

DiallelW 1.0 User Manual

Combining Ability Analysis Tool for Diallel Crosses

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Abstract

DiallelW is a Windows-based tool for analysing general combining ability (GCA) and specific combining ability (SCA) in diallel-cross experimental designs. It adopts fixed-effect linear models and supports unbalanced datasets even with missing cross combinations. It estimates and performs significance tests for general combining ability (GCA), specific combining ability (SCA), reciprocal cross effect (RCA), as well as genotype-by-environment interaction effects. It is compatible with the four Griffing diallel-cross experimental designs.

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1 Core Functions

- Estimate general combining ability (GCA), specific combining ability (SCA), reciprocal cross effect (RCA), GCA-by-environment, SCA-by-environment, and RCA-by-environment interaction effects.
- Overall model F-test and F-tests for each single factor.
- Parameter estimation: effect values, standard errors, t-statistics and P-values.
- Pair-wise t-tests for GCA differences and SCA differences.

- Supports single/multiple blocks, single/multiple environments and allows missing cross combinations.
- Directly reads Excel files; calculation results can be exported and saved as text files.

2 Statistical Models

DiallelW supports eight fixed-effect linear models, as follows:

- **Model 1:**

$$y_{ijk} = \mu + G_i + G_j + S_{ij} + e_{ijk}$$

where y_{ijk} is the trait value of the k th individual in the ij th cross; μ is the overall mean; G_i and G_j are the GCAs of the i th and j th parents, respectively; S_{ij} is the SCA for the ij th cross combination; e_{ijk} is the random error effect for the individual observation. This model is suitable for a half-diallel experiment in a single environment with no blocks.

- **Model 2:**

$$y_{ijk} = \mu + G_i + G_j + S_{ij} + R_{ij} + e_{ijk}$$

where R_{ij} is the ij th reciprocal effect, and all other notations are the same as in Model 1. Copared with Model 1, Model 2 is suitable for a full-diallel experiment.

- **Model 3:**

$$y_{ijkl} = \mu + B_k + G_i + G_j + S_{ij} + e_{ijkl}$$

where y_{ijkl} is the trait value of the l th individual of the ij th cross in the k th block; e_{ijkl} is the corresponding random error; B_k is the k th block effect; and all other notations are the same as in previous models. Model 3 is extended from Model 1 by incorporating block effects at a single experimental site and is suitable for a half-diallel cross experimental design.

- **Model 4:**

$$y_{ijkl} = \mu + B_k + G_i + G_j + S_{ij} + R_{ij} + e_{ijkl}$$

where R_{ij} is the ij th reciprocal effect, and all other notations are the same as in Model 3. This model is suitable for a full-diallel cross experimental design with blocks at a single experimental site.

- **Model 5:**

$$y_{ijlkm} = \mu + E_k + B_{l(k)} + G_i + G_j + S_{ij} + e_{ijlkm}$$

where y_{ijlkm} is the m th observation of the l th block within the k th environment for the ij th cross; μ is the overall mean; E_k is the k th environment effect; $B_{l(k)}$ is the l th block effect in the k th environment; G_i , G_j and S_{ij} are the same as in previous models; e_{ijlkm} is the random error within a plot. This model is suitable for a half-diallel cross design with blocks at different environmental sites.

- **Model 6:**

$$y_{ijlkm} = \mu + E_k + B_{l(k)} + G_i + G_j + S_{ij} + GE_{ik} + GE_{jk} + SE_{ijk} + e_{ijlkm}$$

where GE_{ik} and GE_{jk} are the interaction effects of the k th environment with parents i and j , respectively; SE_{ijk} is the interaction effect of the k th environment with the combination of parents i and j ; all other notations are the same as in Model 5. Like Model 5, this model is also suitable for a half-diallel cross design, but it incorporates interaction effects between genotype and environment.

- **Model 7:**

$$y_{ijklm} = \mu + E_k + B_{l(k)} + G_i + G_j + S_{ij} + R_{ij} + e_{ijklm}$$

where R_{ij} is the ij th reciprocal effect; all other notations are the same as in Model 5. This model is suitable for a full-diallel cross experimental design with blocks at different experimental sites, without considering genotype-by-environment effects.

- **Model 8:**

$$y_{ijklm} = \mu + E_k + B_{l(k)} + G_i + G_j + S_{ij} + R_{ij} + GE_{ik} + GE_{jk} + SE_{ijk} + RE_{ijk} + e_{ijklm}$$

where RE_{ijk} is the interaction effect between the k th environment effect and the reciprocal effect of R_{ij} ; GE_{ik} , GE_{jk} and SE_{ijk} are the genotype-by-environment effects as described in Model 6; all other notations are the same as in Model 7. This model is suitable for a full-diallel cross experimental design, incorporating not only the reciprocal effects but also the genotype-by-environment effects.

Note that all effects in the above linear models are fixed effects, except the random errors. To make these effects estimable, they must satisfy some sum-to-zero linear restrictions. For example, the linear restrictions for Model 8 are somewhat more complex, as follows:

$$\left\{ \begin{array}{ll} \sum E_k = 0 & \\ \sum_l B_{l(k)} = 0 & \text{for each } k \\ \sum G_i = 0 & \\ S_{ij} = S_{ji} & \text{for all } i \text{ and } j \\ \sum_i S_{ij} = 0 & \text{for each } j \\ \sum_j S_{ij} = 0 & \text{for each } i \\ R_{ij} + R_{ji} = 0 & \text{for all } i \text{ and } j \\ \sum_i GE_{ik} = 0 & \text{for each } k \\ \sum_k GE_{ik} = 0 & \text{for each } i \\ SE_{ijk} = SE_{jik} & \text{for all } i, j \text{ and } k \\ \sum_i SE_{ijk} = 0 & \text{for all } j \text{ and } k \\ \sum_j SE_{ijk} = 0 & \text{for all } i \text{ and } k \\ \sum_k SE_{ijk} = 0 & \text{for all } i \text{ and } j \\ RE_{ijk} + RE_{jik} = 0 & \text{for all } i, j \text{ and } k, i \neq j \\ \sum_k RE_{ijk} = 0 & \text{for all } i \text{ and } j, i \neq j \end{array} \right.$$

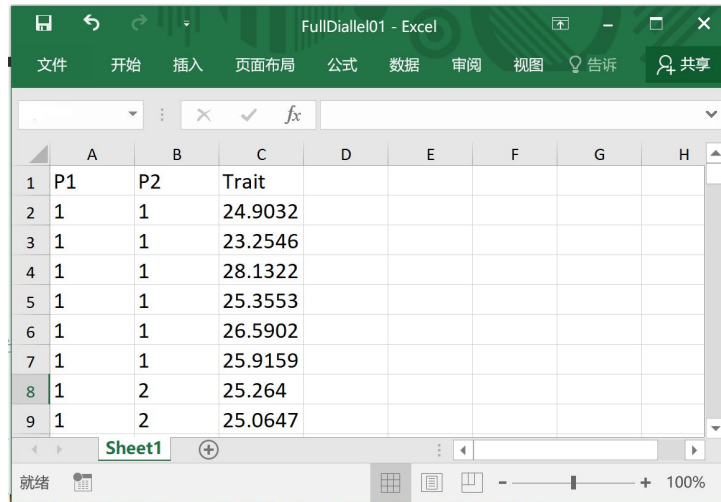
3 Data Preparation

DiallelW reads Excel data files directly. **Header names must remain unchanged.** All data must be stored in the first worksheet of the Excel file. Example input files are provided in the **example** sub-folder under the installation directory; users may prepare their spreadsheets following these templates. Permitted header labels:

- P1: Maternal parent ID
- P2: Paternal parent ID
- Blk: Block
- Env: Environment
- Trait: Target phenotypic trait

3.1 Format 1: Single location and single block

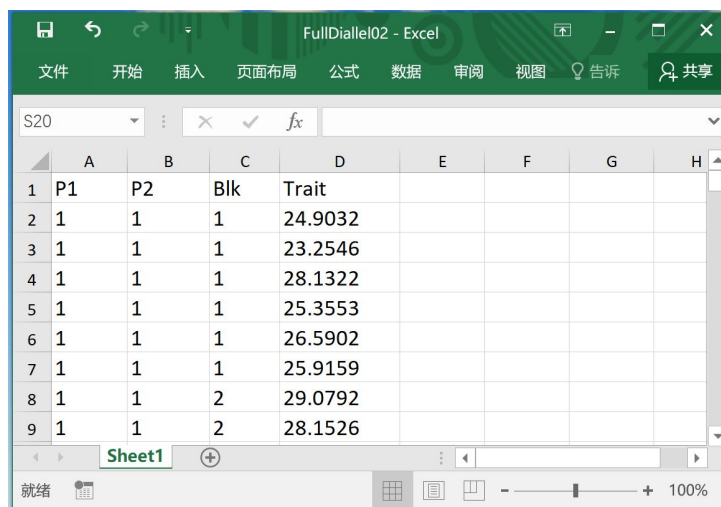
If the experiment is arranged at a single location with one block, the input data format is as shown in the figure below. It can be applied to Model 1 or Model 2.



	A	B	C	D	E	F	G	H
1	P1	P2	Trait					
2	1	1	24.9032					
3	1	1	23.2546					
4	1	1	28.1322					
5	1	1	25.3553					
6	1	1	26.5902					
7	1	1	25.9159					
8	1	2	25.264					
9	1	2	25.0647					

3.2 Format 2: Single location and multiple blocks

If the experiment is arranged at a single location with multiple blocks, the input data format is as shown in the figure below. It can be applied to Model 3 or Model 4.



	A	B	C	D	E	F	G	H
1	P1	P2	Blk	Trait				
2	1	1	1	24.9032				
3	1	1	1	23.2546				
4	1	1	1	28.1322				
5	1	1	1	25.3553				
6	1	1	1	26.5902				
7	1	1	1	25.9159				
8	1	1	2	29.0792				
9	1	1	2	28.1526				

3.3 Format 3: Multi locations and multiple blocks

If the experiment is arranged at multiple locations with multiple blocks, the input data format is as shown in the figure below. It can be applied to Model 5, Model 6, Model 7 or Model 8.

	A	B	C	D	E	F	G
1	P1	P2	Blk	Env	Trait		
2	1	1	1	1	29.5713		
3	1	1	1	1	28.1184		
4	1	1	1	1	25.4861		
5	1	1	1	1	26.1067		
6	1	1	1	1	28.6841		
7	1	1	1	1	27.4834		
8	1	1	2	1	25.1610		
9	1	1	2	1	24.6863		

3.4 Key Points for Data Entry

- Each row represents one individual observation. Multiple replicates for the same cross occupy multiple separate rows.
- Do **not** create rows for missing cross combinations; the software automatically handles unbalanced datasets.
- Avoid blank rows and extra comment lines inside the Excel worksheet.

4 Workflow

- **Open dataset:** Launch DiallelW. Click menu **File** → **Open** and select your prepared Excel file for data import.
- **Run genetic analysis:** Click menu **Analysis** → **Fixed-Effect Linear Model**. The software auto-detects data structure and opens a dialogue listing valid linear models. Select the model matching your experimental design.
- Click **OK** to execute computation.
- **View and save results:** Output appears in the right-hand panel. Export results as a *.txt text file for backup.

5 Output

The output results of DiallelW are divided into six sections. As an example, we run the software with the built-in data file HalfDiallel02.xlsx, and present the output results as follows.

- Displaying the fitted linear model and computation timestamp

```
Analysis of Diallel Mating Design for the fixed linear model as following:

Yijkl = u + Bk + Gi + Gj + Sij + eijkl

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```

- Overall model test

Test for the model					
Source	DF	Sum of Squares	Mean Squares	F Value	Pr>F
Model	11	2263.0720	205.7338	5.8433	0.0000
Error	168	5915.0589	35.2087		
Total	179	8178.1309			

- F-test for each factor

Test for factors					
Source	DF	Sum of Squares	Mean Squares	F Value	Pr>F
BLK	2	432.8629	216.4315	6.1471	0.0027
GCA	4	1496.6370	374.1593	10.6269	0.0000
SCA	5	333.5720	66.7144	1.8948	0.0977

- Presenting each parameter estimate, standard error, t-statistic, and P-value

Parameter Estimates				
Parameter	Estimate	Std Error	T Value	Pr> T
u	33.7840	0.4423	76.3876	0.0000
B1	1.3970	0.6255	2.2335	0.0268
B2	-2.1626	0.6255	-3.4575	0.0007
B3	0.7656	0.6255	1.2240	0.2227
G1	-2.5435	0.7222	-3.5217	0.0006
G2	1.8735	0.7222	2.5940	0.0103
G3	2.7789	0.7222	3.8477	0.0002
G4	0.9191	0.7222	1.2726	0.2049
G5	-3.0281	0.7222	-4.1927	0.0000
S1x2	0.5847	0.9889	0.5913	0.5551
S1x3	0.0342	0.9889	0.0346	0.9725
S1x4	-1.4881	0.9889	-1.5047	0.1343
S1x5	0.8691	0.9889	0.8789	0.3807
S2x3	1.5564	0.9889	1.5738	0.1174
S2x4	-1.3642	0.9889	-1.3794	0.1696
S2x5	-0.7770	0.9889	-0.7857	0.4331
S3x4	0.6769	0.9889	0.6844	0.4947
S3x5	-2.2675	0.9889	-2.2928	0.0231
S4x5	2.1754	0.9889	2.1997	0.0292

- Presenting t-tests for pairwise GCA differences

T values of test for difference between any two GCAs				
	G1	G2	G3	G4
G2	3.8679**			
G3	4.6608**	0.7929		
G4	3.0322**	0.8358	1.6287	
G5	0.4244	4.2923**	5.0852**	3.4565**

*Pr<0.05, **Pr<0.01

- Presenting t-tests for pairwise SCA differences

T values of test for difference between any two SCAs									
	S12	S13	S14	S15	S23	S24	S25	S34	S35
S13	0.3409								
S14	1.2835	0.9426							
S15	0.1761	0.5170	1.4596						
S23	0.6017	0.9426	2.6661**	0.6019					
S24	1.2068	1.2245	0.0767	1.9557	1.8085				
S25	0.8432	0.7104	0.6227	1.0193	1.4449	0.3636			
S34	0.0807	0.3980	1.3405	0.1684	0.5447	1.2638	1.2732		
S35	2.4977*	1.4252	0.6825	1.9422	2.3678*	0.7910	0.9229	1.8232	
S45	1.3929	1.8750	2.2684*	0.8088	0.5420	2.1917*	1.8282	0.9279	2.7511**
*Pr<0.05, **Pr<0.01									

6 Frequently-Asked Questions and Notes

- Excel input data **must reside in the first worksheet (Sheet1)** of the workbook.
- Do not modify header labels; delete entire columns for factors you do not require.
- For half-diallel datasets without reciprocal crosses, avoid selecting Model 2, 4, 7, 8 which include reciprocal-cross terms R_{ij} .
- Severe numbers of missing cross combinations reduce available degrees of freedom and weaken statistical power of hypothesis tests.
- DiallelW outputs fixed-effect estimates and **does not directly provide variance components**. Use software such as ASReml or R for random-effect variance-component estimation.
- DiallelW analyses one trait per run; multi-trait datasets must be analysed trait-by-trait.
- Always save results as a text *.txt file after computation completes to prevent data loss upon closing the program.

References

- [1] Tong C F, Liu G X, Yang L W, et al. GSCA: new software and algorithms to analyse diallel mating designs based on restricted linear model[J]. Silvae Genet, 2012,61(3):126-132.