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Research Article

Some New Construction of Diallel Crosses

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Abstract
One of the fundamental goals of crop genetics research is the development of improved crop varieties through the analysis of genetic architecture, particularly when multiple crop strains are involved. Diallel cross experiments, involving the crossing of various inbred parental lines, are commonly used to evaluate these lines' combining ability and identify superior genetic combinations. This study focuses on constructing and applying Balanced Incomplete Block Designs (BIBDs) and Partial Diallel Cross (PDC) designs to optimize genetic evaluation strategies. BIBDs constructed using the method of cyclic shifts will serve as the basis for developing complete diallel cross designs. Additionally, these designs will facilitate control versus test comparisons among crop lines. The study employs cyclic regular graph designs derived through cyclic shifts to construct partial diallel crosses. To estimate General Combining Ability (GCA) with precision, the study proposes using two associated Partial Balanced Incomplete Block Designs (PBIBDs). These PBIBDs will support contrasts such as gi−gjg_i-g_jgi−gj, ensuring that only two types of variances are associated with such estimates. The methodological framework outlined in this study aims to enhance the efficiency and accuracy of genetic investigations, ultimately contributing to the development of high-yielding and resilient crop varieties.

Keywords: Diallel crosses, Partial Diallel Cross, Balanced Incomplete Block Designs, contrasts, variations, cyclic shifts

Introduction
The field of statistics addresses uncertainty and random variations, forming a foundational pillar of scientific inquiry across diverse disciplines (Romero et al., 2011). Rooted in mathematics and probability theory, the domain of Mathematical Statistics has evolved into an applied science critical for analyzing uncertainty in data collection and interpretation, particularly within fields such as biology, agriculture, and engineering (Skrypnyk and Rybak, 2024). At its core, statistical science is inherently interdisciplinary, serving as a bridge between theoretical models and practical applications.

Sir Ronald Aylmer Fisher is widely regarded as the pioneer of modern statistical techniques, particularly through his early contributions to agricultural research in the 1930s (Yates, 1964). Since then, statistics has grown to influence virtually all scientific disciplines, including genetics, where experimental investigations are predominantly driven by statistical design and analysis. In crop genetics, the principal aim is to develop improved varieties through an understanding of genetic architecture (Bailey-Serres et al., 2019). This often involves diallel crosses among multiple inbred lines to study their combining abilities and genetic potential.

The term *diallel*, derived from Greek, refers to all possible pairwise crosses among a given set of genotypes. According to Hyman (1954a,b), diallel crosses involve clones, homozygous lines, and other genetic forms to systematically assess genotype interactions. These crosses are essential for analyzing the genetic components of quantitative traits and estimating General Combining Ability (GCA) and Specific Combining Ability (SCA) among the parental lines. First introduced by Sprague and Tatum (1942), GCA refers to the average performance of a line across combinations, while SCA captures deviations of specific combinations from the expected GCA effects. Diallel crosses offer balanced testing frameworks and are particularly useful for evaluating early-generation performance and parental selection.

As the number of parental lines increases, conducting a full diallel cross becomes impractical. In such cases, Partial Diallel Cross (PDC) designs are preferred, which involve a subset of all possible crosses while maintaining a balanced representation of each parent. Kempthorne and Curnow (1961) highlighted the advantages of PDC designs, including more accurate estimation of GCA variances, broader parental selection, and greater potential for genetic gains. Studies by Sharma (1998) and Singh and Hinkelmann (1995) employed cyclic and incomplete block designs to efficiently manage large-scale crossing schemes, thereby increasing the feasibility and robustness of genetic investigations.

Diallel hybrid designs are essential tools for exploring genetic properties and conducting reproduction studies in seed plants. However, conventional designs often assume a linear framework and may struggle with large numbers of genotypes or missing cross data. Environmental interactions and random blocking further complicate analysis, particularly when no aggregate results are available across intercrosses. This necessitates the development of more efficient and structured designs to overcome these limitations.

The study aims to enhance diallel and partial diallel crossing designs using principles from combinatorial design theory, particularly Balanced Incomplete Block Designs (BIBD) and Partial BIBDs (PBIBD). The specific objectives are:

- To construct BIBDs using cyclic shift methods for the development of complete diallel cross designs.
- To apply BIBD-based diallel designs for control versus test comparisons among genotypes.
- To utilize cyclic regular graph designs for constructing partial diallel cross schemes.
- To develop partial diallel cross plans that allow efficient estimation of GCA using two-associate PBIBDs, ensuring controlled variance structures in contrasts such as gi−gjg_i - g_jgi−gj.

Methodology

Method of Cyclic Shifts

In this study, method of cyclic shifts (Rule I) is used to construct BIBDs and PBIBDs with two associate scheme. Method of Cyclic Shifts was introduced by Iqbal (1991). Itis used to construct several types of designs such as BIBDs, PBIBDs, circular polygonal designs, neighbor designs and Balanced RMDs, etc. Method of cyclic shifts (Rule I)is explained here only for the construction of BIBDs and PBIBDs with two associate scheme.

Rule I: Let $S_j = [q_{j1}, q_{j2}, \ldots, q_{j(k-1)}]$ be a set of shifts where $1 \le q_{j1}, q_{j2}, \ldots, q_{j(k-1)} \le v-1$, then initial blocks of design will be $I_j = (0, q_{j1}, q_{j1}+q_{j2}, \ldots, (q_{j1}+q_{j2}+ \ldots + q_{j(k-1)}))$ mod v. A design is balanced incomplete block if each element of S_j^* along with its complement contains all elements 1, 2, …,v-1 equally often, say, λ times. Where $S_j^* = [q_{j1}, q_{j2}, \ldots, q_{j(k-1)}, (q_{j1}+q_{j2}), (q_{j2}+q_{j3}), \ldots, (q_{j(k-2)}+q_{j(k-1)}), (q_{j1}+q_{j2}+q_{j3}), (q_{j2}+q_{j3}+q_{j4}), \ldots, (q_{j(k-3)}+q_{j(k-2)}+q_{j(k-1)}), \ldots, (q_{j1}+q_{j2}+ \ldots + q_{j(k-1)})]$, here complement of q_i is $v-q_i$. A design is PBIBDwith two associate scheme if each element of S_j^* along with its complement contains all elements (1, 2, …,v-1)λ_1 and λ_2 times where $\lambda_2 = \lambda_1+1$.

Example 1. Following BIBD is constructed from the initial block (0,1,3,5,6,7,8,9,10) obtained from set of shifts [1,2,2,1,1,1,1,1] for v =13 and k = 9.

B1	B2	B3	B4	B5	B6	B7	B8	B9	B10	B11	B12	B13
0	1	2	3	4	5	6	7	8	9	10	11	12
1	2	3	4	5	6	7	8	9	10	11	12	0
3	4	5	6	7	8	9	10	11	12	0	1	2
5	6	7	8	9	10	11	12	0	1	2	3	4
6	7	8	9	10	11	12	0	1	2	3	4	5
7	8	9	10	11	12	0	1	2	3	4	5	6
8	9	10	11	12	0	1	2	3	4	5	6	7
9	10	11	12	0	1	2	3	4	5	6	7	8
10	11	12	0	1	2	3	4	5	6	7	8	9

Example 2. Following PBIBD is constructed is for v = 12 and k = 4 from the initial block (0,2,5,6) obtained from set of shifts.

B1	B2	B3	B4	B5	B6	B7	B8	B9	B10	B11	B12
0	1	2	3	4	5	6	7	8	9	10	11
2	3	4	5	6	7	8	9	10	11	0	1
5	6	7	8	9	10	11	0	1	2	3	4
6	7	8	9	10	11	0	1	2	3	4	5

Construction of BIBD from given symmetric BIBD

The following three ways are available in literature to obtain a new BIBD from a given symmetric BIBD.

- Residual design
- Derived design
- Complementary design

Residual design

Residual design is another BIB design that can be derived from a symmetric BIB design in the following manner.

- Select a block from the original design.
- Remove it and all of its treatments from the remaining blocks.

- All new blocks have size k-λ.
- Each treatment appears r = k blocks, and any pair of remaining treatments will still appear together in λ blocks.
- The new design then has v-k treatments and b-1 blocks.

Example 3. Residual design is obtained from the symmetric design presented as example 1 by deleting its 8th column.

B1	B2	B3	B4	B5	B6	B7	B8	B9	B10	B11	B12
5	6	5	6	5	5	6	5	9	5	5	5
6	9	9	9	9	6	9	9	5	6	6	6
9	11	11	11	11	11	11	11	6	11	11	9

After labeling the remaining treatments 5, 6, 9, and 11 as 0, 1, 2, and 3, respectively, the following is the resultant BIB design (residual design) for v = 4 and k = 3.

B1	B2	B3	B4	B5	B6	B7	B8	B9	B10	B11	B12
0	1	0	1	0	0	1	0	2	0	0	0
1	2	2	2	2	1	2	2	0	1	1	1
2	3	3	3	3	3	3	3	1	3	3	2

Derived design

Derived design is another BIB design derived from a symmetric BIB design in the following manner.

- Select a block from the original design.
- Remove it and all the treatments from the remaining blocks that do not appear in the deleted block.
- All new blocks have size λ.
- The new design then has k treatments and b-1 blocks.

Example 4. The derived design is obtained from the symmetric design presented in example 1 by deleting its 8th column.

B1	B2	B3	B4	B5	B6	B7	B8	B9	B10	B11	B12
0	1	2	3	4	8	7	8	10	10	12	12
1	2	3	4	7	10	12	0	12	0	1	0
3	4	7	8	10	12	0	1	1	2	3	2
7	7	8	10	12	0	1	2	2	3	4	4
8	8	10	12	0	1	2	3	3	4	7	7
10	10	12	0	1	2	3	4	4	7	8	8

Relabeling the remaining treatments 0, 1, 2, 3, 4, 7, 8, 10, 12 as 0, 1, 2, 3, 4, 5, 6, 7 and 8 respectively, following is the resultant BIB design (Derived design) for v = 9 and k = 6.

B1	B2	B3	B4	B5	B6	B7	B8	B9	B10	B11	B12
0	1	2	3	4	6	5	6	7	7	8	8
1	2	3	4	5	7	8	0	8	0	1	0
3	4	5	6	7	8	0	1	1	2	3	2
5	5	6	7	8	0	1	2	2	3	4	4
6	6	7	8	0	1	2	3	3	4	5	5
7	7	8	0	1	2	3	4	4	5	6	6

Complementary Design

Complementary design is another BIBD derived from BIB design in the following manner.

- Replace treatments in a block by those that do not occur in that block. All blocks will be replaced in the same way.
- All new blocks have size *v*-k.
- The new design then has *v* treatments and b blocks.

Example 5. Complementary design is obtained from the symmetric BIBD given in example 3.1.1 for v =13 and k = 4.

B1	B2	B3	B4	B5	B6	B7	B8	B9	B10	B11	B12	B13
2	0	0	1	2	3	4	5	6	0	1	0	1
4	3	1	2	3	4	5	6	7	7	8	2	3
11	5	4	5	6	7	8	9	10	8	9	9	10
12	12	6	7	8	9	10	11	12	11	12	10	11

Results

Hayman (1954, 1958) developed diallel analysis. The study of diallel crosses has received considerable attention in several plant breeding programs because it fulfills certain specific needs of plant breeders.

A diallel cross is a mating design used by plant and animal breeders. Two methods for the construction of diallel crosses designs, (i) row-wise Construction and (ii) column-wise construction, are described.

Row wise Construction of Diallel crosses Design

The method is illustrated by the following PBIBD example. The following PBIBD is generated for v = 16 and k = 3 in 16 blocks using the initial block (0,1,6).

Blocks															
B_1	**B_2**	**B_3**	**B_4**	**B_5**	**B_6**	**B_7**	**B_8**	**B_9**	**B_{10}**	**B_{11}**	**B_{12}**	**B_{13}**	**B_{14}**	**B_{15}**	**B_{16}**
0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	0
6	7	8	9	10	11	12	13	14	15	0	1	2	3	4	5

The diallel design's interaction is given below. To create the interaction across the block, horizontal (row) interactions were constructed.

(0×1) (0×2) (0×3) (0×4) (0×5) (0×6) (0×7) (0×8) (0×9) (0×10) (0×11) (0×12) (0×13) (0×14) (0×15) (1×2) (1×3) (1×4) (1×5) (1×6) (1×7) (1×8) (1×9) (1×10) (1×11) (1×12) (1×13) (1×14) (1×15) (2×3) (2×4) (2×5) (2×6) (2×7) (2×8) (2×9) (2×10) (2×11) (2×12) (2×13) (2×14) (2×15) (3×4) (3×5) (3×6) (3×7) (3×8) (3×9) (3×10) (3×11) (3×12) (3×13) (3×14) (3×15) (4×5) (4×6) (4×7) (4×8) (4×9) (4×10) (4×11) (4×12) (4×13) (4×14) (4×15) (5×6) (5×7) (5×8) (5×9) (5×10) (5×11) (5×12) (5×13) (5×14) (5×15) (6×7) (6×8) (6×9) (6×10) (6×11) (6×12) (6×13) (6×14) (6×15) (7×8) (7×9) (7×10) (7×11) (7×12) (7×13) (7×14) (7×15) (8×9) (8×10) (8×11) (8×12) (8×13) (8×14) (8×15) (9×10) (9×11) (9×12) (9×13) (9×14) (9×15) (10×11) (10×12) (10×13) (10×14) (10×15) (11×12) (11×13) (11×14) (11×15) (12×13) (12×14) (12×15) (13×14) (13×15) (14×15)

(1×2) (1×3) (1×4) (1×5) (1×6) (1×7) (1×8) (1×9) (1×10) (1×11) (1×12) (1×13) (1×14) (1×15) (1×0) (2×3) (2×4) (2×5) (2×6) (2×7) (2×8) (2×9) (2×10) (2×11) (2×12) (2×13) (2×14) (2×15) (2×0) (3×4) (3×5) (3×6) (3×7) (3×8) (3×9) (3×10) (3×11) (3×12) (3×13) (3×14) (3×15) (3×0) (4×5) (4×6) (4×7) (4×8) (4×9) (4×10) (4×11) (4×12) (4×13) (4×14) (4×15) (4×0) (5×6) (5×7) (5×8) (5×9) (5×10) (5×11) (5×12) (5×13) (5×14) (5×15) (5×0) (6×7) (6×8) (6×9) (6×10) (6×11) (6×12) (6×13) (6×14) (6×15) (6×0) (7×8) (7×9) (7×10) (7×11) (7×12) (7×13) (7×14) (7×15) (7×0) (8×9) (8×10) (8×11) (8×12) (8×13) (8×14) (8×15) (8×0) (9×10) (9×11) (9×12) (9×13) (9×14) (9×15) (9×0) (10×11) (10×12) (10×13) (10×14) (10×15) (10×0) (11×12) (11×13) (11×14) (11×15) (11×0) (12×13) (12×14) (12×15) (12×0) (13×14) (13×15) (13×0) (14×15) (14×0)

(6×7) (6×8) (6×9) (6×10) (6×11) (6×12) (6×13) (6×14) (6×15) (6×0) (6×1) (6×2) (6×3) (6×4) (6×5) (7×8) (7×9) (7×10) (7×11) (7×12) (7×13) (7×14) (7×15) (7×0) (7×1) (7×2) (7×3) (7×4) (7×5) (8×9) (8×10) (8×11) (8×12) (8×13) (8×14) (8×15) (8×0) (8×1) (8×2) (8×3) (8×4) (8×5) (9×10) (9×11) (9×12) (9×13) (9×14) (9×15) (9×0) (9×1) (9×2) (9×3) (9×4) (9×5) (10×11) (10×12) (10×13) (10×14) (10×15) (10×0) (10×1) (10×2) (10×3) (10×4) (10×5) (11×12) (11×13) (11×14) (11×15) (11×0) (11×1) (11×2) (11×3) (11×4) (11×5) (12×13) (12×14) (12×15) (12×0) (12×1) (12×2) (12×3) (12×4) (12×5) (13×14) (13×15) (13×0) (13×1) (13×2) (13×3) (13×4) (13×5) (14×15) (14×0) (14×1) (14×2) (14×3) (14×4) (14×5) (15×0) (15×1) (15×2) (15×3) (15×4) (15×5) (0×1) (0×2) (0×3) (0×4) (0×5) (1×2) (1×3) (1×4) (1×5) (2×3) (2×4) (2×5) (3×4) (3×5) (4×5)

Column wise construction of Diallel crosses Design

The interaction of the diallel design is given as under. In order to create the interaction across the block, column-wise interaction was constructed.

(0×1) (0×6) (1×6) (1×2) (1×7) (2×7) (2×3) (2×8) (3×8) (3×4) (3×9) (4×9) (4×5) (4×10) (5×10) (5×6) (5×11) (6×11) (6×7) (6×12) (7×12) (7×8) (7×13) (8×13) (8×9) (8×14) (9×14) (9×10) (9×15) (10×15) (10×11) (10×0) (11×0) (11×12) (11×1) (12×1) (12×13) (12×2) (13×2) (13×14) (13×3) (14×3) (14×15) (14×4) (15×4) (15×0) (15×5) (0×5)

Blocks															
B_1	**B_2**	**B_3**	**B_4**	**B_5**	**B_6**	**B_7**	**B_8**	**B_9**	**B_{10}**	**B_{11}**	**B_{12}**	**B_{13}**	**B_{14}**	**B_{15}**	**B_{16}**
0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	0
6	7	8	9	10	11	12	13	14	15	0	1	2	3	4	5

Partial Diallel Crosses

Partial Diallel Cross design is used in Plant and Breeding in order to explore the genetic characteristics. The partial diallel cross is considered a significant alternative to a diallel cross, which is a mating design often used by plant breeders (Kemfthone and Curnow, 1961). The entailing strengths of the partial diallel established it as an alternative to diallel cross, which had limitation that number of crosses escalate vastly with he increases in number of parents. Partial cross has numerous statistical, economic, and genetic advantages, and these advantages are widely accepted around the world (Kemfthone and Curnow, 1961; Drillon, 1975). In this study, two methods for the construction of Partial diallel crosses designs, (i) row-wise Construction and (ii) column-wise construction, are described.

Row wise construction of Partial Diallel Crosses

The method is illustrated with the help of the following example of a PBIBD. Following PBIBD is generated forfor*v* = 29 and k = 4 in 29 blocks using initial block (0,1,3,11)

Blocks														
B_1	B_2	B_3	B_4	B_5	B_6	B_7	B_8	B_9	B_{10}	B_{11}	B_{12}	B_{13}	B_{14}	B_{15}
0	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

B_{16}	B_{17}	B_{18}	B_{19}	B_{20}	B_{21}	B_{22}	B_{23}	B_{24}	B_{25}	B_{26}	B_{27}	B_{28}	B_{29}
15	16	17	18	19	20	21	22	23	24	25	26	27	28
16	17	18	19	20	21	22	23	24	25	26	27	28	0
18	19	20	21	22	23	24	25	26	27	28	0	1	2
26	27	28	0	1	2	3	4	5	6	7	8	9	10

The interaction of the partial dialed design is given as under. In order to create the interaction across the block, horizontal (row-wise) interaction was constructed

(0×1) (1×2) (2×3) (3×4) (4×5) (5×6) (6×7) (7×8) (8×9) (9×10) (10×11) (11×12) (12×13) (13×14) (14×15) (15×16) (16×17) (17×18) (18×19) (19×20) (20×21) (21×22) (22×23) (23×24) (24×25) (25×26) (26×27) (27×28) (28×0)

(1×2) (2×3) (3×4) (4×5) (5×6) (6×7) (7×8) (8×9) (9×10) (10×11) (11×12) (12×13) (13×14) (14×15) (15×16) (16×17) (17×18) (18×19) (19×20) (20×21) (21×22) (22×23) (23×24) (24×25) (25×26) (26×27) (27×28) (28×0) (0×1)

(3×4) (4×5) (5×6) (6×7) (7×8) (8×9) (9×10) (10×11) (11×12) (12×13) (13×14) (14×15) (15×16) (16×17) (17×18) (18×19) (19×20) (20×21) (21×22) (22×23) (23×24) (24×25) (25×26) (26×27) (27×28) (28×0) (0×1) (1×2) (2×3)

(11×12) (12×13) (13×14) (14×15) (15×16) (16×17) (17×18) (18×19) (19×20) (20×21) (21×22) (22×23) (23×24) (24×25) (25×26) (26×27) (27×28) (28×0) (0×1) (1×2) (2×3) (3×4) (4×5) (5×6) (6×7) (7×8) (8×9) (9×10) (10×11)

Column wise construction of Partial Diallel Crosses

The interaction of the partial dialled design is given below. To create the interaction across the block, a column-wise interaction was constructed.

(0×1), (1×2),(2×3),(3×4),(4×5),(5×6),(6×7),(7×8),(8×9),(9×10),(10×11)
(0×3), (1×4), (2×5), (3×6), (4×7), (5×8), (6×9), (7×10), (8×11),(9×12), (10×13)
(0×11),(1×12),(2×13), (3×14), (4×15),(5×16),(6×17),(7×18),(8×19),(9×20),(10×21)
(1×3),(2×4),(3×5),(4×6),(5×7),(6×8),(7×9),(8×10),(9×11),(10×12),(11×13)
(1×11),(2×12),(3×13),(4×14),(5×15),(6×16),(7×17),(8×18),(9×19),(10×20),(11×21)
(3×11),(4×12),(5×13),(6×14),(7×15),(8×16),(9×17),(10×18),(11×19),(12×20),(13×21),
(11×12),(12×13),(13×14), (14×15),(15×16),(16×17),(17×18),(18×19),(19×20),(20×21)
(11×14),(12×15),(13×16),(14×17),(15×18),(16×19),(17×20),(18×21),(19×22),(20×23)
(11×22),(12×23),(13×24),(14×25),(15×26),(16×27),(17×28),(18×0),(19×1),(20×2)
(12×14),(13×15),(14×16),(15×17),(16×18),(17×19),(18×20),(19×21),(20×22),(21×23)
(12×22),(13×23),(14×24),(15×25),(16×26),(17×27),(18×28),(21×0),(20×1),(23×2)
(14×22),(15×23),(16×24),(17×25),(18×26),(19×27),(20×28),(0×21),(22×1),(23×2)

(21×22),(22×23),(23×24),(24×25),(25×26),(26×27),(27×28),(28×0)
(21×24),(22×25),(23×26),(24×27),(25×28),(26×0),(27×1),(28×2)
(21×3),(22×4),(23×5),(24×6),(25×7),(26×8),(27×9),(28×10)
(22×24),(23×25),(24×26),(25×27),(26×28),(27×0),(28×1),(0×2)
(22×3),(23×4),(24×5),25×6),(26×7),(27×8),(28×9),(0×10),
(24×3),(25×4),(26×5),(27×6),(28×7),(0×8),(1×9),(2×10)

Blocks														
B_1	**B_2**	**B_3**	**B_4**	**B_5**	**B_6**	**B_7**	**B_8**	**B_9**	**B_{10}**	**B_{11}**	**B_{12}**	**B_{13}**	**B_{14}**	**B_{15}**
0	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

B_{16}	**B_{17}**	**B_{18}**	**B_{19}**	**B_{20}**	**B_{21}**	**B_{22}**	**B_{23}**	**B_{24}**	**B_{25}**	**B_{26}**	**B_{27}**	**B_{28}**	**B_{29}**
15	16	17	18	19	20	21	22	23	24	25	26	27	28
16	17	18	19	20	21	22	23	24	25	26	27	28	0
18	19	20	21	22	23	24	25	26	27	28	0	1	2
26	27	28	0	1	2	3	4	5	6	7	8	9	10

Conclusion

This study proposes an innovative application of Balanced Incomplete Block Designs (BIBDs) and Partial Balanced Incomplete Block Designs (PBIBDs), developed through the method of cyclic shifts, to construct efficient and systematic diallel and partial diallel cross designs. The use of BIBDs enables the formulation of complete diallel crosses, facilitating structured control versus test comparisons among genotypic lines. Additionally, cyclic regular graph designs derived through cyclic shifts are employed to construct partial diallel cross designs. These partial schemes are particularly significant for estimating General Combining Ability (GCA) by maintaining only two types of contrast variances, such as gi−gjg_i - g_jgi−gj, using two-associate PBIBDs.

This research's significance lies in its theoretical foundations and practical applications. From a theoretical perspective, the study advances combinatorial design theory in the context of genetics experiments. Practically, it contributes to crop genetics by offering improved experimental strategies for studying genetic variability and combining abilities among inbred parental lines. As one of the primary goals in crop genetic investigations is to develop superior crop varieties through the strategic crossing of different strains, the proposed designs provide a scientifically sound and resource-efficient framework for evaluating such genetic potential. Ultimately, this approach supports a more effective selection of parental lines and enhances breeding programs aimed at crop improvement.

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