting the absence of an epistatic gene effect. b was statically at par one for days to 50% heading (E_1 and E_4) and 1000-grain weight (E_3 and E_4), which revealed an absence of digenic interactions for these characteristics in the respective environments (Table 2).

The graphical analyses are presented in Figures 3–6 and are described as follows.

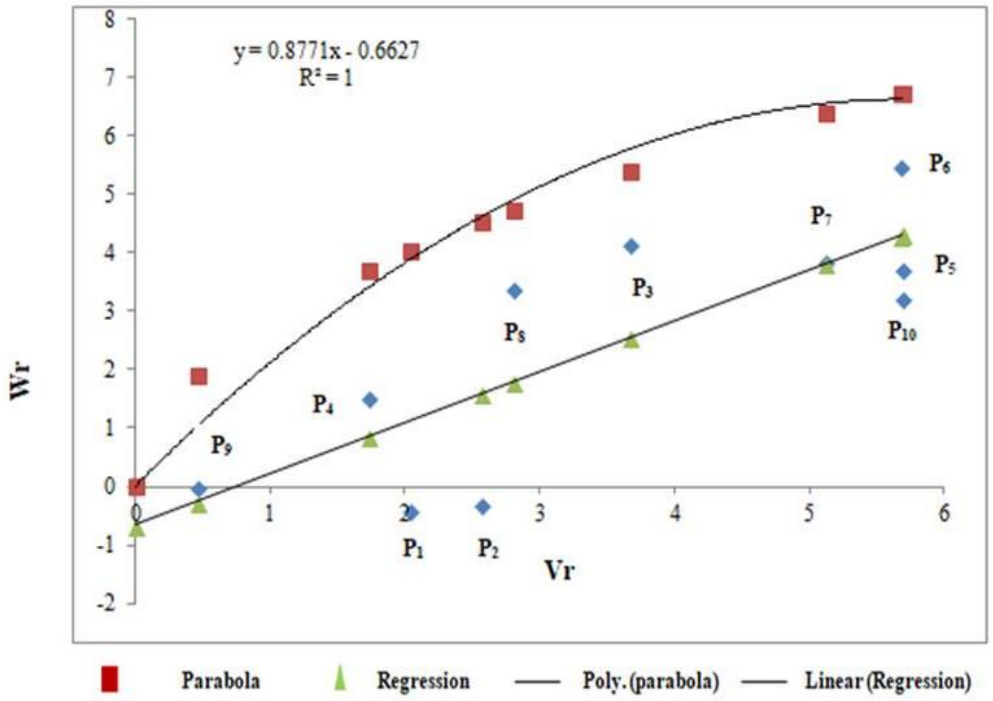

Figure 3. Wr-Vr graph for days to 50% heading in E_2. P1 = GW 451; P2 = GW 496; P3 = LOK 1; P4 = GW 322; P5 = GW 366; P6 = HI 1544; P7 = GW 173; P8 = GW 11; P9 = HD 2864; P10 = UAS 385 blue quadrilateral: parental genotypes).

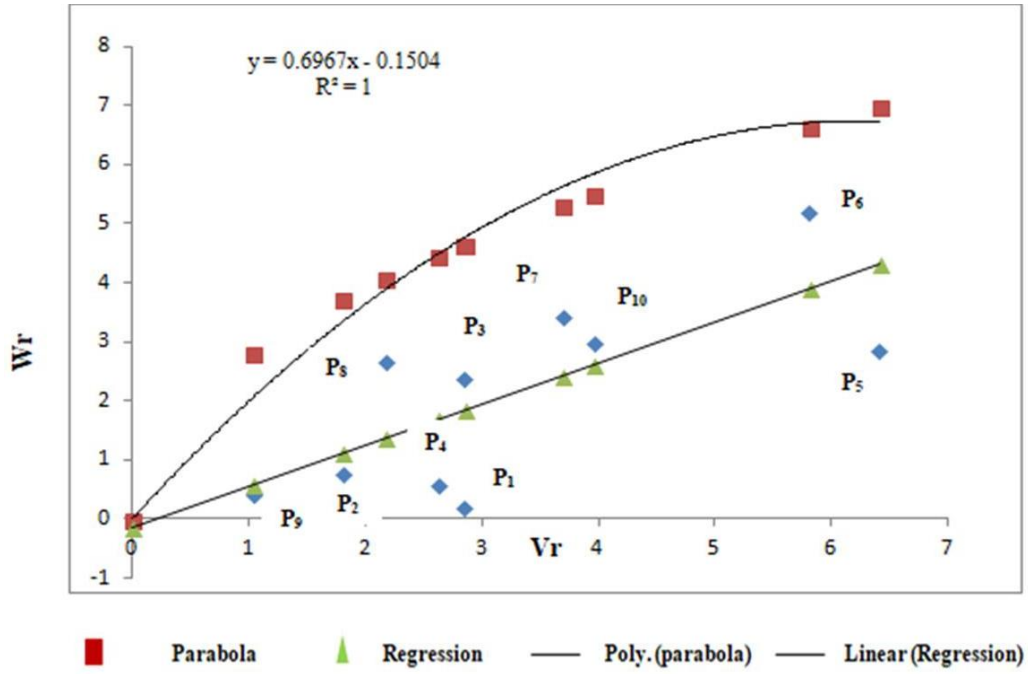

Figure 4. Wr-Vr graph for days to 50% heading in E_4. P1 = GW 451; P2 = GW 496; P3 = LOK 1; P4 = GW 322; P5 = GW 366; P6 = HI 1544; P7 = GW 173; P8 = GW 11; P9 = HD 2864; P10 = UAS 385 (blue quadrilateral: parental genotypes).

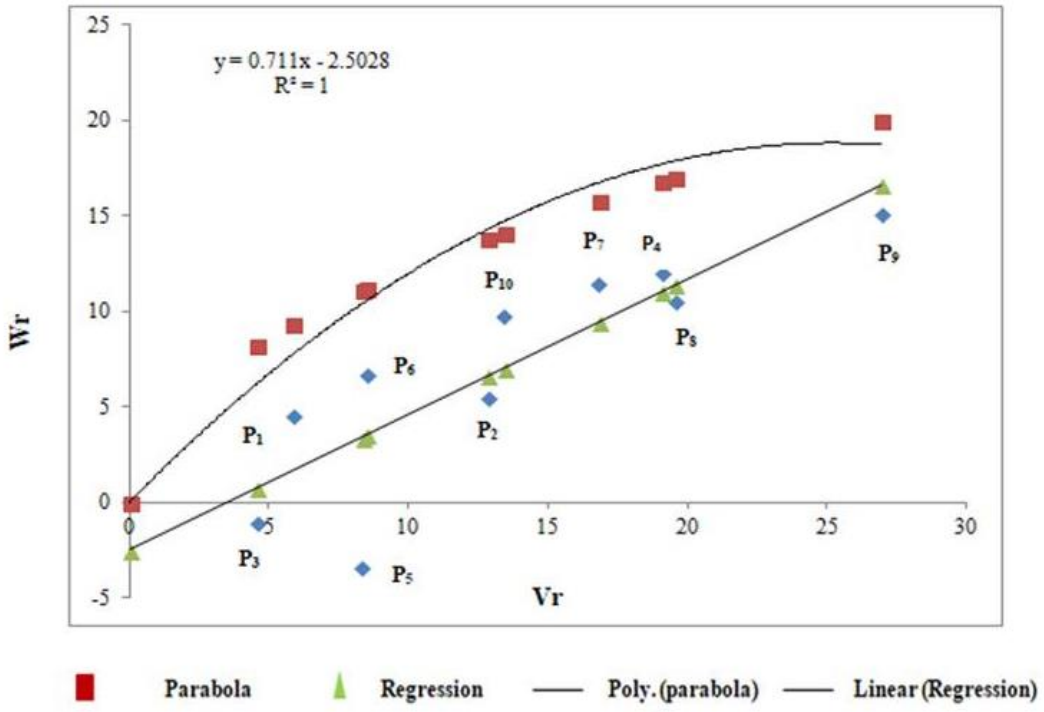

Figure 5. Wr-Vr graph for 1000-grain weight in E_3. P1 = GW 451; P2 = GW 496; P3 = LOK 1; P4 = GW 322; P5 = GW 366; P6 = HI 1544; P7 = GW 173; P8 = GW 11; P9 = HD 2864; P10 = UAS 385 (blue quadrilateral: parental genotypes).

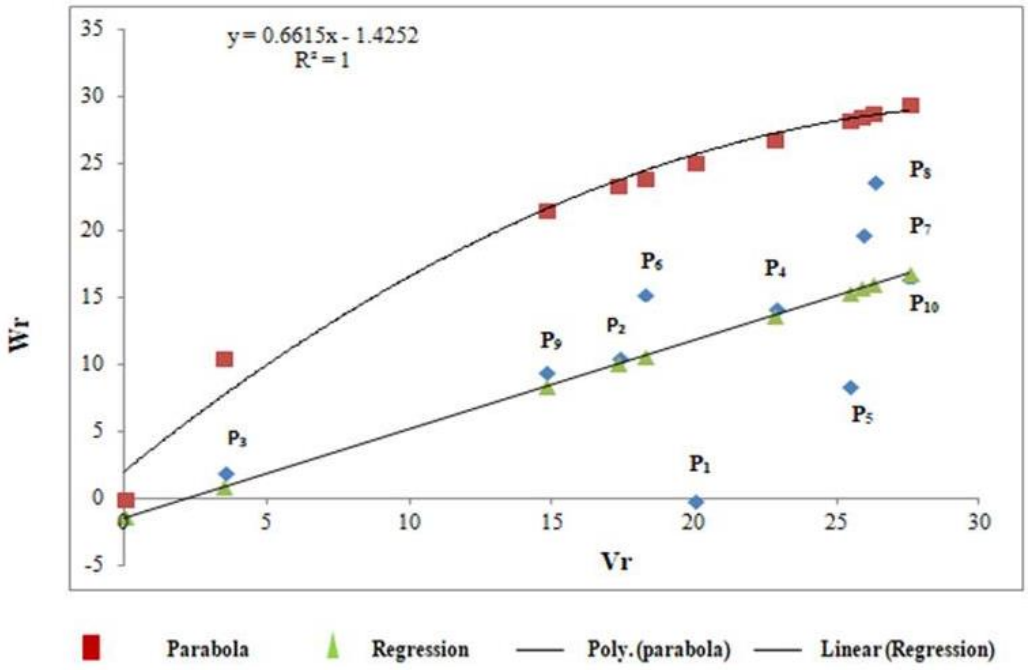

Figure 6. Wr-Vr graph for 1000-grain weight in E_4. P1 = GW 451; P2 = GW 496; P3 = LOK 1; P4 = GW 322; P5 = GW 366; P6 = HI 1544; P7 = GW 173; P8 = GW 11; P9 = HD 2864; P10 = UAS 385 (blue quadrilateral: parental genotypes).

3.2.1. Days to 50% Heading

In E_2, the regression line (Y = 0.8771x − 0.6627) was intercepted by the Wr axis below the origin, indicating the presence of overdominance (Figure 3). Among the parents, HD 2864 had a higher frequency of dominant genes, as these parents occupied the nearest position to the origin of the regression line. Accordingly, the parents GW 366, HI 1544, and UAS 385 had a higher frequency of recessive genes, as they occupied the farthest position from the origin, whereas LOK 1, GW 322, GW 173, and GW 11 had an equal proportion of dominant and recessive genes as they occupied an intermediate position on the regression line. The parents GW 451 and GW 496 may carry the genes, causing inter-allelic interaction as they occupied the positions outside the truncated area of the graph. The slope of the regression line of the Wr-Vr graph was statistically equal to unity in E_4 (Y = 0.6967x − 0.1504), indicating the absence of digenic interactions (Figure 4). Similarly, the regression line intercepted by the Wr axis passed through the origin, indicating the presence of complete dominance.

Among the parents, HD 2864 and GW 496 had a higher frequency of dominant genes as they occupied the nearest position to the origin of the regression line, whereas GW 366 and HI 1544 had a higher frequency of recessive genes as they occupied the farthest position from the origin; GW 451, LOK 1, GW 322, GW 11, GW 173, and UAS 385 had an equal proportion of dominant and recessive genes as they occupied an intermediate position on the regression line.

3.2.2. 1000-Grain Weight

The regression line (Y = 0.711x – 2.5028) was intercepted by the Wr axis below the origin, indicating overdominance for the characteristic in E_3 (Figure 5). The array point of parent GW 451 was closest to the origin, thereby indicating its contribution to the several dominant genes, whereas the parent HD 2864 occupied a position at the tail of the regression line, indicating it as a carrier of the several recessive genes. Moreover, the rest of the parents, GW 451, GW 496, GW 322, HI 1544, GW 173, GW 11, and UAS 385, occupied intermediate positions on the regression line, indicating an equal distribution of dominant and recessive genes within them. The parents LOK 1 and GW 366 could be carriers of genes

causing inter-allelic interaction as they occupied positions outside the truncated area of the graph.

In E_4, the slope of the regression line of the Wr-Vr graph was linear and probably at par to one. The regression line (Y = 0.6615x – 1.4252) intercepted the Wr axis below the origin, indicating the presence of overdominance. The scattered array points of the parents on and around the regression line revealed the existence of sufficient variability among the parents. The array point of LOK 1 occupied a position closer to origin, indicating that it would likely contribute dominant genes in high frequency; whereas the parents, GW 173, GW 11, and UAS 385, occupied positions at the tail of the regression line, indicating their contribution to the high frequency of recessive genes. Moreover, the rest of the parents occupied intermediate positions on the regression line within the truncated area, indicating an equal distribution of dominant and recessive genes within them (Figure 6).

4. Discussion

4.1. Numerical Approach

Components of the gene effect revealed that most of the characteristics were governed by both additive and dominance gene action across the environments with a greater influence of the dominance gene effect, except for days to 50% heading in E_1, E_2, E_3, and E_4; days to maturity in E_2, E_3, and E_4; grain yield per main spike in E_4. For the number of effective tillers per plant (E_1 and E_3), length of main spike (E_2 and E_3), number of spikelets per main spike (E_3), number of grains per main spike (E_1), and harvest index (E_1), only the dominant component (H_1 and H_2) of the gene effect was significant. The findings also indicated the involvement of both additive and non-additive gene action in the inheritance of yield and related traits in bottle gourd [19,21,22].

The values of the average degree of dominance varied across the environments. The overdominance behavior of interacting alleles was depicted for days to 50% heading (E_1, E_2, E_3, and E_4), days to maturity (E_2, E_3, and E_4), number of effective tillers per plant (E_1 and E_3), length of main spike (E_2 and E_3), number of spikelets per main spike (E_2, E_3, and E_4), number of grains per main spike (E_1, E_2, and E_4), grain yield per main spike (E_2 and E_4), 1000-grain weight (E_1, E_2, E_3, and E_4), and harvest index (E_1). The higher proportions of dominant genes observed in most of the characteristics are in agreement with the earlier findings of [23]. Thus, both the additive and dominant variances were the predominant components governing the expression of yield and its components in accordance with [24]. He also reported that non-additive gene action plays important roles in controlling grain yield under both drought stress and favorable growing environments [25].

An asymmetrical distribution of positive–negative and dominance–recessive genes was depicted for most of the characteristics. However, days to 50% heading (E_2, E_3, and E_4), days to maturity (E_2, E_3, and E_4), length of main spike (E_3), number of spikelets per main spike (E_4), number of grains per main spike (E_1, E_2, and E_4), grain yield per main spike (E_2 and E_4), 1000-grain weight (E_2 and E_4), and harvest index (E_1) exhibited a lack of dominant genes; whereas days to 50% heading (E_1), number of effective tillers per plant (E_1 and E_3), length of main spike (E_2), number of spikelets per main spike (E_2 and E_3), and 1000-grain weight (E_1 and E_3) exhibited an excess of recessive genes. $H_2/4H_1$ indicated a symmetrical distribution of positive and negative dominant genes in parents in all the studied characteristics and the result is in agreement with [26].

The estimates of narrow-sense heritability were low for days to 50% heading (E_1 and E_3), days to maturity (E_1 and E_3), number of effective tillers per plant (E_1 and E_3), length of main spike (E_2 and E_3), number of spikelets per main spike (E_2, E_3, and E_4), number of grains per main spike (E_1, E_2, and E_4), grain yield per main spike (E_2 and E_4), 1000-grain weight (E_1, E_2, E_3, and E_4), and harvest index (E_1), which indicated that these characteristics were under greater influence of the dominant gene effect. The narrow-sense heritability was moderate for days to 50% heading (E_2 and E_4), which confirmed that this characteristic was under the control of both additive and dominant genes. Narrow-sense heritability was generally small and ranged from 0.86 to 66.67%.

4.2. Graphical Approach

In graphical analysis, b was unity for days to 50% heading (E_1 and E_4) and 1000-grain weight (E_3 and E_4), which revealed an absence of digenic interactions for these characteristics in the respective environments. Based on the interception of the regression line on the Wr axis, the degree of dominance was depicted as overdominance for days to 50% heading (E_2) and 1000-grain weight (E_3 and E_4), whereas it was complete dominance for days to 50% heading (E_4). The dispersion of parents around the regression line revealed that parents LOK 1, GW 451, and GW 496 were close to the origin of the coordinate, and accordingly had >75% of dominant genes; parents GW 322 and HI 1544 had 50% dominant genes; while parent GW 366 was far from the origin and, therefore, mostly had recessive genes [26].

Environmental influence is an important factor affecting yield potential, especially temperature and precipitation. Understanding the interactions between environment and genotype, and environmental conditions and nutrition are a prerequisite for the improvement of the wheat crop [27–29].

5. Conclusions

Components of the gene effect revealed that the number of spikelets per main spike in E_2 and E_4, and the number of grains per main spike in E_2 were governed by both additive and dominance gene action across the environments with a greater influence of the dominance gene effect, except for days to 50% heading in E_1, E_2, E_3, and E_4; days to maturity in E_2, E_3, and E_4; grain yield per main spike in E_4. Grain yield per plant was influenced by the overdominance gene effect. Selection may be delayed by the time, dominance will be diluted, and transgressive segregants could be identified.

In graphical analysis, b was unity for days to 50% heading (E_1 and E_4) and 1000-grain weight (E_3 and E_4), which revealed an absence of digenic interactions for these characteristics in the respective environments. The remaining characteristics exhibited a non-random distribution of genes at different loci among the parents or the presence of inter-allelic interaction at different loci. The contradiction between the approaches of the genetic component of variation and Wr-Vr graph analysis could be ascribed to the presence of correlated gene distribution.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/agriculture13010171/s1, Table S1: Crossing pattern in 10 × 10 half-diallel crosses in wheat. Table S2: Nutrient management and irrigation in wheat at Regional Research Station, AAU, Anand.

Author Contributions: Conceptualization, G.R.C. and D.A.P.; data curation, A.D.K.; formal analysis, G.R.C.; investigation, D.A.P.; methodology, G.R.C., D.A.P., A.D.K. and S.K.; software, A.D.K.; supervision, D.A.P. and S.K.; validation, D.A.P. and S.K.; visualization, A.D.K.; writing—original draft, G.R.C.; writing—review and editing, D.A.P., A.D.K. and S.K. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Institutional Review Board Statement: Not applicable.

Data Availability Statement: The original contributions presented in this study are included in the article/Supplementary Material; further inquiries can be directed to the corresponding author/s.

Acknowledgments: We would like to thank Anand Agricultural University for providing resources.

Conflicts of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

References

1. Khodadadi, E.; Aharizad, S.; Sabzi, M.; Khodadadi, E. Studding the genetic control of the bread quality related traits of wheat using Hayman graphical method. *Ann. Biol. Res.* **2012**, *3*, 5446–5449.
2. Khan, M.; Riaz, K.; Khan, A.S. Graphical analysis of spike characters related to grain yield in bread wheat (*Triticum aestivum* L.). *Pak. J. Biol. Sci.* **1999**, *2*, 340–343.
3. Gami, R.A.; Chauhan, B.B.; Patel, R.N. Hayman's diallel analysis for yield and attributing traits in sesame (*Sesamum indicum* L.). *Electron. J. Plant Breed.* **2020**, *11*, 359–366. [CrossRef]
4. Jaiswal, K.K.; Marker, S.; Kumar, B. Combining ability analysis in diallel crosses of wheat (*Triticum aestivum* L.). *Bioscan* **2013**, *8*, 1557–1560.
5. Owusu, E.Y.; Mohammed, H.; Manigben, K.A.; Adjebeng-Danquah, J.; Kusi, F.; Karikari, B.; Sie, E.K. Diallel Analysis and Heritability of Grain Yield, Yield Components, and Maturity Traits in Cowpea (*Vigna unguiculata*(L.) Walp.). *Sci. World J.* **2020**, *2020*, 9390827. [CrossRef]
6. Griffing, B. A general treatment of the use of diallel cross in quantitative inheritance. *Heredity* **1956**, *10*, 31–50. [CrossRef]
7. Hayman, B.I. The theory and analysis of diallel crosses. *Genetics* **1954**, *39*, 789–809. [CrossRef]
8. Patel, A.L.; Kathiria, K.B. Graphical analysis for fruit yield and its component traits in chilli (*Capsicum annuum* L.). *Electron. J. Plant Breed.* **2018**, *9*, 926. [CrossRef]
9. Kearsey, M.J. Biometrical analysis of a random mating population: A comparison of five experimental designs. *Heredity* **1965**, *20*, 205–235. [CrossRef]
10. Jinks, J.L.; Hayman, B.I. The analysis of diallel crosses. *Maize Genet. Newsl.* **1953**, *27*, 48–54.
11. Pooni, H.S.; Jinks, J.L.; Singh, R.K. Methods of analysis and the estimation of the genetic parameters from a diallel set of crosses. *Heredity* **1984**, *52*, 243–253. [CrossRef]
12. Wright, A.J. Diallel designs, analysis and reference populations. *Heredity* **1985**, *54*, 307–311. [CrossRef]
13. Hayman, B.I. The analysis of variation of diallel tables. *Biometrics* **1954**, *10*, 235–244. [CrossRef]
14. Ahuja, S.; Malhotra, P.K.; Bhatia, V.K.; Prasad, R. Statistical Package for Agricultural Research (SPAR 2.0). *J. Ind. Soc. Agril. Statist.* **2008**, *62*, 65–74.
15. Hayman, B.I. The theory and analysis of diallel crosses. III. *Genetics* **1960**, *45*, 155–172. [CrossRef]
16. Jinks, J.L. The analysis of continuous variation in a diallel cross of nicotiana rustica varieties. *Genetics* **1954**, *39*, 767–788. [CrossRef]
17. Jinks, J.L. The F2 and backcross generations from a set of diallel crosses. *Heredity* **1956**, *10*, 1–30. [CrossRef]
18. Mather, K.; Jinks, J.L. *Biometrical Genetics, the Study of Continuous Variation*, 3rd ed.; Chapman and Hall Ltd.: London, UK, 1982.
19. Singh, R.K.; Chaudhary, B.D. *Biometrical Methods in Quantitative Genetic Analysis*; Kalyani Publishers: Ludhiana/Delhi, India, 1985; pp. 262–282.
20. Hayman, B.I. The separation of epistasis from additive and dominance variation in generation means. *Heredity* **1958**, *12*, 371–390. [CrossRef]
21. Kushwaha, M.L.; Ram, H.H. Vr, Wr graphical analysis in bottlegourd. *Veg. Sci.* **1996**, *23*, 162–165.
22. Dubey, S.K.; Maurya, I.B. Studies on heterosis and combining ability in bottlegourd. *Indian J. Genet.* **2003**, *63*, 148–152.
23. Maurya, I.B.; Singh, S.P. Studies on gene action in long fruited bottlegourd. *Crop Res.* **1994**, *8*, 100–104.
24. Dubey, R.K.; Ram, H.H. Graphical analysis (Vr-Wr) and numerical approach for a diallel analysis of yield components in Bottlegourd (*Lagenaria siceraria* (Mol.) Standl.). *Int. J. Plant Breed.* **2007**, *1*, 65–69.
25. Derera, J.; Tongoona, P.; Vivek, B.S.; Laing, M. Gene action controlling grain yield and secondary traits in southern African maize hybrids under drought and non-drought environments. *Euphytica* **2008**, *162*, 411–422. [CrossRef]
26. Al-Naggar, A.M.M.; Atta, M.M.M.; Ahmed, M.A.; Younis, A.S.M. Numerical and Graphical Diallel Analyses of Maize (*Zea mays* L.) Agronomic and Yield Traits under Well Watering and Water Deficit at Silking. *Arch. Curr. Res. Int.* **2016**, *5*, 1–18. [CrossRef]
27. Ljubičić, N.; Popović, V.; Ćirić, V.; Kostić, M.; Ivošević, B.; Popović, D.; Pandžić, M.; El Musafah, S.; Janković, S. Multivariate Interaction Analysis of Winter Wheat Grown in Environment of Limited Soil Conditions. *Plants* **2021**, *10*, 604. [CrossRef]
28. Popović, V.; Ljubičić, N.; Kostić, M.; Radulović, M.; Blagojević, D.; Ugrenović, V.; Popović, D.; Ivošević, B. Genotype × Environment Interaction for Wheat Yield Traits Suitable for Selection in Different Seed Priming Conditions. *Plants* **2020**, *9*, 1804. [CrossRef]
29. Glamočlija, Đ.; Popović, V.; Markoski, M.; Janković, S.; Ikanović, J.; Lončarević, V.; Strugar, V.; Bačkonja, B. Climatic change effect on wheat production "Biotechnology and modern approach in growing and breeding plants". *Smeder. Palanka* **2022**, 212–223.

Disclaimer/Publisher's Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.