

Chapter 3

Diallel Analysis for an Additive-Dominance Model with Genotype-by-Environment Interaction Effects

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Purpose

To analyze balanced or unbalanced data of an additive x dominance (AD) genetic model for estimating components of variance, covariance, heritability, and selection response.

Definitions

Mating Design

A set of inbred lines are sampled from a reference population. These parents are used to produce F_1 crosses. If it is difficult to use F_1 crosses for some crops, F_2 crosses can be used as an alternative. Experiments with parents and F_1 s (or F_2 s) are conducted in multiple environments using a randomized complete block design.

Genetic Model

The genetic model for a genetic entry derived from parents i and j in the k th block within the h th environment is

$$y_{hijk} = \mu + E_h + G_{ij} + GE_{hij} + B_{hk} + e_{hijk}$$

where μ = population mean, E_h = environment effect, G_{ij} = total genotypic effect, GE_{hij} = genotype \times environment interaction effect, B_{hk} = block effect, and e_{hijk} = residual effect.

For parent (P_i):

$$G_{ii} + GE_{hii} = 2A_i + D_{ii} + 2AE_{hi} + DE_{hii}$$

For F_1 ($P_i \times P_j$):

$$G_{ij} + GE_{hij} = A_i + A_j + D_{ij} + AE_{hi} + AE_{hj} + DE_{hij}$$

For F_2 ($F_1 \otimes$):

$$G_{ij} + GE_{hij} = A_i + A_j + \frac{1}{4}D_{ij} + \frac{1}{4}D_{ii} + \frac{1}{2}D_{jj} \\ + AE_{hi} + AE_{hj} + \frac{1}{4}DE_{hii} + \frac{1}{4}DE_{hjj} + \frac{1}{2}DE_{hij}$$

where A = additive effect, D = dominance effect, AE = additive by environment interaction effect, DE = dominance by environment interaction effect.

Analysis Methodology

Mixed Linear Model

The phenotypic mean of the genetic model can be expressed by a mixed linear model as

$$y = Xb + U_A e_A + U_D e_D + U_{AE} e_{AE} + U_{DE} e_{DE} + U_B e_B + e_e \\ = Xb + \sum_u^6 U_u e_u$$

with variance-covariance matrix

$$\text{var}(y) = \sigma_A^2 U_A U_A^T + \sigma_D^2 U_D U_D^T + \sigma_{AE}^2 U_{AE} U_{AE}^T + \sigma_{DE}^2 U_{DE} U_{DE}^T \\ + \sigma_B^2 U_B U_B^T + \sigma_e^2 I \\ = \sum_{u=1}^6 \sigma_u^2 U_u U_u^T = \sum_{u=1}^6 \sigma_u^2 V_u.$$

Variance Components

Unbiased estimation of variances can be obtained by the following MINQUE(1) equations (Zhu, 1992; Zhu and Weir, 1996):

$$[tr(Q_{(1)}V_uQ_{(1)}V_v)] [\hat{\sigma}_u^2] = [y^T Q_{(1)}V_uQ_{(1)}y]$$

where

$$Q_{(1)} = V_{(1)}^{-1} - V_{(1)}^{-1}X(X^T V_{(1)}^{-1}X)^+ X^T V_{(1)}^{-1}$$

$$V_{(1)} = \sum_u V_u = \sum_u U_u U_u^T$$

When experimental variances (σ_u^2) are estimated, genetic variance components can be obtained by $V_A = 2\sigma_A^2$, $V_D = \sigma_D^2$, $V_{AE} = 2\sigma_{AE}^2$, $V_{DE} = \sigma_{DE}^2$, and $V_e = \sigma_e^2$. The total phenotypic variance is $V_P = V_A + V_D + V_{AE} + V_{DE} + V_e$.

Covariance Components and Correlation

Unbiased estimation of covariances $\sigma_{u/1u}$ between two traits (y_1 and y_2) can be obtained by MINQUE(1) approaches (Zhu, 1992; Zhu and Weir, 1996):

$$[tr(Q_{(1)}V_uQ_{(1)}V_v)] [\hat{\sigma}_{u/1u}] = [y_1^T Q_{(1)}V_uQ_{(1)}y_2]$$

When experimental covariances ($\sigma_{u/1u}$) are estimated, genetic covariance components can be obtained by $C_A = 2\sigma_{A/A}$, $C_D = \sigma_{D/D}$, $C_{AE} = 2\sigma_{AE/AE}$, $C_{DE} = \sigma_{DE/DE}$, and $C_e = \sigma_{e/e}$. The total phenotypic covariance is $C_P = C_A + C_D + C_{AE} + C_{DE} + C_e$. For trait 1 and trait 2, correlation coefficient of genetic components can be estimated by $r_A = C_A / \sqrt{V_{A(1)}V_{A(2)}}$, $r_D = C_D / \sqrt{V_{D(1)}V_{D(2)}}$, $r_{AE} = C_{AE} / \sqrt{V_{AE(1)}V_{AE(2)}}$, $r_{DE} = C_{DE} / \sqrt{V_{DE(1)}V_{DE(2)}}$, and $r_e = C_e / \sqrt{V_{e(1)}V_{e(2)}}$.

Heritability Components

For the genetic model with *GE* interaction effects, the total heritability (h^2) can be partitioned into two components ($h^2 = h_G^2 + h_{GE}^2$), where $h_G^2 = V_A / V_P$ is general heritability and $h_{GE}^2 = V_{AE} / V_P$ is interaction heritability

(Zhu, 1997). General heritability is applicable to multiple environments whereas interaction heritability is applicable only to specific environments.

Selection Response

The total selection response ($R = ih^2 \sqrt{V_P}$) can be partitioned into two components (Zhu, 1997):

$$R = R_G + R_{GE}$$

where $R_G = ih_G^2 \sqrt{V_P}$ is general response and $R_{GE} = ih_{GE}^2 \sqrt{V_P}$ is interaction response.

Heterosis Components

Prediction of genetic merits can be obtained by using the linear unbiased prediction (LUP) method (Zhu, 1992; Zhu and Weir, 1996) or adjusted unbiased prediction (AUP) method (Zhu, 1993; Zhu and Weir, 1996). Predicted genotypic effects and *GE* interaction effects can be further used in analyzing heterosis of different generations (Zhu, 1997). Heterosis in specific environments consists of two components. General heterosis is due to genotypic effects and can be expected in overall environments, and interaction heterosis is a deviant of *GE* interaction relative to specific environments. The two components of heterosis based on midparent or better parent can be calculated as

General heterosis of F_n relative to midparent: $H_M(F_n) = (\frac{1}{2})^{n-1} \Delta_D$

Interaction heterosis of F_n relative to midparent: $H_{ME}(F_n) = (\frac{1}{2})^{n-1} \Delta_{DE}$

General heterosis of F_n relative to better parent (P_i):

$$H_B(F_n) = (\frac{1}{2})^{n-1} \Delta_D - \frac{1}{2} \omega_G$$

Interaction heterosis of F_n relative to better parent (P_i):

$$H_{BE}(F_n) = (\frac{1}{2})^{n-1} \Delta_{DE} - \frac{1}{2} \omega_{GE}$$

where $\Delta_D = D_{ij} - \frac{1}{2}(D_{ii} + D_{jj})$ is dominance heterosis, $\Delta_{DE} = DE_{hij} - \frac{1}{2}(DE_{hii} + DE_{hjj})$ is *DE* interaction heterosis, $\omega_G = |G(P_i) - G(P_j)|$ is parental genotypic difference, and $\omega_{GE} = |GE(P_i) - GE(P_j)|$ is parental interaction difference.

Heterosis based on population mean ($H_{PM} = \frac{1}{\mu} H_M$, $H_{PME} = \frac{1}{\mu} H_{ME}$, $H_{PB} = \frac{1}{\mu} H_B$, or $H_{PBE} = \frac{1}{\mu} H_{BE}$) can be used to compare proportion of heterosis among different traits.

Originators

- Zhu, J. (1992). Mixed model approaches for estimating genetic variances and covariances. *Journal of Biomathematics* 7(1):1-11.
- Zhu, J. (1993). Methods of predicting genotype value and heterosis for offspring of hybrids (Chinese). *Journal of Biomathematics* 8(1):32-44.
- Zhu, J. (1997). *Analysis Methods for Genetic Models*. Agricultural Publication House of China, Beijing.
- Zhu, J. and Weir, B.S. (1996). Diallel analysis for sex-linked and maternal effects. *Theoretical and Applied Genetics* 92(1):1-9.

Software Available

- Zhu, J. (1997). GENAD.EXE for constructing AD model, GENVAR1.EXE for estimating components of variance and heritability, GENCOV1.EXE for estimating components of covariance and correlation, GENHET1.EXE for predicting genetic effects and components of heterosis. *Analysis Methods for Genetic Models* (pp. 278-285), Agricultural Publication House of China, Beijing (program free of charge). Contact: Dr. Jun Zhu, Department of Agronomy, Zhejiang University, Hangzhou, China. E-mail: <jzhu@zju.edu.cn>.

EXAMPLE

Unbalanced data (COTDATA.TXT) to be analyzed (Parent = 4, Year = 2, Blk = 2):

Env	Fem	Male	Cross	Blk	Bolls	Fiber Yield
1	1	1	0	1	14.5	54.4
1	1	1	0	2	11.2	29.7
1	1	2	1	1	10.9	54.3
1	1	2	1	2	12.4	55.1
1	1	3	1	1	12.7	43.7
1	1	3	1	2	10.4	51.2
1	1	4	1	1	15.5	58.3
1	1	4	1	2	14.3	38.5
1	2	1	1	1	15.9	62.5
1	2	1	1	2	14.0	56.8
1	2	2	0	1	14.0	34.8
1	2	2	0	2	14.9	35.0
1	2	3	1	1	12.7	34.3

1	2	3	1	2	10.0	24.1
1	2	4	1	1	14.7	34.9
1	2	4	1	2	18.2	34.1
1	3	1	1	1	10.0	26.9
1	3	1	1	2	11.4	28.1
1	3	2	1	1	13.9	23.9
1	3	2	1	2	11.1	33.5
1	3	3	0	1	6.3	12.5
1	3	3	0	2	9.1	22.3
1	3	4	1	1	11.4	19.8
1	3	4	1	2	11.0	21.4
1	4	1	1	1	13.3	43.8
1	4	1	1	2	12.0	42.0
1	4	2	1	1	15.9	31.5
1	4	2	1	2	16.7	40.2
1	4	3	1	1	13.6	39.9
1	4	3	1	2	14.9	19.6
1	4	4	0	1	10.0	28.5
1	4	4	0	2	15.0	28.1
2	1	1	0	1	19.4	55.1
2	1	1	0	2	24.1	56.3
2	1	2	1	1	21.7	69.2
2	1	2	1	2	25.1	79.5
2	1	3	1	1	15.1	76.8
2	1	3	1	2	16.6	42.7
2	1	4	1	1	22.9	72.7
2	1	4	1	2	19.2	62.7
2	2	2	0	1	17.2	60.6
2	2	2	0	2	19.6	71.6
2	2	3	1	1	18.9	36.8
2	2	3	1	2	17.2	47.8
2	2	4	1	1	32.8	61.9
2	2	4	1	2	30.7	78.3
2	3	3	0	1	13.6	27.8
2	3	3	0	2	8.4	19.1
2	3	4	1	1	16.8	37.9
2	3	4	1	2	17.0	34.2
2	4	4	0	1	21.5	49.5
2	4	4	0	2	19.9	57.1

1. Run GENAD.EXE to create mating design matrix files and data files for additive-dominance (AD) model. Before running this program, you should create a file for your analysis with five design columns followed by trait columns. The first five columns are: (1) environment, (2) maternal, (3) paternal, (4) generation, and (5) replication. There is a limitation (<100 traits) for the number of trait columns. An example of a data file is provided with the name COTDATA.TXT.
2. Run programs for variance and covariance analyses. Standard errors of estimates are calculated using jackknife procedures. If you have multiple blocks for your experiments, you can use GENVAR1R.EXE or GENCOV1R.EXE for jackknifing over blocks. Otherwise you can use

- GENVAR1C.EXE or GENCOV1C.EXE for jackknifing over cell means.
3. Run GENVAR1R.EXE or GENVAR1C.EXE for estimating variance components and predicting genetic effects before estimating covariance and correlation. These two programs will allow you to choose the parental type (inbred or outbred) and the prediction methods (LUP or AUP). You also need to input coefficients (1, 0, or -1) for conducting linear contrasts for genetic effects of parents.
 4. After you finish variance analysis, you can run GENCOV1R.EXE or GENCOV1C.EXE for estimating covariance components and coefficients of correlation among all the traits analyzed.
 5. If you want to predict heterosis and genotypic value for each F_1 or F_2 cross by an AD model, you can run GENHET1R.EXE or GENHET1C.EXE.
 6. The results from the analyses will be automatically stored in text files for later use or printing. Examples of result files are provided with the names COTDATA.VAR for analysis of variance and genetic effects, COTDATA.PRE for heterosis, and COTDATA.COR for analysis of covariances and correlation.

Output 1 for Variance Analysis

Traits = , 2
 Variance components = , 6
 Degree of freedom = , 3
 File name is cotdata.VAR
 Date and Time for Analysis: Thu Jun 22 21:43:19 2000

Variance Components Estimated by MINQUE(1) with GENVAR1R.EXE.
 Jackknifing Over Block Conducted for Estimating S.E.
 Predicting Genetic Effects by Adjusted Unbiased Prediction (AUP)
 Method.

NS = Not significant; S+ = Significant at 0.10 level.
 S* = Significant at 0.05 level; S** = Significant at 0.01 level.

Linear Contrasts:
 + <1> + <2> - <3> + <4>

Diallel Analysis of Trait 'Bolls' for Public Users

Var Comp	Estimate	S. E.	P-value	
(1): Additive Var	7.30438	1.4425	0.00743	S**
(2): Dominance Var	3.29038	0.935764	0.0195	S*
(3): Add. * Env. Var	0.866547	0.683906	0.147	NS
(4): Dom. * Env. Var	4.82384	1.71492	0.0336	S*
(6): Residual Var	4.18772	0.555651	0.00242	S**

(7): Var (Pheno.)	20.4729	2.79941	0.00264	S**
Proportion of Var(G)/Var(T) Estimate				
(1): Additive Var/Vp	0.356783	0.0888328	0.0139	S*
(2): Dominance Var/Vp	0.160719	0.0275068	0.005	S**
(3): Add. * Env. Var/Vp	0.0423266	0.0244	0.0906	S+
(4): Dom. * Env. Var/Vp	0.235621	0.0667933	0.0194	S*
(6): Residual Var/Vp	0.20455	0.0209314	0.00114	S**
Heritability				
(7): Heritability(N)	0.356783	0.0888328	0.0139	S*
(8): Heritability(B)	0.517502	0.0661515	0.00217	S**
(9): Heritability(NE)	0.0423266	0.0244	0.0906	S+
(10): Heritability(BE)	0.277948	0.0575567	0.00846	S**
Genetic Predictor, S. E., P-value for Two-tail t-test				
(1): Random Effect is Additive Effect				
A1	0.392019	0.632218	0.579	NS
A2	1.326158	0.211643	0.0082	S**
A3	-2.917664	0.353084	0.00371	S**
A4	1.199422	0.548514	0.117	NS
Linear Contrast	3.05342	0.470211	0.00741	S**
(2): Random Effect is Dominance Effect				
D1*1	0.263665	0.437706	0.589	NS
D2*2	-2.176718	0.509854	0.0236	S*
D3*3	-1.244060	0.786988	0.212	NS
D4*4	-1.836773	0.495630	0.0341	S*
D1*2	0.388935	0.399988	0.403	NS
D1*3	-0.349309	0.311425	0.344	NS
D1*4	-0.273600	0.915662	0.785	NS
D2*3	0.210065	0.829160	0.816	NS
D2*4	4.888072	0.707825	0.00622	S**
D3*4	0.129694	0.666849	0.858	NS
Heterosis <Delta>	1.37653	0.337286	0.0266	S*
(3): Random Effect is Add. * Env. Effect				
AE1 in E1	0.089686	0.496245	0.868	NS
AE2 in E1	0.242420	0.070750	0.0416	S*
AE3 in E1	-0.079016	0.182773	0.695	NS
AE4 in E1	-0.253113	0.407134	0.578	NS
AE1 in E2	-0.136729	0.705758	0.859	NS
AE2 in E2	0.342004	0.648600	0.634	NS
AE3 in E2	-1.257717	1.654640	0.502	NS
AE4 in E2	1.052433	0.508793	0.13	NS
Linear Contrast	-1.76747e-005	6.70577e-006	0.0779	S+
(4): Random Effect is Dom. * Env. Effect				
DE11 in E1	-0.349740	0.559982	0.577	NS
DE22 in E1	2.063640	0.515148	0.0279	S*
DE33 in E1	-0.889553	1.186821	0.508	NS
DE44 in E1	-0.318622	1.006553	0.772	NS
DE12 in E1	-1.294414	0.520453	0.0887	S+
DE13 in E1	0.562069	0.405746	0.26	NS
DE14 in E1	1.114442	1.050572	0.367	NS
DE23 in E1	-0.217579	1.660683	0.904	NS
DE24 in E1	-2.368299	0.651167	0.0358	S*

DE34 in E1	1.698030	0.881687	0.15	NS
DE11 in E2	0.751202	0.780806	0.407	NS
DE22 in E2	-4.653504	1.121175	0.0254	S*
DE33 in E2	-0.744776	1.086469	0.542	NS
DE44 in E2	-1.890872	0.707435	0.0755	S+
DE12 in E2	1.815819	0.552480	0.0462	S*
DE13 in E2	-0.926615	0.698261	0.276	NS
DE14 in E2	-1.611676	1.678116	0.408	NS
DE23 in E2	0.437429	0.800245	0.623	NS
DE24 in E2	8.238749	1.841553	0.0208	S*
DE34 in E2	-1.415766	1.261023	0.343	NS
Heterosis <Delta>	0.971038	0.40929	0.0983	S+

Fixed Effect , 12.8719

Fixed Effect , 19.885

Results of Fiber Yield are not presented.

Time Used (Hour) = 0.001389

Output 2 for Covariance Analysis

Traits = , 2

Variance components = , 6

Degree of freedom = , 3

File name is cotdata.COV

Date and Time for Analysis: Thu Jun 22 22:00:24 2000

Variance Components Estimated by MINQUE(1) with GENVAR1R.EXE.
Jackknifing Over Block Conducted for Estimating S.E.

NS = Not significant; S+ = Significant at 0.10 level.

S* = Significant at 0.05 level; S** = Significant at 0.01 level.

Covariances and Correlations Between Bolls & FibYield, for Public Users:

Covariances	Estimates	S.E.	P-value	
Additive Cov	26.4031	15.0422	0.177	NS
Dominance Cov	3.68996	4.09328	0.434	NS
Add. * Env. Cov	5.2684	5.4782	0.407	NS
Dom. * Env. Cov	0.725936	6.15727	0.914	NS
Residual Cov	5.74197	4.7088	0.31	NS

Cov 1=Genotypic

Cov2=Phenotypic

	Estimates	S.E.	P-value	
Cov 2	41.8294	20.9549	0.14	NS
Cov 1	36.0874	21.3383	0.189	NS

Correlation	Estimates	S.E.	P-value	
Additive Cor	0.905414	0.326942	0.0696	S+
Dominance Cor	0.275228	0.243147	0.34	NS
Add. * Env. Cor	1.000000	0.288675	0.0405	S*
Dom. * Env. Cor	0.000000	0	1	NS

Residual Cor	0.318575	0.229826	0.26	NS
Cor 1=Genotypic				
Cor2=Phenotypic	Estimates	S.E.	P-value	
Cor 2	0.556778	0.215421	0.0815	S+
Cor 1	0.635333	0.26869	0.099	S+

Time Used (Hour) = 0.000000

Output 3 for Heterosis Analysis

Traits = , 2

Variance components = , 6

Degree of freedom = , 3

File name is cot8185.

Date and Time for Analysis: Thu Jun 22 22:15:40 2000

Variance Components Estimated by MINQUE(1) with GENVAR1R.EXE.
Jackknifing Over Block Conducted for Estimating S.E.
Genetic Effects by Adjusted Unbiased Prediction (AUP) Method.

NS = Not significant; S+ = Significant at 0.10 level.

S* = Significant at 0.05 level; S** = Significant at 0.01 level.

Diallel Analysis of Trait, Bolls, for Public Users.

Var Comp	Estimate	S. E.	P-value	
Additive Var	7.30429	1.4425	0.00743	S**
Dominance Var	3.29035	0.935764	0.0195	S*
Add. * Env. Var	0.866537	0.683909	0.147	NS
Dom. * Env. Var	4.82386	1.71492	0.0336	S*
Residual Var	4.18772	0.555651	0.00242	S**

Heterosis Analysis of Trait, Bolls, for F2 Seeds with total mean =,
15.312341

No.	Cro	(F ₁) (GE)	S.E.	P- value	Sig- nif. (F ₂)	(F ₂) (GE)	S.E.	P- value	Sig- nif.
Cro 1 <E1>	<1 * 2>	-0.962	0.471	0.134	NS	-0.113	0.578	0.857	NS
Cro 2 <E1>	<1 * 3>	0.573	0.406	0.253	NS	-0.018	0.213	0.938	NS
Cro 3 <E1>	<1 * 4>	0.951	1.020	0.420	NS	0.227	0.366	0.579	NS
Cro 4 <E1>	<2 * 3>	-0.054	1.673	0.976	NS	0.348	0.530	0.558	NS
Cro 5 <E1>	<2 * 4>	-2.379	0.984	0.094	S+	-0.759	0.930	0.474	NS
Cro 6 <E1>	<3 * 4>	1.366	0.489	0.068	S+	0.215	0.630	0.756	NS
Cro 7 <E2>	<1 * 2>	2.021	1.222	0.197	NS	0.138	1.488	0.932	NS
Cro 8 <E2>	<1 * 3>	-2.321	0.646	0.037	S*	-1.856	0.366	0.015	S*
Cro 9 <E2>	<1 * 4>	-0.696	1.562	0.686	NS	-0.175	0.708	0.821	NS
Cro 10 <E2>	<2 * 3>	-0.478	1.110	0.696	NS	-2.047	0.629	0.047	S*
Cro 11 <E2>	<2 * 4>	9.633	1.556	0.008	S**	3.878	0.469	0.004	S**
Cro 12 <E2>	<3 * 4>	-1.621	0.806	0.138	NS	-1.572	0.610	0.082	S+

Significance of F1 or F2 is over Population Mean 15.312341

No.	Cro	(F ₁) (G)	S.E.	P- value	Sig- nif. (F ₂)	(F ₂) (G)	S.E.	P- value	Sig- nif.
Cro 1	<1 * 2>	17.420	1.118	0.156	NS	16.747	1.233	0.329	NS
Cro 2	<1 * 3>	12.437	0.868	0.045	S*	12.367	0.732	0.028	S*

Cro 3	<1 * 4>	16.630	1.075	0.308	NS	16.374	0.748	0.251	NS
Cro 4	<2 * 3>	13.931	1.064	0.285	NS	12.971	0.832	0.067	S+
Cro 5	<2 * 4>	22.726	0.625	0.001	S**	19.279	0.832	0.018	S*
Cro 6	<3 * 4>	13.724	0.814	0.146	NS	12.889	1.033	0.101	NS

No.	Cro	$H_{pm}(F_1)$	S.E.	P-value	Sig-nif.	$H_{pm}(F_2)$	S.E.	P-value	Sig-nif.
Cro 1 <E1>	<1 * 2>	-0.140	0.034	0.027	S*	-0.070	0.017	0.027	S*
Cro 2 <E1>	<1 * 3>	0.077	0.030	0.079	S+	0.039	0.015	0.079	S+
Cro 3 <E1>	<1 * 4>	0.095	0.087	0.355	NS	0.047	0.043	0.355	NS
Cro 4 <E1>	<2 * 3>	-0.053	0.140	0.733	NS	-0.026	0.070	0.733	NS
Cro 5 <E1>	<2 * 4>	-0.212	0.059	0.038	S*	-0.106	0.030	0.038	S*
Cro 6 <E1>	<3 * 4>	0.150	0.115	0.283	NS	0.075	0.058	0.283	NS
Mean for Env. Cro No. = 6		-0.014	0.059	0.830	NS	-0.007	0.029	0.830	NS

Cro 7 <E2>	<1 * 2>	0.246	0.052	0.018	S*	0.123	0.026	0.018	S*
Cro 8 <E2>	<1 * 3>	-0.061	0.056	0.361	NS	-0.030	0.028	0.361	NS
Cro 9 <E2>	<1 * 4>	-0.068	0.153	0.686	NS	-0.034	0.076	0.686	NS
Cro 10 <E2>	<2 * 3>	0.205	0.074	0.071	S+	0.102	0.037	0.071	S+
Cro 11 <E2>	<2 * 4>	0.752	0.200	0.033	S*	0.376	0.100	0.033	S*
Cro 12 <E2>	<3 * 4>	-0.006	0.113	0.958	NS	-0.003	0.057	0.958	NS

Significance of F1 or F2 is over Population Mean 15.312341

No.	Cro	$H_{pm}(F_1)$	S.E.	P-value	Sig-nif.	$H_{pm}(F_2)$	S.E.	P-value	Sig-nif.
Cro 1	<1 * 2>	0.088	0.031	0.067	S+	0.044	0.016	0.067	S+
Cro 2	<1 * 3>	0.009	0.027	0.754	NS	0.005	0.013	0.754	NS
Cro 3	<1 * 4>	0.033	0.078	0.696	NS	0.017	0.039	0.696	NS
Cro 4	<2 * 3>	0.125	0.072	0.181	NS	0.063	0.036	0.181	NS
Cro 5	<2 * 4>	0.450	0.083	0.012	S*	0.225	0.042	0.012	S*
Cro 6	<3 * 4>	0.109	0.075	0.241	NS	0.055	0.037	0.241	NS

No.	Cro	$H_{pb}(F_1)$	S.E.	P-value	Sig-nif.	$H_{pb}(F_2)$	S.E.	P-value	Sig-nif.
Cro 1 <E1>	<1 * 2>	-0.229	0.003	0.000	S**	-0.159	0.019	0.004	S**
Cro 2 <E1>	<1 * 3>	0.049	0.012	0.025	S*	0.010	0.017	0.595	NS
Cro 3 <E1>	<1 * 4>	0.073	0.107	0.542	NS	0.026	0.069	0.732	NS
Cro 4 <E1>	<2 * 3>	-0.170	0.128	0.277	NS	-0.144	0.068	0.123	NS
Cro 5 <E1>	<2 * 4>	-0.322	0.077	0.025	S*	-0.216	0.054	0.029	S*
Cro 6 <E1>	<3 * 4>	0.143	0.114	0.297	NS	0.068	0.056	0.315	NS
Cro 7 <E2>	<1 * 2>	0.101	0.048	0.128	NS	-0.022	0.034	0.563	NS
Cro 8 <E2>	<1 * 3>	-0.183	0.118	0.219	NS	-0.152	0.095	0.206	NS
Cro 9 <E2>	<1 * 4>	-0.077	0.163	0.670	NS	-0.043	0.087	0.657	NS
Cro 10 <E2>	<2 * 3>	0.182	0.116	0.215	NS	0.079	0.126	0.573	NS
Cro 11 <E2>	<2 * 4>	0.615	0.151	0.027	S*	0.239	0.055	0.023	S*
Cro 12 <E2>	<3 * 4>	-0.120	0.165	0.520	NS	-0.117	0.111	0.369	NS

Significance of F1 or F2 is over Population Mean 15.312341

No.	Cro	$H_{pb}(F_1)$	S.E.	P-value	Sig-nif.	$H_{pb}(F_2)$	S.E.	P-value	Sig-nif.
Cro 1	<1 * 2>	0.069	0.040	0.183	NS	0.025	0.029	0.445	NS
Cro 2	<1 * 3>	-0.256	0.081	0.050	S+	-0.261	0.091	0.064	S+
Cro 3	<1 * 4>	0.018	0.088	0.854	NS	0.001	0.049	0.987	NS
Cro 4	<2 * 3>	-0.121	0.092	0.278	NS	-0.184	0.071	0.081	S+
Cro 5	<2 * 4>	0.447	0.076	0.010	S**	0.222	0.036	0.008	S**
Cro 6	<3 * 4>	-0.140	0.082	0.184	NS	-0.195	0.050	0.030	S*

Significance of Heterosis is over Population Mean 15.312341

Pre(F ₁)	16.4871	0.580926	0.136	NS
Pre(F ₂)	15.4467	0.665146	0.853	NS
Hpm(F ₁)	0.135267	0.030647	0.0216	S*
Hpm(F ₂)	0.067634	0.015324	0.0216	S*
Hpb(F ₁)	-0.04533	0.042593	0.365	NS
Hpb(F ₂)	-0.11297	0.035282	0.0493	S*

Results of Fiber yield are not presented.

Time Used (Hour) = 0.000278