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ASSESSMENT OF TWO APPROACHES FOR THE CONSTRUCTION AND ANALYSIS OF DIALLEL CROSS DESIGNS THROUGH INCOMPLETE BLOCK DESIGNS

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ABSTRACT

In this article we compared two approaches: one is Griffing approach for numerical components and other is Hyman's approach for graphical representation of the components through the mating design of Complete Diallel Cross design for p=5 parental lines. Griffing (1956) approach was a numerical approach based on the estimates of combining ability effects. Here use his fourth method. Hayman (1954) approach also have four components namely (i) complete, (ii) partial, (iii) over-dominance and (iv) no dominance. Hayman's approach based on the estimation of parts of variation. We use three mutually orthogonal Latin squares design of order 5 for the construction of mating designs. ANOVA and estimates of combining ability derived and analyzed. We demonstrate the numerical accuracy of the proposed design Griffing method I and Hayman's method by using Turnip data of 5x5 crosses of plant height.

KEY WORDS

Diallel Cross, Incomplete Block Design, Mutually Orthogonal Latin Square, Griffing and Hayman Approach, General Combining Ability, Specific Combining Ability.

1. INTRODUCTION

Latin square designs usually utilized in experiments to control random variation in two directions. For Latin square design it is necessary that the total number of treatments must be equal the total numbers of replications of the treatments. The Graeco Latin squares, balanced incomplete block designs and square lattice designs etc. constructed through Orthogonal Latin squares. If 'p' is a prime positive integer or a power of prime positive integer, then a set of p-1 orthogonal Latin squares of order p can be constructed.

Mating design represents "rules" for arranging different controlled crossings. When the same parents are used as females and males in breeding, the mating design is called diallel. The design is the most commonly used in crop plants to estimate General Combining Ability (GCA), Specific Combining Ability (SCA) and variances.

GCA of a parent is parallel to main effect in a factorial design (either complete or incomplete) while SCA for a mating is parallel to interaction effect. "Method of' Diallel

Crossing" or "Method of' Complete Intercrossing" was firstly presented by Danish geneticist Schmidt (1919).

Sprague and Tatum (1942) initially presented concept of diallel cross for plant breeding.

After that Jinks and Hayman (1953) introduced diallel cross to plants and animal breeders. Numerous researchers worked upon theory and statistical analysis for diallel mating design Jinks and Hayman (1953), Srivastav and Shankar (2007) and Labdi et al. (2015). Makumbi, et al. (2018) frequently employs a variety of diallel crossing techniques in Plant breeding. Furthermore, Hallauer and Filho ((1988) used diallel mating design in various plant species. Griffing (1956) classified CDC system into four types based on the inclusion of parental lines / reciprocal cross. Mudassir et al. (2021) suggested numerous fields, including biology and plant breeding, could benefit from the use of the Diallel Cross designs. Aleksoski (2022) examines the heterotic effect and inheritance in ten F1 crosses of five parent. These crosses follow diallel plan. Mamun et al. (2022) measure the inherited distinction of fiber yield components by diallel analysis.

Zhang and Kang (1997) suggested that Breeders could develop effective breeding and selection techniques by using genetic information from parallel mating designs, such as GCA and SCA. Intended for odd value of ‘p’ parents, Parsad, et al. (2005) used nested balanced incomplete block (NBIB) designs and suggested optimal row–column designs for double cross experiments and for CDC method IV. Mutually orthogonal Latin (MOL) squares designs of order p used by Sharma and Fanta (2009) whereas p represents prime or prime power to obtain optimal incomplete block designs for CDC method II.

In this article, we proposed a diallel cross design through mutually orthogonal latin square design. We establish an optimal as well as efficient design. We assess Griffing method I and full diallel Hayman’s approach. We apply our suggested design to the Turnip data.

The rest of the paper is organized as follows. In section 2, we provide methodology to develop the balanced incomplete block design. In section 3, we apply our proposed design to a real-life example and in section 4, we present the conclusion of this research work.

2. MATERIALS AND METHODS

2.1 Approaches of Diallel Analysis

Diallel analysis has two approaches one is Hayman (1954) approach and other is Griffing(1956) approach. Griffing(1956) could be utilizes for combining ability analysis whereas Hayman(1954) method can be used to understand the action of genes, genetic components and heritability. For complementary data interpretation, Griffing and Hayman data analysis frequently utilized collectively.

2.1.1 Hayman’s Graphical Approach

Jinks and Hayman (1953) initially developed graphical approach that based on the estimation of parts of variation.

2.1.1.1 Variance-Covariance (Vr-Wr) Graph

Within Hayman's method for diallel assessment a graph illustrated through assistance of arrays variances (Vr) as well as covariances among oldsters along with their offspring (Wr), named as Vr-Wr graph. Array describes crosses within which a unique common parent exists.

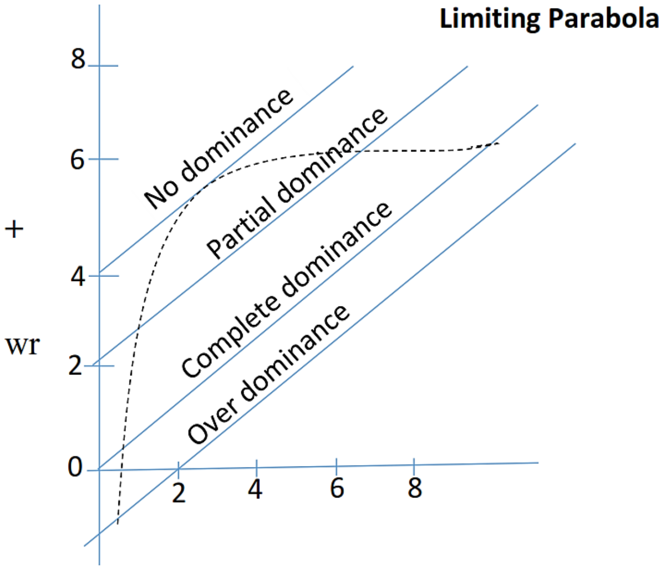

Figure 1: Vr – Wr Graph

Explanation of Vr – Wr Graph

The information related to the average dominance degree is required. It suggested using location of regression line upon Vr-Wr graph

- Complete dominance: While regression line when travels via origin.
- Partial dominance: When it passes above the origin thus cutting Wr axis.
- No dominance: When line travels over origin, it cuts Wr axis and touches the restricting parabola.
- Over dominance: While regression line when travels under origin, it cuts down Vr axis.

2.1.2 Griffing's Numerical Approach

Griffing (1956) developed detailed numerical approach of diallel analysis of all CDC systems in a randomized block design. The numerical approach focused upon its approximation of common and particular combining ability effects and variances. Griffing (1956) suggested four different techniques for diallel analysis based on the material (s) involved in the experimentation:

Table 1
Griffing Methods

Methods	**Materials included in the Experiment of Entries in the Experiment (F_1's + parents)**	**Number**
Method 1	Parents, $F1's$ and Reciprocals	$p2$
Method 2	Parents and $F1's$ (w/o Reciprocals)	$p\ (p\ +\ 1)/2$
Method 3	$F1's$ and Reciprocals (w/o Parents)	p (p – 1)
Method 4	$F1's$ (w/o parents & w/o Reciprocals)	p (p – 1)/2

2.2 Construction of Design Model

For the CDC experimental model 1 for $p = 5$ parents, let us assume a mating design. We obtain designs through considering three MOL squaresL_1 , L_2, and L_3 of semi-standard order 5 and superimposing any one over other two squares.

2.2.1 Development of Design Model

Example 1

Suppose to think the mating design for Complete Diallel Cross testing model 1 designed for P=5 parents. For semi standard forms are regarded as three MOLS L_1, L_2 and L_3 of order 5 and super-impose any one across other two squares, we obtain designs after superimposition of L_1 over the other L_2, and L_3, we achieve different design as specified below:

L_1	**L_2**	**L_3**
0 1 2 3 4	0 1 2 3 4	0 1 2 3 4
1 2 3 4 0	2 3 4 0 1.	3 4 0 1 2
2 3 4 0 1	4 0 1 2 3+-	1 2 3 4 0
3 4 0 1 2	1 2 3 4 0	4 0 1 2 3
4 0 1 2 3	3 4 0 1 2	2 3 4 0 1

The design for CDC experiment method 1 obtained from L_1 and L_2 by taking all cross. The D_1 in Table 2:

Table 2
$D_1$for CDC Experiment Method 1

B_I	**B_2**	**B_3**	**B_4**	**B_5**	**B_6**	**B_7**	**B_8**	**B_9**	**B_{10}**
0×0	1×1	2×2	3×3	4×4	0×0	1×1	2×2	3×3	4×4
1×2	2×3	3×4	4×0	0×1	2×3	3×4	4×0	0×1	1×2
2×4	3×0	4×1	0×2	1×3	4×1	0×2	1×3	2×4	3×0
3×1	4×2	0×3	1×4	2×0	1×4	2×0	3×1	4×2	0×3
4×3	0×4	1×0	2×1	3×2	3×2	4×3	0×4	1×0	2×1

In Table 3 we construct design D_2 for CDC experiment method 3 is acquired from D_1 after deleting the cross $l = m, m = 0{,}1{,}2{,}3{,}4$ The D_2 is given below:

Table 3
D_2 for CDC Experiment Method 2

B_I	**B_2**	**B_3**	**B_4**	**B_5**	**B_6**	**B_7**	**B_8**	**B_9**	**B_{10}**
1×2	2×3	3×4	4×0	0×1	2×3	3×4	4×0	0×1	1×2
2×4	3×0	4×1	0×2	1×3	4×1	0×2	1×3	2×4	3×0
3×1	4×2	0×3	1×4	2×0	1×4	2×0	3×1	4×2	0×3
4×3	0×4	1×0	2×1	3×2	3×2	4×3	0×4	1×0	2×1

Next design D_3 for CDC experiment method 4 acquired from D_2 after deleting the cross, $and\ l > m, m = 0{,}1{,}2{,}3{,}4$. The D_3 gave in Table 4:

Table 4
$D_3$for CDC Experiment Method 4

B_I	**B_2**	**B_3**	**B_4**	**B_5**	**B_6**	**B_7**	**B_8**	**B_9**	**B_{10}**
1×2	2×3	3×4	0×2	0×1	2×3	3×4	1×3	0×1	1×2
2×4	0×4	0×3	1×4	1×3	1×4	0×2	0×4	2×4	0×3

2.3 Model and Estimation

We followed methodology of Sharma and Fanta (2009). On behalf of the study of facts taken from design D_1, D_2 and D_3 there are two-step measures for estimate GCA, SCA effect and RCA effects with some variation introduced by Singh and Hinkelmann (1998).

The first step is to understand the proposed design to approximate Cross effect, say, $\tau = (\tau_{00}, \tau_{01}, \ldots, \tau_{(p-1)(p-1)})'$ for D_1

$$y = \mu 1 + X\tau + D\beta + e, \tag{1}$$

where y is $n \times 1$ vector of observations, 1 is $n \times 1$vector of ones, X is $n \times v$ treatments design matrix and blocks design matrix D is $n \times b$, which is, $(h, u)^{th}$ element of X is 1 if h^{th} observation relates to u^{th} cross, and is zero else ($h = 1, \dots, n; u = 1, \dots, v$; and $l = 1, \dots, b$);, μ shows general mean, τ a $v \times 1$ represents treatment parameters vector, block parameters vector β is $(b \times 1)$ and residuals *vector* e is an $n \times 1$. This supposed that β is indeed a constant vector and e follow normal distribution with $E(e) = 0$, and $V(e) = \sigma^2 I$ and $Cov(\beta, e) = 0$, for which I will be an identity matrix of corresponding order.

Rao (1973) used least square methodology for the analysis of a proposed design corresponds to reduced normal model equations for the model (1)

$$C_{d1} \tau = Q_{d1}, \tag{2}$$

where $C_{d1} = r^{\delta} - Nk^{-\delta} N'$ and $Q_{d1} = (Q_{1d1} \dots Q_{vd1})' = T - Nk^{-\delta} B$

In Eq (2), the terminology r^{δ} and k^{δ} be the diagonal matrices of order v x v and b x b with elements 2 and p in the diagonal, correspondingly to D_1. $N = X'D$ is $v \times b$ incidence matrix to design D_1, $T = X'Y$ and $B = D'Y$ are the vector of cross totals with block totals of order $v \times 1$ and $b \times 1$ correspondingly for designs D_1. So answer to (2) known via

$$\hat{\tau} = C_{d1}^{-} Q_{d1} , \tag{3}$$

where $C_{d1}^{-}$is the G-inv of C_{d1} among assets $CC\neg C = C$. The S.S appropriate to cross be $\acute{Q}_{d1} C_{d1}^{-} Q_{d1}$, with d.f. = Rank ($C_{d1}$) for designs D_1 and expectation and variance Q_{d1}

$$E\,(Q_{d1}) = C_{d1}\tau \text{ and } V(Q_{d1}) = \sigma^2 C_{d1} \tag{4}$$

Currently we shall use the equation (4) to evaluate the genetic parameters in planned designs.

2.3.1 Estimation of GCA, SCA and RCA in design D_1.

Now in second step, utilize the aspect that the crosses effect expressed in terms of GCA, SCA and RCA. Hence τ_{lm} stated as

$$\tau_{lm} = g_l + g_m + s_{lm} + r_{lm}, \tag{5}$$

where gi (gj) is GCA for the $l^{th}(m^{th})$ parent, $s_{lm} (s_{lm} = s_{ml})$ is SCA for cross among $l^{th}$and m^{th}parent and r_{lm} be RCA $(r_{lm} = -r_{ml})$ used for cross involving the $l^{th}$and m^{th}parents, where $(l, m = 0, 1, \dots, p - 1)$for design D_1

$$\tau = Zg + s + r, \tag{6}$$

where as $Z = (Z_{ul})(u = 1, 2, \dots, v; l = 1, 2, \dots, p)$ is cross and gca relation matrix. Z_{ul} = 2 if the u^{th} cross contains both parent l, Z_{ul} = 1 if the u^{th} cross contains only single parent *l, and* Z_{ul} = 0 else.

Below techniques used in Kempthorne and Curnow (1962), model (6) shown as

$$E\,(Q_{d1}) = C_{d1} Z_g + C_{d1} s + C_{d1} r \,, V(Q_{d1}) = \sigma^2 C_{d1} \tag{7}$$

As the matrix C_{d1} is singular, we apply Least Square due to Rao (1973). Estimators for general combining ability g obtained by.

$$\hat{g} = (Z'C_{d1}C_{d1}^{-}C_{d1}Z)^{-}Z'Q_{d1} = (Z'C_{d1}Z)^{-}Z'C_{d1}\hat{\tau} = P_1\hat{\tau}, \quad (8)$$

where $P_1 = (Z'C_{d1}Z)^{-}Z'C_{d1}$ with

$$(Z'C_{d1}Z) = 2r\,p\left[I_p - \frac{1}{p}1_p 1_p'\right] \quad (9)$$

and generalized inverse of $(Z'C_{d1}Z)$ is as given below.

$$(Z'C_{d1}Z)^{-} = \frac{1}{2rp}I_p,$$

where, for positive integers t, I_t is a t × t identity matrix, 1_t is t×1 vector with all elements unity.

$$\text{With } V(\hat{g}) = P_1 C_{d1}^{-} P_1' \sigma^2 = \frac{1}{2rp} I_p \sigma^2 \quad (10)$$

This shows that the all-uncomplicated compare amid G.ca property through design d_1 is predictable along the same σ. Thus, the design d_1 is VB.

The SS because of GCA given by

$$SS_{gca} = Q_{d1}' Z(Z'C_{d1}Z)^{-}Z'Q_{d1} \quad (11)$$

Since estimator of τ contain the reciprocal effects of reciprocal crosses that exist with it in r blocks. The effects of reciprocal crosses eliminate for getting the correct estimate of s. So, firstly estimate effects of reciprocal crosses. The contrast $(\tau_{lm} - \tau_{ml})$ $(l, m = 0,1,\ldots, p-1)$is estimable and provides the estimate of reciprocal crosses effects. So,

$$\hat{r}_{lm} = \hat{\tau}_{lm} - \hat{\tau}_{ml}$$

Because $r_{lm} = -r_{ml}$, then $\hat{\tau}_{lm} - \hat{\tau}_{ml} = 2\hat{r}_{lm}$ from equation (5), in matrix representation, the overhead expression may be expressed as below

$$\frac{1}{2}S\hat{\tau} = \hat{r} \quad (12)$$

where S = (S_{ul}) is a v×v matrix among row along with column in index into couples $(l \times m)$ where l, $m = 0,1,2,\ldots, p-1$ or $(l \times m, l \times m)$ entrance of S is 2 if $(l \times m, l \times m) = (l \times l, l \times l)$ otherwise 0. If $(l \times m, l \times m) = (l \times m, l \times m)$ then $(l \times m, l \times m)$ entry of S is 1 and if $(l \times m, l \times m) = (m \times l, l \times m)$ then $(m \times l, l \times m)$ is -1 otherwise 0. Currently substitute to estimator of g and r in the equations' (6) and applying simple calculus. Then obtain $\hat{s}$

$$(Z'C_{d1}C_{d1}^{-}C_{d1}Z)^{-}Z'Q_{d1} = (Z'C_{d1}Z)^{-}Z'C_{d1}\hat{\tau} = P_1\hat{\tau}$$

$$\hat{\tau} = C_{d1}^{-}Q_{d1}\ ,$$

$$\hat{s} = C_{d1}^{-}Q_{d1} - Z\,(Z'C_{d1}Z)^{-}Z'Q_{d1} - \frac{1}{2}\,SC_{d1}^{-}Q_{d1}$$

$$\hat{s} = \left\{C_{d1}^{-}C_{d1} - Z(Z'C_{d1}Z)^{-}Z'C_{d1} - \frac{1}{2}SC_{d1}^{-}C_{d1}\right\}\hat{\tau} = P_2\hat{\tau}. \quad (13)$$

where

$$P_2 = \left\{C_{d1}^{-}C_{d1} - Z(Z'C_{d1}Z)^{-}Z'C_{d1} - \frac{1}{2}SC_{d1}^{-}C_{d1}\right\}$$

and

$$V(\hat{s}) = P_2 C_{d1}^{-} P_2' \sigma^2.$$

The SS(sca) is obtain through

$$SS(sca) = \frac{1}{2}\sum_{l\neq m} s_{lm} Q_{ld1}. \quad (14)$$

Now recalling (12), we obtain

$$\hat{r} = \left(\frac{1}{2}SC_{d1}^{-}Q_{d1}\right)$$
$$= \left(\frac{1}{2}SC_{d1}^{-}C_{d1}\right)\hat{\tau} \Rightarrow \hat{r} = P_3\hat{\tau}.$$

where $P_3 = \left(\frac{1}{2}SC_{d1}^{-}C_{d1}\right)$

$$V(\hat{r}) = P_3 C_{d1}^{-} P_3' \sigma^2.$$

The SS(rca) is obtain through

$$SS\ (\text{reciprocal effects}) = \frac{1}{2}\sum_{l\neq m} \hat{r}_{lm} Q_{ld1}\ . \quad (15)$$

Since $P_1 1_v = P_2 1_v = P_3 1_v = 0$ and rank $(P_1) = p - 1$and rank (P_2)= rank $(P_3) = p\,(p-1)/2$, it followed $\hat{g}$, $\hat{s}$ and $\hat{r}$ are signify through treatment contrasts which contains (p−1) degrees of freedom and p (p−1)/2 degrees of freedom correspondingly. The future design d1 allows for GCA, SCA and RCA, theses estimated independently. The ANOVA given in Table 5:

Table 5
The Analysis of Variance of D_1 Method 1

S.O.V	DF	SS
Blocks	2p-1	$B'B/p-G^2/2p^2$
Crosses	$Rank(C_{d1})=p^2-1$	$Q_{d1}'C_{d1}^{-}Q_{d1}$
GCA	$Rank(Z'C_{d1}Z)=p-1$	$Q_{d1}'Z(Z'C_{d1}Z)^{-}Z'Q_{d1}$
SCA	$Rank(p_2)=p(p-1)/2$	$Q_{d1}'P_2Q_{d1}$
Reciprocal Effect	$Rank(p_2)=p(p-1)/2$	$Q_{d1}'P_3Q_{d1}$
Residuals	By Subtraction	By Subtraction
Total	n-1	$y'y-G^2/2p^2$

2.4 Efficiency Factor (EF) and Optimality

2.4.1 Efficiency Factor

If one adopts IBD by $r = 2$, every block have altogether $\frac{p(p-1)}{2}$ crosses. Efficiency factor of design D_1 (obtain by MOLS) to RCBD, with the assumption of equal number of crosses and of equal intra-block variances, is given below,

$$E = \frac{\frac{1}{P(P+1)}}{1/P(P+1)} = 1,$$

$$E = 1$$

Therefore, the proposed design D_1 is best in logic of Kempthorne (1956).

2.4.2 Optimality

Here C matrix for the designs D_1 is $(Z'C_{d1}Z)$ that is entirely symmetric. The trace of design D_1 is 2rp (p−1) which is equal to 2(n−b) i.e. 2rp (p−1).

3. ANALYSIS

The plant height data of Turnip cross varieties taken from Sincik, et al. (2014). Each cross replicate two times. 5 × 5 DC were evaluated through BIBD in 2 replications. The layout with observations given in Table 6.

Table 6
The D1 of Griffing Method 1 Model 1 of Turnip Cross (Plant Height)

B_1	B_2	B_3	B_4	B_5	B_6	B_7	B_8	B_9	B_{10}
0×0 (122.7)	1×1 (124.3)	2×2 (129.3)	3×3 (132)	4×4 (126.3)	0×0 (151.3)	1×1 (140.01)	2×2 (156.3)	3×3 (173.7)	4×4 (156.0)
1×2 (143.7)	2×3 (152.7)	3×4 (144)	4×0 (122.01)	0×1 (134)	2×3 (179)	3×4 (176)	4×0 (172.7)	0×1 (168)	1×2 (174.3)
2×4 (141.3)	3×0 140.3	4×1 (122.3)	0×2 (156.3)	1×3 (131.7)	4×1 (164.7)	0×2 (176.3)	1×3 (158.7)	2×4 (173)	3×0 (177.3)
3×1 (132)	4×2 158.7	0×3 (150.3)	1×4 (136.7)	2×0 (154.7)	1×4 (175.7)	2×0 (180.3)	3×1 (171.3)	4×2 (176.7)	0×3 (178.0)
4×3 (142)	0×4 143.3	1×0 (98.7)	2×1 (134)	3×2 (172)	3×2 (174.3)	4×3 (181.7)	0×4 (177.3)	1×0 (176.7)	2×1 (177.7)

These show the Vector of treatment total and blocks total using Griffing method 1.

T = (274, 302, 332.6, 328.3, 320.6, 275.4, 264.31, 318, 290.4, 312.4, 335, 311.7, 285.6, 331.7, 314.3, 317.6, 303.3, 346.3, 305.7, 320, 294.71, 287, 335.4, 323.7, 282.3)'

B = (681.7, 719.3, 644.6, 681.01, 718.7, 845, 854.31, 836.3, 868.1, 863.3)'

Table 7
The ANOVA of D_1 of Griffing Method 1 Model 1 of TURNIP Cross (Plant Height)

S.O.V	DF	SS	MS	F_{cal}	F_{cri} $\alpha = 0.05$
Blocks	9	14417.13	1601.903	18.62768**	2.54
Crosses	24	5832.126	243.0053	2.825778**	1.95
GCA	4	2277.398	569.3495	6.620661**	3.01
SCA	10	354.2994	35.42994	0.411996^{ns}	2.49
Reciprocal Effect	10	1423.064	142.3064	1.654805^{ns}	2.49
Residuals	16	1375.93	85.99588		
Total	49	21625.19			

Table 8
The Estimates of GCA and their S.E of D1 of Griffing Method 1 Model of Turnip Cross (Plant Height)

Parent	Estimates of (GCA)	S.E
1	-1.5359	1.854
2	-7.8054	1.854
3	5.5636	1.854
4	4.3886	1.854
5	-0.6109	1.854

Table 9
The Estimates of SCA and their S.E on of D_1 of Griffing method 1 Model 1 of Turnip Cross (Plant Height)

SCA	E(SCA)	S.E	SCA	E(SCA)	S.E
S_{01}	-4.6101	4.9070	S_{13}	-5.7786	4.9070
S_{02}	11.0094	4.9070	S_{14}	10.2694	4.9070
S_{03}	4.4114	4.9070	S_{23}	3.9219	4.9070
S_{04}	0.2339	4.9070	S_{24}	-2.0686	4.9070
S_{12}	6.799	4.9070	S_{34}	9.1277	4.9070

Table 10
RCA and their S.E on D_1 of Griffing Method 1
Model 1 of Turnip Cross (Plant Height)

RCA	E(RCA)	S.E	RCA	E(RCA)	S.E
R_{01}	2.2250	2.7820	R_{13}	-5.7900	2.7820
R_{02}	3.2245	2.7820	R_{14}	5.7495	2.7820
R_{03}	6.4795	2.7820	R_{23}	-3.0295	2.7820
R_{04}	3.2685	2.7820	R_{24}	-3.3305	2.7820
R_{12}	0.3155	2.7820	R_{34}	0.2572	2.7820

The inbred and their hybrids were tested, and performance of all characters was investigated. Analysis of variance of combining ability indicated that effects of general combining ability (GCA) were found to be significant for plant height (Table 7). Dominance effects, tested by SCA, were insignificant for plant height (Table 7). Analysis of variance for reciprocal effects (R) showed that insignificant effects were found (Table 7). The estimates of the GCA effects for the parents indicated that Parent 3 was a good general combiner (Table 8). The highest SCA positive value for plant height was found at P1 × P3 (11.0094) (Table 9). Meanwhile the highest positive reciprocal effect (R) value was observed in reciprocal hybrid, P4 × P1 (6.4795) (Table 10).

3.1 Vr-WrGraph

Mean squares from diallel analysis for plant height of Turnip cross. (Hayman's Model I Method 1).

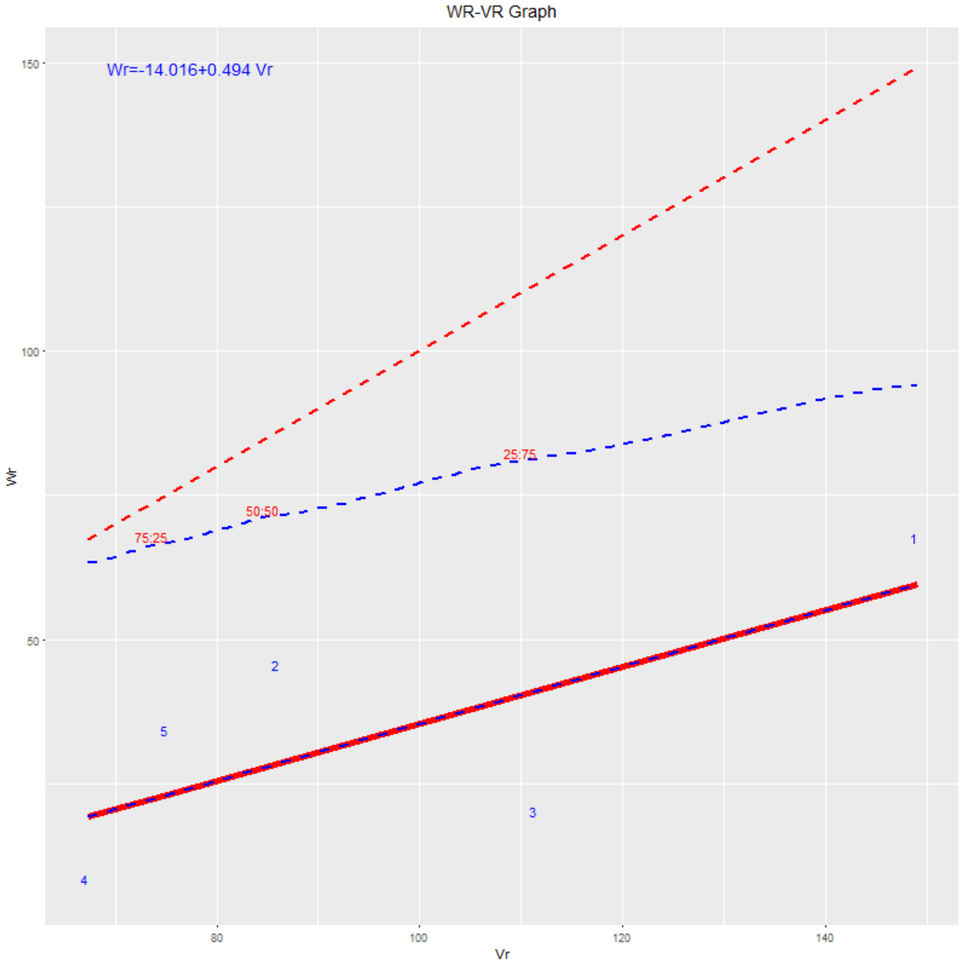

Figure 2: Plant Height

The result of graphical analysis, which carried out for the characters, revealed partial dominance for plant height,

The full diallel hayman analysis exposed that the regression line intercepted Wr axis above the point of origin showing partial dominance. The regression line on the graph of Wr -Vr has a value of intercept a = 14.016, so cut the Wr axis above the origin (0). Cutting point at that position indicates a partially dominant gene action (Figure 2). The parents 1, 4 were nearby to the point of origin signifying leading genes in these parents. However, the parents 3, 4 were located below the regression line suggesting complementary type of gene interaction played role in expression of this trait in above parents. Since all the parents are well scatter, therefore they considered diverse.

4. CONCLUSION

We presented the methodology for the construction of Griffing's full diallel cross design 1 through mutually orthogonal Latin square design. The constructed design 1 is efficient and optimal design as well. From Griffing's numerical approach, parents used in this study exhibited positive GCA effects for parent 3 of turnip cross. Therefore, they considered as promising parents in the production of F1 hybrids and in further breeding studies. From Hayman's analysis, the order of dominance is also reflected in the relationship of covariance (Wr) and variance (Vr) of image. The more close to the zero point the parents of these genes the more dominant, whereas farther from the zero point is the parents containing the most widely recessive genes.

5. CONFLICT OF INTEREST

The authors declare that they have no conflicts of interest.

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