ALA 3.3
Exercise in Analysis of GCA and SCA - Griffing Method 4 Diallel

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Griffing methods (1956)

1. One set of F1's and reciprocals [p^2 genotypes] plus parents

2. One set of F1's, no reciprocals [$p(p+1)/2$ genotypes] plus parents

3. One set of F1's and reciprocals [$p(p-1)$ genotypes], no parents

4. One set of F1's, no reciprocals [$p(p-1)/2$ genotypes] no parents

Mathematical model for RCB

$$x_{ijkl} = \mu + v_{ij} + b_k + (bv)_{ijk} + e_{ijkl}$$

where μ is the population mean effect

v_{ij} is the effect for the ijth variety (i.e. genotype)

b_k is the kth block effect

$(bv)_{ijk}$ is the interaction between the ijth genotype and the jth block

e_{ijkl} is the environmental effect associated with the $ijkl$th individual

In this model, there are a varieties randomized to b blocks with c individual measurements taken in each of the ab plots

The variety effects in the model

$$x_{ijkl} = \mu + v_{ij} + b_k + (bv)_{ijk} + e_{ijkl}$$

are considered in terms of GCA and SCA:

For methods in which reciprocal F1's are included

$$v_{ij} = g_i + g_j + s_{ij} + r_{ij}$$

where g_i is the GCA effect of the ith parent,

s_{ij} is the SCA effect for the cross of the ith and jth parents, and

r_{ij} is the reciprocal effect involving the ith and jth parents.

For methods in which reciprocal F1's are not included, r_{ij} is zero

$$v_{ij} = g_i + g_j + s_{ij}$$

Models

I. All effects except error are regarded as 'fixed'

II. All effects except μ are considered 'random'

In Model 1, inferences are limited to the experimental materials. Useful in comparing combining abilities among the parent lines. Can identify good hybrid combinations.

In Model 2, inferences are not about the individual lines in the sample but rather extend to the population of lines. Useful in estimating genetic components of the population variance.

Expected Means Square table for RCB

Source of Variation	Degrees of Freedom	Mean Square	Model I	Model II
Varieties	a-1	M_v	$\sigma_e^2 + bc\left(\dfrac{1}{a-1}\sum v_i^2\right)$	$\sigma_e^2 + c\sigma_{bv}^2 + bc\sigma_v^2$
Blocks	b-1	M_b	$\sigma_e^2 + ac\left(\dfrac{1}{b-1}\sum_k b_k^2\right)$	$\sigma_e^2 + c\sigma_{bv}^2 + ac\sigma_b^2$
Varieties x blocks	(a-1)(b-1)	M_{bv}	$\sigma_e^2 + c\left(\dfrac{1}{(a-1)(b-1)}\sum_{i<}\sum_j \sum_k bv_{ijk}^2\right)$	$\sigma_e^2 + c\sigma_{bv}^2$
Error	ab(c-1)	M_e	σ_e^2	σ_e^2

Note that if $c=1$ (i.e. no subsampling), then M_{bv} becomes the error term M_e

Expected Means Square table for Method 4

Source of Variation	Degrees of Freedom	Mean Square	Model I	Model II
GCA	p-1	M_g	$\sigma^2 + (p-2)\left(\dfrac{1}{p-1}\right)\sum_i g_i^2$	$\sigma^2 + \sigma_s^2 + (p-2)\sigma_g^2$
SCA	$p(p-3)/2$	M_s	$\sigma^2 + \left(\dfrac{2}{p(p-3)}\right)\sum_{i<}\sum_j s_{ij}^2$	$\sigma^2 + \sigma_s^2$
Error	m	M_e'	σ^2	σ^2

Note $M_e' = Me/bc$
with the same number of d.f.'s: m

To test for GCA effects: $F_{[(p-1),m]} = M_g / M_e'$

To test for SCA effects: $F_{[p(p-3)/2,m]} = M_s / M_e'$

Compute estimates of effects for Method 4

$$x_{ijkl} = \mu + v_{ij} + b_k + (bv)_{ijk} + e_{ijkl}$$

$$v_{ij} = g_i + g_j + s_{ij}$$

Of particular interest is the estimate of GCA effects for parents, g_i, and the SCA effects for specific hybrid combinations of parents, s_{ij}

$$g_i = \frac{1}{p(p-2)}\left(pX_{i.} - 2X_{..}\right) \qquad s_{ij} = x_{ij} - \frac{1}{(p-2)}\left(X_{i.} + X_{j.}\right) + \frac{2}{(p-1)(p-2)}X_{..}$$

given $\quad X_{i.} = \sum_{j \neq i} x_{ij} \quad$ where $\quad x_{ij} = x_{ji} \quad$ e.g. $\quad X_{2.} = x_{12} + x_{23}$

And

$$X_{..} = \sum_{i<j}\sum x_{ij}$$

Estimating breeding value (BV)

Once estimated GCA effects for parents, g_i, are obtained, the expected values of progeny resulting from hybrid combinations of parents can be calculated:

$$E(x_{ij}) = \mu + g_i + g_j$$

Note that SCA effects are not included. Why? Because non-additive effects cannot be transmitted to progeny in the case of diploids.

Also note that $E(x_{ij})$ is the same as an estimated breeding value (EBV). The predicted performance of the progeny is the average of the breeding values of the parents. Thus, the breeding value of a parent line is twice its GCA:

BV = 2 GCA

The SCA effect for specific hybrid combinations of parents, s_{ij}, can be calculated as difference between actual and expected performance:

$$s_{ij} = x_{ij} - E(x_{ij})$$

Exercise

Data were gathered on potato leaf roll virus (PLRV) resistance from crosses among 7 lines from a native regional population of potato, *Solanum tuberosum* ssp *andigena* (Mihovilovich et al.2007). The 7 lines were crossed in a diallel design, Griffing Method 4 (no reciprocals, F1 crosses only) and evaluated under greenhouse conditions using viruliferous aphids as an inoculation source. An RCB design with 3 replications was employed.

The mean percentage of resistance to PLRV infection was scored and data were transformed to arc sen (>80% resistance equivalent to >70 transformed arc sen). Table 1 displays the mean arc sen for percentage PLRV resistance for the F1 crosses among the 7 lines. Table 2 is the ANOVA table from the data analysis.

TABLE 1. Mean are sen percentage PLRV resistance

CROSS	L1	L2	L3	L4	L5	L6	L7	TOTAL
L1		18.05	35.00	26.14	65.95	41.07	39.18	225.40
L2			22.97	12.50	66.84	26.45	21.14	167.96
L3				40.00	67.21	38.24	28.54	231.97
L4					70.69	36.07	30.29	215.70
L5						66.84	63.85	401.39
L6							30.95	239.62
L7								213.96
GRAND TOTAL								848.00

TABLE 2. ANOVA of the diallel for the transformed data of response to PLRV infection

SOURCE	DF	DF	SS	MS	F VALUE	Pr>F	EMS
Varieties	20		20923.3100	1046.1660	21.41	**	
Blocks	2		138.4938	69.2500	1.42	ns	
Error (e)	40		1954.5000	48.8625			
GCA	6		6549.3700	1091.5600	35.94	**	
SCA	14		425.2420	30.3700	1.86	ns	
Error (e')	40			16.2875			

TABLE 3. GCA effects (diagonal elements) and SCA effects (off diagonal)

CROSS	L1	L2	L3	L4	L5	L6	L7
L1							
L2							
L3							
L4							
L5							
L6							
L7							

Exercise

1. What is a, b, c, p? Show formulas.

2. What are the formulas for the d.f.'s? Hint: show how the number of d.f. given were computed.

3. Show how M_e' was calculated.

4. Was the analysis performed as a Model 1 (fixed) or Model 2 (random)? How do you know? What this appropriate?

5. Based on the ANOVA, what do you conclude about gene action controlling PLRV in potato? Why?

6. Compute the GCA and SCA effects to populate Table 3.

7. If you were to select 3 lines based on their GCA, which lines would you choose?

8. Which F1 cross showed the highest SCA?

9. What is the expected value of progeny resulting from L1 x L7?

Exercise – ANSWER KEY

1. What is p, a, b, c? Show formulas.

p=7; a = p(p-1)/2 = 7(6)/2 = 21; b=3; c=1

2. What are the formulas for the d.f.'s? Hint: show how the number of d.f. given were computed.

See ANSWER KEY TABLE 2

3. Show how M_e' was calculated.

$M_e' = M_e/bc$ = 48.8625 / 3(1) = 16.2875

4. Was the analysis performed as a Model 1 (fixed) or Model 2 (random)? How do you know? What this appropriate?

Model 2 was used; the lines were sampled from a native regional population of potatoes. See EMS terms for GCA and SCA behind F test in ANSWER KEY TABLE 2

5. Based on the ANOVA, what do you conclude about gene action controlling PLRV in potato? Why?

The ANOVA indicates that GCA is highly statistically significant, whereas SCA is not significant. Because GCA reflects mainly additive effects, we can conclude that additive gene action is largely controlling PLRV resistance and non-additive effects (dominance and epistasis) are not involved to any significant extent.

Exercise – ANSWER KEY (cont)

6. Compute the GCA and SCA effects to populate Table 3.

See ANSWER KEY TABLE 3

7. If you were to select 3 lines based on their GCA, which lines would you choose?

By rank: L5, L6, L3 have highest GCA. L5 is outstanding at 31.82

8. Which F1 cross showed the highest SCA? L2 x L5 with SCA at 9.50

9. What is the expected value of progeny resulting from L1 x L7?

$$E(x_{17}) = \mu + g_1 + g_7 = 40.38 + -3.38 + -5.67 = 31.33$$

Also note that

$$s_{17} = x_{17} - E(x_{17}) = 39.18 - 31.33 = 7.84$$

Exercise – ANSWER KEY (cont)

TABLE 2. ANSWER KEY

SOURCE	DF	DF	SS	MS	F VALUE	Pr>F	EMS
Varieties	20	a-1	20923.3100	1046.1660	21.41	**	
Blocks	2	b-1	138.4938	69.2500	1.42	ns	
Error (e)	40	(a-1)(b-1)	1954.5000	48.8625			
GCA	6	p-1	6549.3700	1091.5600	35.94	**	$\sigma^2 + \sigma_s^2 + (p-2)\sigma_g^2$
SCA	14	p(p-3)/2	425.2420	30.3700	1.86	ns	$\sigma^2 + \sigma_s^2$
Error (e')	40	(a-1)(b-1)		16.2875			σ^2

TABLE 3. ANSWER KEY   GCA   SCA

CROSS	L1	L2	L3	L4	L5	L6	L7
L1	-3.38	-4.09	0.06	-5.54	-2.87	4.60	7.84
L2		-14.87	-0.48	-7.70	9.50	1.47	1.29
L3			-2.06	7.00	-2.93	0.46	-4.11
L4				-5.32	3.81	1.54	0.89
L5					31.82	0.30	-2.68
L6						-0.53	-3.24
L7							-5.67

TABLE 1. Mean are sen percentage PLRV resistance

$s = \frac{1}{N-1}[N^2-1]$

CROSS	L1	L2	L3	L4	L5	L6	L7	TOTAL
L1		18.05	35.00	26.14	65.95	41.07	39.18	225.40
L2			22.97	12.50	66.84	26.45	21.14	167.96
L3				40.00	67.21	38.24	28.54	231.97
L4					70.69	36.07	30.29	215.70
L5						66.84	63.85	401.39
L6							30.95	239.62
L7								213.96
GRAND TOTAL								848.00

ANSWER KEY (cont)

Example calculations of GCA and SCA effects for Table 3

$$g_i = \frac{1}{p(p-2)}\left(pX_{i.} - 2X_{..}\right)$$

g_1 = 1/35 [7(225.4) − 2(848)] = 1/35 [1577.8 − 1696] = -3.38

g_7 = 1/35 [7(213.96) − 1696)] = -5.67

$$s_{ij} = x_{ij} - \frac{1}{(p-2)}\left(X_{i.} + X_{j.}\right) + \frac{2}{(p-1)(p-2)}X_{..}$$

s_{17} = 39.18 − 1/(5) [225.40 + 213.96] + 2/(6)(5) [848]
 = 39.18 − 87.87 + 56.53
 = 7.84

References

Griffing, B. 1956. Concept of general and specific combining ability in relation to diallel crossing systems. Australian J. Biol. Sci. 9: 463-493.

Mihovilovich, E., L. Alarcon , A.L. Perez, J. Alvarado, C. Arellano, and M. Bonierbale. 2007. High levels of heritable resistance to *Potato leafroll virus* (PLRV) in *Solanum tuberosum* subsp. *Andigena*. Crop Science 47: 1091-1103.

FAO GIPB – Pre-breeding to build capacity for effective use of plant genetic resources
http://www.fao.org/fileadmin/templates/agphome/documents/PGR/Announcements/PB-elearningcourse_GIPB_en.pdf

Crow, J.F. 1986. Basic Concepts in Population, Quantitative, and Evolutionary Genetics. W.H. Freeman and Company, New York, USA.

Falconer, D.S. 1989. Introduction to Quantitative Genetics, 3rd ed. John Wiley & Sons, Inc., New York, NY, USA.