

Chapter 2

Diallel Analysis for a Seed and Endosperm Model with Genotype-by-Environment Interaction Effects

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Purpose

To analyze balanced or unbalanced data of diploid seed and triploid endosperm models 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 and F_2 seeds. Experiments with parents, F_1 s, and F_2 s are conducted in multiple environments using a randomized complete-block design.

Genetic Model

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

$$y_{hijkl} = \mu + E_h + G_{ijk} + GE_{hijk} + B_{nl} + e_{hijkl}$$

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

Genetic partitioning for the diploid seed model (Zhu and Weir, 1994a; Zhu, 1996):

For parent (P_i , $k = 0$):

$$G_{ii0} + GE_{hii0} = 2A_i + D_{ii} + C_i + 2Am_i + Dm_{ii} + 2AE_{hi} + DE_{hiii} + CE_{hi} + 2AmE_{hi} + DmE_{hii}$$

For F_1 ($P_i \times P_j$, $k = 1$):

$$G_{ij1} + GE_{hij2} = A_i + A_j + D_{ij} + C_i + 2Am_i + Dm_{ii} + AE_{hi} + AE_{hj} + DE_{hij} + CE_{hi} + 2AmE_{hi} + DmB_{hii}$$

For F_2 ($F_1 \otimes$, $k = 2$):

$$G_{ij2} + GE_{hij2} = A_i + A_j + \frac{1}{4}D_{ii} + \frac{1}{4}D_{jj} + \frac{1}{2}D_{ij} + C_i + Am_i + Am_j + Dm_{ij} + AE_{hi} + AE_{hj} + \frac{1}{4}DE_{hii} + \frac{1}{4}DE_{hjj} + \frac{1}{2}DE_{hij} + CE_{hi} + AmE_{hi} + AmE_{hj} + DmE_{hij}$$

Genetic partitioning for triploid endosperm model (Zhu and Weir, 1994b; Zhu, 1996):

For parent (P_i , $k = 0$):

$$G_{ii0} + GE_{hii0} = 3A_i + 3D_{ii} + C_i + 2Am_i + Dm_{ii} + 3AE_{hi} + 3DE_{hii} + CE_{hi} + 2AmE_{hi} + DmE_{hii}$$

For F_1 ($P_i \times P_j$, $k = 1$):

$$G_{ij1} + GE_{hij1} = 2A_i + A_j + D_{ii} + 2D_{ij} + C_i + 2Am_i + Dm_{ii} + 2AE_{hi} + AE_{hj} + DE_{hii} + 2DE_{hij} + CE_{hi} + 2AmE_{hi} + DmE_{hii}$$

For F_2 ($F_1 \otimes$, $k = 2$):

$$\begin{aligned} G_{ij2} + GE_{hij2} = & 1\frac{1}{2}A_i + 1\frac{1}{2}A_j + D_{ii} + D_{jj} + D_{ij} + C_i + Am_i + Am_j + Dm_{ij} \\ & + 1\frac{1}{2}AE_{hi} + 1\frac{1}{2}AE_{hj} + DE_{hii} + DE_{hjj} + DE_{hij} + CE_{hi} \\ & + AmE_{hi} + AmE_{hj} + DmE_{hij} \end{aligned}$$

where A = direct additive effect, D = direct dominance effect, C = cytoplasm effect, Am = maternal additive effect, Dm = maternal dominance effect, AE = direct additive by environment interaction effect, DE = direct dominance by environment interaction effect, CE = cytoplasm by environment interaction effect, AmE = maternal additive by environment interaction effect, DmE = maternal dominance by environment interaction effect.

Other generations, such as BC_1 s and BC_2 s and their reciprocals (RBC_1 s and RBC_2 s) can also be used for analyzing seed traits (Zhu and Weir, 1994a; Zhu, 1996).

Analysis Methodology

Mixed Linear Model

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

$$\begin{aligned} y = & Xb + U_A e_A + U_D e_D + U_C e_C + U_{Am} e_{Am} + U_{Dm} e_{Dm} + U_{AE} e_{AE} + U_{DE} e_{DE} \\ & + U_{CE} e_{CE} + U_{AmE} e_{AmE} + U_{DmE} e_{DmE} + U_B e_B + e_e \\ = & Xb + \sum_u^{12} U_u e_u \end{aligned}$$

with variance-covariance matrix

$$\begin{aligned} \text{var}(y) = & \sigma_A^2 V_1 + \sigma_D^2 V_2 + \sigma_C^2 V_3 + \sigma_{Am}^2 V_4 + \sigma_{Dm}^2 V_5 + \sigma_{AE}^2 V_6 + \sigma_{DE}^2 V_7 \\ & + \sigma_{CE}^2 V_8 + \sigma_{AmE}^2 V_9 + \sigma_{DmE}^2 V_{10} + \sigma_B^2 V_{11} + \sigma_{A.Am} V_{12} + \sigma_{D.Dm} V_{13} \\ & + \sigma_{AE.AmE} V_{14} + \sigma_{DE.DmE} V_{15} + \sigma_e^2 V_{16} \\ = & \sum_{u=1}^{16} \theta_u V_u \end{aligned}$$

where $V_u = U_u U_u^T$ ($u = 1, 2, \dots, 11$), $V_{12} = (U_1 U_4^T + U_4 U_1^T)$, $V_{13} = (U_2 U_5^T + U_5 U_2^T)$, $V_{14} = (U_6 U_9^T + U_9 U_6^T)$, $V_{15} = (U_7 U_{10}^T + U_{10} U_7^T)$, $V_{16} = I$.

Variance Components

Unbiased estimation of variances and covariances of the same trait can be obtained by the following MINQUE(0/1) equations (Zhu, 1992; Zhu and Weir, 1994a):

$$\left[\text{tr} \left(Q_{(0/1)} V_u Q_{(0/1)} V_v \right) \right] [\hat{\theta}_u] = [y^T Q_{(0/1)} V_u Q_{(0/1)} y]$$

where

$$Q_{(0/1)} = V_{(0/1)}^{-1} - V_{(0/1)}^{-1} X \left(X^T V_{(0/1)}^{-1} X \right)^+ X^T V_{(0/1)}^{-1}$$

$$V_{(0/1)} = \sum_{u=1}^{11} U_u U_u^T + I$$

For diploid seed of F_2 , genetic variance and covariance components can be obtained by $V_A = 2\sigma_A^2$, $V_D = \frac{3}{8}\sigma_D^2$, $V_C = \sigma_C^2$, $V_{Am} = 2\sigma_{Am}^2$, $V_{Dm} = \sigma_{Dm}^2$, $V_{AE} = 2\sigma_{AE}^2$, $V_{DE} = \frac{3}{8}\sigma_{DE}^2$, $V_{CE} = \sigma_{CE}^2$, $V_{AmE} = 2\sigma_{AmE}^2$, $V_{DmE} = \sigma_{DmE}^2$, $V_e = \sigma_e^2$, $C_{A,Am} = 2\sigma_{A,Am}$, $C_{D,Dm} = \frac{1}{2}\sigma_{D,Dm}$, $C_{AE,AmE} = 2\sigma_{AE,AmE}$, $C_{DE,DmE} = \frac{1}{2}\sigma_{DE,DmE}$.

For triploid endosperm of F_2 , genetic variance and covariance components can be obtained by $V_A = 4\frac{1}{2}\sigma_A^2$, $V_D = 3\sigma_D^2$, $V_C = \sigma_C^2$, $V_{Am} = 2\sigma_{Am}^2$, $V_{Dm} = \sigma_{Dm}^2$, $V_{AE} = 4\frac{1}{2}\sigma_{AE}^2$, $V_{DE} = 3\sigma_{DE}^2$, $V_{CE} = \sigma_{CE}^2$, $V_{AmE} = 2\sigma_{AmE}^2$, $V_{DmE} = \sigma_{DmE}^2$, $V_e = \sigma_e^2$, $C_{A,Am} = 3\sigma_{A,Am}$, $C_{D,Dm} = \sigma_{D,Dm}$, $C_{AE,AmE} = 3\sigma_{AE,AmE}$, $C_{DE,DmE} = \sigma_{DE,DmE}$.

The total phenotypic variance is $V_P = V_A + V_D + V_C + V_{Am} + V_{Dm} + V_{AE} + V_{DE} + V_{CE} + V_{AmE} + V_{DmE} + 2C_{A,Am} + 2C_{D,Dm} + 2C_{AE,AmE} + 2C_{DE,DmE} + V_e$, where $C_{A,Am}$ and $C_{D,Dm}$ are the covariances between direct effects (A and D) and maternal effects (Am and Dm) of the same trait, $C_{AE,AmE}$ and $C_{DE,DmE}$ are the covariances between direct by environment interaction effect (AE and DE) and maternal by environment interaction effect (AmE and DmE) of the same trait.

Covariance Components and Correlation

Unbiased estimation of covariances between two traits (y_1 and y_2) can be obtained by MINQUE(0/1) approaches (Zhu, 1992; Zhu and Weir, 1994a).

$$[tr(Q_{(0|1)} V_u Q_{(0|1)} V_v)] [\hat{\theta}_{u|u}] H [y_1^T Q_{(0|1)} V_u Q_{(0|1)} y_2]$$

For diploid seed of F_2 , genetic covariance components can be obtained by $C_A = 2\sigma_{A/A}$, $C_D = \frac{3}{8}\sigma_{D/D}$, $C_C = \sigma_{C/C}$, $C_{Am} = 2\sigma_{Am/Am}$, $C_{Dm} = \sigma_{D/D}$, $C_{AE} = 2\sigma_{AE/AE}$, $C_{DE} = \frac{3}{8}\sigma_{DE/DE}$, $C_{CE} = \sigma_{CE/CE}$, $C_{AmE} = 2\sigma_{AmE/AmE}$, $C_{DmE} = \sigma_{DE/DE}$, $C_e = \sigma_{e/e}$, $C_{A/Am} = 2\sigma_{A/Am}$, $C_{D/Dm} = \frac{1}{2}\sigma_{D/Dm}$, $C_{AE/AmE} = 2\sigma_{AE/AmE}$, $C_{DE/DmE} = \frac{1}{2}\sigma_{DE/DmE}$.

For triploid endosperm of F_2 , genetic covariance components can be obtained by $C_A = 4\frac{1}{2}\sigma_{A/A}$, $C_D = 3\sigma_{D/D}$, $C_C = \sigma_{C/C}$, $C_{Am} = 2\sigma_{Am/Am}$, $C_{Dm} = \sigma_{D/D}$, $C_{AE} = 4\frac{1}{2}\sigma_{AE/AE}$, $C_{DE} = 3\sigma_{DE/DE}$, $C_{CE} = \sigma_{CE/CE}$, $C_{AmE} = 2\sigma_{AmE/AmE}$, $C_{DmE} = \sigma_{DE/DE}$, $C_e = \sigma_{e/e}$, $C_{A/Am} = 3\sigma_{A/Am}$, $C_{D/Dm} = \sigma_{D/Dm}$, $C_{AE/AmE} = 3\sigma_{AE/AmE}$, $C_{DE/DmE} = \sigma_{DE/DmE}$.

The total phenotypic covariance is $C_P = C_A + C_D + C_C + C_{Am} + C_{Dm} + C_{AE} + C_{DE} + C_{CE} + C_{AmE} + C_{DmE} + 2C_{A/Am} + 2C_{D/Dm} + 2C_{AE/AmE} + 2C_{DE/DmE} + C_e$. For trait 1 and trait 2, correlation coefficients of genetic components can be estimated by $r_A = C_A / \sqrt{V_{A(1)}V_{A(2)}}$, $r_D = C_D / \sqrt{V_{D(1)}V_{D(2)}}$, $r_C = C_C / \sqrt{V_{C(1)}V_{C(2)}}$, $r_{Am} = C_{Am} / \sqrt{V_{Am(1)}V_{Am(2)}}$, $r_{Dm} = C_{Dm} / \sqrt{V_{Dm(1)}V_{Dm(2)}}$, $r_{AE} = C_{AE} / \sqrt{V_{AE(1)}V_{AE(2)}}$, $r_{DE} = C_{DE} / \sqrt{V_{DE(1)}V_{DE(2)}}$, $r_{CE} = C_{CE} / \sqrt{V_{CE(1)}V_{CE(2)}}$, $r_{AmE} = C_{AmE} / \sqrt{V_{AmE(1)}V_{AmE(2)}}$, $r_{DmE} = C_{DmE} / \sqrt{V_{DmE(1)}V_{DmE(2)}}$, $r_e = C_e / \sqrt{V_{e(1)}V_{e(2)}}$.

Heritability Components

The total heritability (h^2) can be partitioned into general heritability (h_G^2) and interaction heritability (h_{GE}^2) with their components (Zhu, 1997),

$$\begin{aligned} h^2 &= h_G^2 + h_{GE}^2 \\ &= h_O^2 + h_C^2 + h_M^2 + h_{OE}^2 + h_{CE}^2 + h_{ME}^2 \end{aligned}$$

where $h_O^2 = (V_A + C_{A,Am}) / V_P$ is direct general heritability, $h_C^2 = V_C / V_P$ is cytoplasm general heritability, and $h_M^2 = (V_{Am} + C_{A,Am}) / V_P$ is maternal general heritability; $h_{OE}^2 = (V_{AE} + C_{AE,AmE}) / V_P$ is direct interaction heritability, $h_{CE}^2 = V_{CE} / V_P$ is cytoplasm interaction heritability, and $h_{ME}^2 = (V_{AmE} + C_{AE,AmE}) / V_P$ is maternal interaction heritability.

Selection Response

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

$$R = R_G + R_{GE} \\ = (R_O + R_C + R_M) + (R_{OE} + R_{CE} + R_{ME})$$

where $R_G = ih_G^2 \sqrt{V_P}$ is general response, which consists of direct general response ($R_O = ih_O^2 \sqrt{V_P}$), cytoplasm general response ($R_C = ih_C^2 \sqrt{V_P}$), and maternal general response ($R_M = ih_M^2 \sqrt{V_P}$); $R_{GE} = ih_{GE}^2 \sqrt{V_P}$ is interaction response, which consists of direct interaction response ($R_{OE} = ih_{OE}^2 \sqrt{V_P}$), cytoplasm interaction response ($R_{CE} = ih_{CE}^2 \sqrt{V_P}$), and maternal interaction response ($R_{ME} = ih_{ME}^2 \sqrt{V_P}$).

Heterosis Components

Prediction of genetic merits can be obtained using the linear unbiased prediction (LUP) method (Zhu, 1992; Zhu and Weir, 1996) or the adjusted unbiased prediction (AUP) method (Zhu, 1993a; 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 relative to midparent or female parent can be calculated as ($x = 1$ for diploid seed and $x = 2$ for triploid endosperm):

General heterosis of F_n relative to midparent:

$$H_M(F_n) = H_{MO} + H_{MC} + H_{MM} \\ = \left(\frac{1}{2}\right)^{n-x} \Delta_O + \frac{1}{2} \Delta_C + \left(\frac{1}{2}\right)^{n-2} \Delta_M$$

Interaction heterosis of F_n relative to midparent:

$$H_{ME}(F_n) = H_{MOE} + H_{MCE} + H_{MME} \\ + \left(\frac{1}{2}\right)^{n-x} \Delta_{OE} + \frac{1}{2} \omega_{CE} + \left(\frac{1}{2}\right)^{n-2} \Delta_{ME}$$

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

$$H_F(F_n) = H_{FO} + H_{FM} \\ = \left[\left(\frac{1}{2}\right)^{n-x} \Delta_O - \frac{1}{2} \omega_O \right] + \left[\left(\frac{1}{2}\right)^{n-2} \Delta_M - \frac{1}{2} \omega_M \right]$$

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

$$H_{FE(F_n)} = H_{FOE} + H_{FME} \\ + \left[\left(\frac{1}{2}\right)^{n-x} \Delta_{OE} - \frac{1}{2} \omega_{OE} \right] + \left[\left(\frac{1}{2}\right)^{n-2} \Delta_{ME} - \frac{1}{2} \omega_{ME} \right]$$

where $\Delta_O = D_{ij} - \frac{1}{2}(D_{ii} + D_{jj})$, $\Delta_M = Dm_{ij} - \frac{1}{2}(Dm_{ii} + Dm_{jj})$, $\Delta_{OE} = DE_{hij} - \frac{1}{2}(DE_{hii} + DE_{hjj})$, $\Delta_{ME} = DmE_{hij} - \frac{1}{2}(DmE_{hii} + DmE_{hjj})$, $\omega_O = 2(A_i - A_j) + (D_{ii} - D_{jj})$ for diploid and $\omega_O = 3(A_i - A_j) + 3(D_{ii} - D_{jj})$ for triploid endosperm, $\omega_C = C_i - C_j$, $\omega_M = 2(Am_i - Am_j) + (Dm_{ii} - Dm_{jj})$.

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

Covariances Between Seed Quality Trait and Plant Agronomic Trait

In plant breeding, breeders usually want to improve seed quality traits while keeping the genetic merit of yield traits. Therefore, understanding the genetic relationship between seed quality traits and plant yield traits is of importance. Seed models and plant models have unequal design matrices. Zhu (1993b) developed a new method for estimating genetic covariance components between seed traits (y_s) and plant traits (y_p). For seed model:

$$y_s = Xb_{(S)} + U_A e_{A(S)} + U_D e_{D(S)} + U_C e_{C(S)} + U_{Am} e_{Am(S)} + U_{Dm} e_{Dm(S)} \\ + U_{AE} e_{AE(S)} + U_{DE} e_{DE(S)} + U_{CE} e_{CE(S)} + U_{AmE} e_{AmE(S)} + U_{DmE} e_{DmE(S)} \\ + U_B e_{B(S)} + e_{e(S)} \\ = Xb_{(S)} + \sum_u^{12} U_u e_{u(S)}$$

The corresponding plants bearing the seeds will have the following mixed linear model:

$$\begin{aligned} y_p &= Xb_{(P)} + U_C e_{C(P)} + U_{Am} e_{Am(P)} + U_{Dm} e_{Dm(P)} \\ &\quad + U_{CE} e_{CE(P)} + U_{AmE} e_{AmE(P)} + U_{DmE} e_{DmE(P)} \\ &\quad + U_B e_{B(P)} + e_{e(P)} \\ &= Xb_{(P)} + \sum_u^8 U_u e_{u(P)} \end{aligned}$$

There are covariances between random factors of seed traits and those of plant traits: $\sigma_{A/Am}$ = covariance between seed direct additive effects and plant additive effects, $\sigma_{D/Dm}$ = covariance between seed direct dominance effects and plant dominance effects, $\sigma_{C/C}$ = covariance between seed cytoplasm effects and plant cytoplasm effects, $\sigma_{Am/Am}$ = covariance between seed maternal additive effects and plant additive effects, $\sigma_{Dm/Dm}$ = covariance between seed maternal dominance effects and plant dominance effects, $\sigma_{AE/AmE}$ = covariance between seed *AE* effects and plant *AmE* effects, $\sigma_{DE/DmE}$ = covariance between seed *DE* effects and plant *DmE* effects, $\sigma_{CE/CE}$ = covariance between seed *CE* effects and plant *CE* effects, $\sigma_{AmE/AmE}$ = covariance between seed *AmE* effects and plant *AmE* effects, $\sigma_{DmE/DmE}$ = covariance between seed *DmE* effects and plant *DmE* effects, $\sigma_{B/B}$ = covariance between seed block effects and plant block effects, $\sigma_{e/e}$ = covariance between seed residual effects and plant residual effects.

If we define $F_1 = (U_A U_A^T + U_{Am} U_A^T)$, $F_2 = (U_D U_D^T + U_{Dm} U_D^T)$, $F_3 = (2U_C U_C^T)$, $F_4 = (2U_{Am} U_{Am}^T)$, $F_5 = (2U_{Dm} U_{Dm}^T)$, $F_6 = (U_{AE} U_{AmE}^T + U_{AmE} U_{AE}^T)$, $F_7 = (U_{DE} U_{DmE}^T + U_{DmE} U_{DE}^T)$, $F_8 = (2U_{CE} U_{CE}^T)$, $F_9 = (2U_{AmE} U_{AmE}^T)$, $F_{10} = (2U_{DmE} U_{DmE}^T)$, $F_{11} = (2U_B U_B^T)$, and $F_{12} = 2I$, covariance components between a seed trait and a plant trait can then be estimated by the following equations:

$$[tr(Q_{(0/1)} F_u Q_{(0/1)} F_v)] [\hat{\sigma}_{u/v}] = [2y_s^T Q_{(0/1)} F_u Q_{(0/1)} y_p]$$

where

$$\begin{aligned} Q_{(0/1)} &= V_{(0/1)}^{-1} - V_{(0/1)}^{-1} X (X^T V_{(0/1)}^{-1} X)^{-1} X^T V_{(0/1)}^{-1} \\ V_{(0/1)} &= 2[U_C U_C^T + U_{Am} U_{Am}^T + U_{Dm} U_{Dm}^T + U_{CE} U_{CE}^T + U_{AmE} U_{AmE}^T + U_{DmE} U_{DmE}^T \\ &\quad + U_B U_B^T + I] \end{aligned}$$

Originators

- Zhu, J. (1992). Mixed model approaches for estimating genetic variances and covariances. *Journal of Biomathematics* 7(1):1-11.
- Zhu, J. (1993a). Methods of predicting genotype value and heterosis for offspring of hybrids (Chinese). *Journal of Biomathematics* 8(1):32-44.
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- Zhu, J. (1996). Analysis methods for seed models with genotype \times environment interactions (Chinese). *Acta Genetica Sinica* 23(1):56-68.
- Zhu, J. (1997). *Analysis Methods for Genetic Models*. Agricultural Publication House of China, Beijing.
- Zhu, J. and Weir, B.S. (1994a). Analysis of cytoplasmic and maternal effects. I. A genetic model for diploid plant seeds and animals. *Theoretical and Applied Genetics* 89:153-159.
- Zhu, J. and Weir, B.S. (1994b). Analysis of cytoplasmic and maternal effects. II. Genetic models for triploid endosperm. *Theoretical and Applied Genetics* 89:160-166.
- 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). GENDIPLD.EXE for constructing seed model, GENVAR0.EXE for estimating components of variance and heritability, GENCOV0.EXE for estimating components of covariance and correlation, GENHET0.EXE for predicting genetic effects and components of heterosis. *Analysis Methods for Genetic Models* (pp. 256-278), 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 (COTSEEDM.TXT) to be analyzed (Parent = 5, Year = 2, Generation = P, F₁, F₂, Blk = 1):

Year	Fema	Male	Gene	Blk	Pro%	Oil%
1	1	1	0	1	37.6	37.4
1	1	3	1	1	37.5	36.5
1	1	3	2	1	38.3	36.1
1	1	4	1	1	38.4	34.6
1	1	4	2	1	37.8	35.3
1	2	2	0	1	42.9	32.5
1	2	3	1	1	39.8	33.1

1	2	3	2	1	39.2	35.5
1	3	1	2	1	37.2	35.9
1	3	2	2	1	37.1	37.1
1	3	3	0	1	38	34.8
1	3	5	1	1	40.6	35.4
1	3	5	2	1	39.8	36.1
1	4	1	1	1	37.2	36.8
1	4	1	2	1	37	36.1
1	4	2	1	1	39.2	38.1
1	4	2	2	1	38.1	35.3
1	4	4	0	1	38.9	35.5
1	4	5	1	1	41	38.1
1	4	5	2	1	40.1	35.6
1	5	5	0	1	45.8	34.5
2	1	1	0	1	37.7	36.5
2	1	3	1	1	37.2	36.5
2	1	3	2	1	37.2	35.6
2	1	4	1	1	36	36.5
2	1	4	2	1	35.9	36.2
2	2	2	0	1	40.5	34.8
2	2	3	1	1	37.4	36.9
2	2	3	2	1	37	36.8
2	2	4	1	1	38.3	36.3
2	2	4	2	1	37.2	36.9
2	3	3	0	1	38.6	35.4
2	3	5	1	1	38.3	35.7
2	3	5	2	1	37.8	35.8
2	4	4	0	1	39.7	35.1
2	4	5	1	1	38.9	35.6
2	4	5	2	1	38.6	34.6
2	5	5	0	1	44	31.2

1. Use one of the following two programs for generating a mating design matrix and data:

GENDIPLD.EXE for traits of diploid seeds or animals.

GENTRIPL.EXE for traits of triploid endosperm.

Before running these programs, create a data file (COTSEEDM.TXT) for your analysis with five design columns followed by trait columns. The five design columns should be labeled (1) environment, (2) maternal, (3) paternal, (4) generation, and (5) replication. There is a limitation (<100 traits) for the number of trait columns.

2. Run programs for variance and covariance analyses. Standard errors of estimates are calculated by jackknifing over cell means.
3. You should always run GENVAR0C.EXE for estimating variance components and predicting genetic effects before estimating covariance and correlation. This program will allow you to choose the prediction methods (LUP or AUP). You also need to input coefficients (1, 0, or -1) for conducting linear contrasts for genetic effects.

4. After finishing variance analysis, run GENCOV0C.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 F₂ seed, you can run GENHET0C.EXE.
6. All results will be automatically stored in text files for later use or printing. Examples of result files are provided with the names COTSEEDM.VAR for analysis of variance and genetic effects, COTSEEDM.PRE for predicting genotype values and heterosis, and COTSEEDM.COR for analysis of covariances and correlation.

Output 1 for Single Trait Test

Traits = , 2
 Variance components = , 15
 Degree of freedom = , 37
 File name is cotseedm.VAR
 Date and Time for Analysis: Fri Jun 23 21:06:32 2000

Variance Components Estimated by MINQUE(0/1) with GENHET0C.EXE.
 Predicting Genetic Effects by Adjusted Unbiased Prediction (AUP)
 Method.

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.

Linear Contrasting Test:
 + <1> + <2> + <3> - <4> - <5>

Genetic Analysis of 1 Trait, Pro%, Public Users.

Var Comp	Estimate	S. E.	P-value	
Direct Additive	4.22578	0.971094	5.11522e-005	S**
Direct Dominance	0.661729	0.187698	0.000572911	S**
Cytoplasm	0.979784	0.316941	0.00188757	S**
Maternal Additive	0	0	0.5	NS
Maternal Dominance	2.14103	0.491783	5.08401e-005	S**
D Add. × Env.	4.14108	1.08163	0.00024065	S**
D Dom. × Env.	0.226718	0.0427548	2.75864e-006	S**
Cyto × Env.	3.08077	0.725817	7.05334e-005	S**
M Add. × Env.	2.1	0.520779	0.000132504	S**
M Dom. × Env.	0	0	0.5	NS
A.Am	0	0.271806	1	NS
D.Dm	0.684771	0.400178	0.0954231	S+
AE.AmE	-2.45518	1.3901	1.91438	NS
DE.DmE	0	0	1	NS
Residual	1.56207	0.341266	2.58189e-005	S**
Var (Phenotype)	15.5781	2.49795	1.50314e-007	S**

Heritability	Estimate	S. E.	P-value	
General Heritability N(A)	0.271263	0.0372287	5.88087e-009	S**

General Heritability B(A+D)	0.357699	0.0380067	-1.37905e-011	S**
General Heritability N(C)	0.0628948	0.0226378	0.00426618	S**
General Heritability N(Am)	0	0	0.5	NS
General Heritability B(Am+Dm)	0.181395	0.0240944	2.80833e-009	S**
Interaction Heritability N(AE)	0.108222	0.0325895	0.00101347	S**
Interaction Heritability B(AE+DE)	0.28038	0.0788095	0.000523146	S**
Interaction Heritability N(CE)	0.197762	0.0388026	5.23056e-006	S**
Interaction Heritability N(AmE)	-0.0227996	0.0252744	0.186424	NS
Interaction Heritability B(AmE+DmE)	0.134804	0.0530296	0.00766977	S**

Genetic Predictor, S. E. , P-value of Two Tail t-test

<1>: Random Effect is Direct Additive

A1	-1.024558	0.602650	0.0975	S+
A2	0.849192	0.492454	0.093	S+
A3	-0.959033	0.579315	0.106	NS
A4	0.023544	0.447671	0.958	NS
A5	1.110611	0.833896	0.191	NS
Linear Contrast	-1.74484	1.15265	0.138582	NS

<2>: Random Effect is Direct Dominance

D1*1	0.430174	0.474310	0.37	NS
D2*2	2.060002	1.236368	0.104	NS
D3*3	0.896631	0.591905	0.138	NS
D4*4	1.637057	0.873815	0.0689	S+
D5*5	1.830764	0.882766	0.0451	S*
D1*3	-0.478229	0.456267	0.301	NS
D1*4	-2.177030	1.321475	0.108	NS
D2*3	-2.215217	1.325812	0.103	NS
D2*4	-0.755464	0.577872	0.199	NS
D3*5	-0.781604	0.580198	0.186	NS
D4*5	-0.447118	0.831929	0.594	NS
Heterosis <Delta>	-2.30767	1.86916	0.225	NS

<3>: Random Effect is Cytoplasm

C1	-0.278965	0.268528	0.306	NS
C2	0.125445	0.666036	0.852	NS
C3	-0.434191	1.217060	0.723	NS
C4	0.022447	0.667609	0.973	NS
C5	0.565182	1.479941	0.705	NS
Linear Contrast	-1.32754	4.23754	0.755827	NS

<4>: Random Effect is Maternal Additive
No Significant Effects.

<5>: Random Effect is Maternal Dominance

Dm1*1	0.328107	0.347168	0.351	NS
Dm2*2	1.334076	0.415525	0.00274	S**
Dm3*3	1.422192	0.519389	0.00944	S**
Dm4*4	1.798117	0.562728	0.00285	S**
Dm5*5	1.842966	0.707409	0.0131	S*
Dm1*3	0.355737	0.403627	0.384	NS
Dm1*4	-0.581557	0.660676	0.384	NS
Dm2*3	-1.434893	0.704201	0.0488	S*
Dm2*4	-1.937210	0.780548	0.0177	S*
Dm3*5	-1.322985	0.768254	0.0934	S+
Dm4*5	-1.804685	0.762519	0.0233	S*

Heterosis <Delta> -2.05554 0.153624 -5.09e-011 S**

<6>: Random Effect is D Add. × Env.

AE1 in E1	-2.254065	0.889523	0.0156	S*
AE2 in E1	0.550176	0.647403	0.401	NS
AE3 in E1	-1.761268	0.848635	0.045	S*
AE4 in E1	0.449786	0.592606	0.453	NS
AE5 in E1	3.015095	1.252800	0.0212	S*
AE1 in E2	0.632488	0.575894	0.279	NS
AE2 in E2	0.874021	0.831909	0.3	NS
AE3 in E2	0.005609	0.629156	0.993	NS
AE4 in E2	-0.596792	0.806521	0.464	NS
AE5 in E2	-0.915384	0.884746	0.308	NS
Linear Contrast	-5.3845	1.32097	0.000233	S**

<7>: Random Effect is D Dom. × Env.

DE1*1 in E1	-0.159850	0.800087	0.843	NS
DE2*2 in E1	0.407181	1.084693	0.71	NS
DE3*3 in E1	-0.132742	0.696827	0.85	NS
DE4*4 in E1	0.001560	0.707096	0.998	NS
DE5*5 in E1	0.110871	0.599268	0.854	NS
DE1*3 in E1	-0.214554	0.706944	0.763	NS
DE1*4 in E1	-0.558690	0.675476	0.413	NS
DE2*3 in E1	-0.403386	1.054141	0.704	NS
DE2*4 in E1	0.075915	0.482125	0.876	NS
DE3*5 in E1	0.105371	1.002477	0.917	NS
DE4*5 in E1	0.768304	1.301119	0.558	NS
DE1*1 in E2	0.508888	1.015302	0.619	NS
DE2*2 in E2	0.623124	1.464434	0.673	NS
DE3*3 in E2	0.853831	1.248241	0.498	NS
DE4*4 in E2	0.310951	1.774209	0.862	NS
DE5*5 in E2	0.149658	1.260388	0.906	NS
DE1*3 in E2	-0.242427	0.585483	0.681	NS
DE1*4 in E2	-0.388505	2.125310	0.856	NS
DE2*3 in E2	-0.489308	1.570559	0.757	NS
DE2*4 in E2	-0.455681	0.679028	0.506	NS
DE3*5 in E2	-0.711946	1.394222	0.613	NS
DE4*5 in E2	-0.158580	1.360425	0.908	NS
Heterosis <Delta>	1.00932	2.70601	0.711	NS

<8>: Random Effect is Cyto × Env.

CE1 in E1	0.776034	0.458734	0.0991	S+
CE2 in E1	2.165781	1.241707	0.0894	S+
CE3 in E1	-1.300904	1.205518	0.288	NS
CE4 in E1	-1.491405	0.967790	0.132	NS
CE5 in E1	-0.149753	1.093888	0.892	NS
CE1 in E2	-1.444760	0.686140	0.0421	S*
CE2 in E2	-1.573186	0.812138	0.0604	S+
CE3 in E2	-0.538525	0.951240	0.575	NS
CE4 in E2	0.589799	1.194278	0.624	NS
CE5 in E2	2.966626	1.385019	0.0388	S*
Linear Contrast	2.09064	1.35549	0.131499	NS

<9> : Random Effect is M Add. × Env.

AmE1 in E1	0.164594	0.421542	0.698	NS
AmE2 in E1	-0.132997	0.439265	0.764	NS

AmE3 in E1	1.211076	0.516050	0.0244	S*
AmE4 in E1	-2.478739	1.117579	0.0328	S*
AmE5 in E1	1.235679	0.732488	0.1	NS
AmE1 in E2	-1.227880	0.750977	0.111	NS
AmE2 in E2	-1.586811	0.633135	0.0167	S*
AmE3 in E2	-0.309359	0.516714	0.553	NS
AmE4 in E2	-0.003356	0.573114	0.995	NS
AmE5 in E2	3.127315	1.394990	0.0311	S*
Linear Contrast	2.71224	3.94209	0.495730	NS

<10>: Random Effect is M Dom. × Env.
No Significant Effects.

Results of Oil% are not presented.

Time Used (Hour) = 0.001389

Output 2 for Covariance Analysis

Traits = , 2

Variance components = , 15

Degree of freedom = , 37

File name is cotseedm.COV

Date and Time for Analysis: Fri Jun 23 21:06:49 2000

Variance Components Estimated by MINQUE(0/1) with GENHETOC.EXE.

Jackknifing Over Block Conducted for Estimating S.E.

For statistical methods, see the following references:

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, Pro% &, Oil% for, Public Users.:

Covariances	Estimates	S.E.	P-value	
Direct Additive Cov	-0.12332	0.785577	0.876	NS
Direct Dominance Cov	-0.18046	0.223768	0.425	NS
Cytoplasm Cov	-0.0560615	0.946456	0.953	NS
Maternal Additive Cov	-0.247106	0.497206	0.622	NS
Maternal Dominance Cov	-0.76196	0.363677	0.0431	S*
D Add. × Env. Cov	0.238753	1.25031	0.85	NS
D Dom. × Env. Cov	0.0696955	0.201047	0.731	NS
Cyto × Env. Cov	-0.748348	0.966985	0.444	NS
M Add. × Env. Cov	-0.567987	0.712327	0.43	NS
M Dom. × Env. Cov	0.139297	0.400729	0.73	NS
A.Am Cov	0.0209709	0.592716	0.972	NS
D.Dm Cov	-0.317895	0.181318	0.0878	S+
AE.AmE Cov	0.538553	0.864524	0.537	NS
DE.DmE Cov	-0.104535	0.150625	0.492	NS
Residual Cov	-0.125117	0.335582	0.711	NS

Cov <1=Genotypic>

Cov <2=Phenotypic>

Cov	Estimates	S.E.	P-value	
Cov 2	-2.08843	1.00453	0.0446	S*
Cov 1	-1.96331	1.0037	0.058	S+

Correlation	Estimates	S.E.	P-value	
Direct Additive Cor	0.000000	0	1	NS
Direct Dominance Cor	-0.313393	0.0713042	8.97e-005	S**
Cytoplasm Cor	0.000000	0	1	NS
Maternal Additive Cor	0.000000	0	1	NS
Maternal Dominance Cor	-0.527223	0.0751039	2.66e-008	S**
D Add. × Env. Cor	0.064792	0.0855313	0.454	NS
D Dom. × Env. Cor	0.225062	0.0669711	0.00182	S**
Cyto × Env. Cor	-0.302136	0.0755769	0.000294	S**
M Add. × Env. Cor	-0.271364	0.0710278	0.000493	S**
M Dom. × Env. Cor	0.000000	0	1	NS
Residual Cor	-0.379882	0.0634317	6.5e-007	S**

Cor <1=Genotypic>

<2=Phenotypic>

	Estimates	S.E.	P-value	
Cor 2	-0.157513	0.0580681	0.0101	S*
Cor 1	-0.154315	0.0587436	0.0125	S*

Time Used (Hour) = 0.000556

Output 3 for Heterosis Analysis

Traits = , 2

Variance components = , 15

Degree of freedom = , 37

File name is cotseedm.PRE

Date and Time for Analysis: Fri Jun 23 21:07:07 2000

Variance Components Estimated by MINQUE(0/1) with GENHETOC.EXE.
Predicting Genetic Effects by Adjusted Unbiased Prediction (AUP)
Method.

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.

Genetic Analysis of 1 Trait, Pro%, for Public Users.

Var Comp	Estimate	S. E.	P-value	
Direct Additive	4.22543	0.971079	5.12e-005	S**
Direct Dominance	0.661737	0.187698	0.000573	S**
Cytoplasm	0.979678	0.316932	0.00189	S**
Maternal Additive	0	0	0.5	NS
Maternal Dominance	2.141	0.491782	5.08e-005	S**
D Add. × Env.	4.14101	1.08162	0.000241	S**
D Dom. × Env.	0.226713	0.042754	2.76e-006	S**
Cyto × Env.	3.08084	0.725821	7.05e-005	S**
M Add. × Env.	2.10002	0.520781	0.000132	S**
M Dom. × Env.	0	0	0.5	NS
A.Am	0	0	1	NS
D.Dm	0.684787	0.400178	0.0954	S+
AE.AmE	-2.45513	1.3901	0.0856	S+
DE.DmE	0	0	1	NS

Residual	1.5621	0.341269	2.58e-005	S**
Var(Phenotype)	15.5779	2.49795	1.5e-007	S**

Genetic Advance(for 0.05)	Estimate	S. E.	P-value	
General Genetic Advance (A)	5.69401	0.844563	3.13324e-008	S**
General Genetic Advance (C)	1.32017	0.382756	0.000709897	S**
General Genetic Advance (Am)	0	0	0.5	NS
Interaction Genetic Advance (AE)	2.27182	0.576013	0.00017183	S**
Interaction Genetic Advance (CE)	4.15161	0.768543	2.0263e-006	S**
Interaction Genetic Advance (AmE)	0.478526	0.466339	0.155745	NS

Heterosis Analysis of Trait, Pro%, for F2 Seeds with total mean =, 38.731644

No.	Cro	G(T)	S.E.	Pv	Sig	G(O)	S.E.	Pv	Sig	G(C)	S.E.	Pv	Sig	G(M)	S.E.	Pv	Sig
Cro<1>	<1*3>	-1.810.71	0.01	0.01	S*	-1.89	0.69	0.01	S**	-0.28	0.19	0.15	NS	0.36	0.34	0.30	NS
Cro<2>	<1*4>	-2.430.67	0.00	0.00	S**	-1.57	0.59	0.01	S*	-0.28	0.19	0.15	NS	-0.58	0.40	0.16	NS
Cro<3>	<2*3>	-1.790.75	0.02	0.02	S*	-0.48	0.37	0.21	NS	0.13	0.40	0.76	NS	-1.43	0.66	0.04	S*
Cro<4>	<2*4>	-0.390.99	0.69	0.69	NS	1.42	0.57	0.02	S*	0.13	0.40	0.76	NS	-1.94	0.76	0.02	S*
Cro<5>	<3*5>	-1.311.39	0.35	0.35	NS	0.44	0.32	0.18	NS	-0.43	0.89	0.63	NS	-1.32	0.76	0.09	S+
Cro<6>	<4*5>	0.001.04	1.00	1.00	NS	1.78	0.58	0.00	S**	0.02	0.40	0.96	NS	-1.80	0.74	0.02	S*

No.	Cro	Hm(T)	S.E.	Pv	Sig	Hm(O)	S.E.	Pv	Sig	Hm(C)	S.E.	Pv	Sig	Hm(M)	S.E.	Pv	Sig
Cro<1>	<1*3>	-0.03	0.02	0.22	NS	-0.01	0.01	0.07	S+	0.00	0.01	0.83	NS	-0.01	0.01	0.33	NS
Cro<2>	<1*4>	-0.09	0.02	0.00	S**	-0.04	0.02	0.04	S*	0.00	0.00	0.24	NS	-0.04	0.02	0.02	S*
Cro<3>	<2*3>	-0.11	0.04	0.01	S*	-0.05	0.02	0.06	S+	0.01	0.02	0.66	NS	-0.07	0.02	0.00	S**
Cro<4>	<2*4>	-0.12	0.04	0.00	S**	-0.03	0.02	0.05	S*	0.00	0.01	0.89	NS	-0.09	0.03	0.00	S**
Cro<5>	<3*5>	-0.12	0.05	0.04	S*	-0.03	0.01	0.03	S*	-0.01	0.03	0.62	NS	-0.08	0.03	0.02	S*
Cro<6>	<4*5>	-0.13	0.05	0.01	S**	-0.03	0.01	0.00	S**	-0.01	0.02	0.73	NS	-0.09	0.03	0.00	S**

No.	Cro	Hf(T)	S.E.	Pv	Sig	Hf(O)	S.E.	Pv	Sig	Hf(M)	S.E.	Pv	Sig	Gen.	S.E.	Pv	Sig
Cro<1>	<1*3>	-0.01	0.02	0.75	NS	-0.01	0.01	0.60	NS	0.00	0.01	0.96	NS	0.00	0.00	2.00	NS
Cro<2>	<1*4>	-0.02	0.02	0.33	NS	0.00	0.02	0.95	NS	-0.02	0.02	0.15	NS	0.00	0.00	2.00	NS
Cro<3>	<2*3>	-0.18	0.06	0.01	S**	-0.11	0.05	0.03	S*	-0.07	0.02	0.00	S**	0.00	0.00	2.00	NS
Cro<4>	<2*4>	-0.14	0.05	0.01	S*	-0.06	0.04	0.11	NS	-0.08	0.03	0.00	S**	0.00	0.00	2.00	NS
Cro<5>	<3*5>	-0.03	0.03	0.33	NS	0.04	0.03	0.15	NS	-0.07	0.03	0.02	S*	0.00	0.00	2.00	NS
Cro<6>	<4*5>	-0.09	0.03	0.00	S**	0.00	0.02	0.90	NS	-0.09	0.03	0.00	S**	0.00	0.00	2.00	NS

Interaction Heterosis Analysis of Trait, Pro%, for F2 Seeds with total mean =, 38.731644

No.	Cro	GE(T)	S.E.	Pv	Sig	GE(O)	S.E.	Pv	Sig	GE(C)	S.E.	Pv	Sig	GE(M)	S.E.	Pv	Sig
Env.<1>	<1*3>	-2.04	1.06	0.06	S+	-4.20	1.25	0.00	S**	0.78	0.32	0.02	S*	1.38	0.50	0.01	S**
Env.<1>	<1*4>	-3.66	1.30	0.01	S**	-2.12	0.77	0.01	S**	0.78	0.43	0.08	S+	-2.31	1.12	0.05	S*
Env.<1>	<2*3>	1.90	1.69	0.27	NS	-1.34	0.87	0.13	NS	2.17	1.82	0.24	NS	1.08	0.98	0.28	NS
Env.<1>	<2*4>	0.70	1.99	0.73	NS	1.14	1.11	0.31	NS	2.17	1.82	0.24	NS	-2.61	1.03	0.02	S*
Env.<1>	<3*5>	2.45	1.57	0.13	NS	1.30	0.95	0.18	NS	-1.30	1.23	0.30	NS	2.45	0.91	0.01	S*
Env.<1>	<4*5>	1.14	1.06	0.29	NS	3.88	1.45	0.01	S*	-1.49	0.69	0.04	S*	-1.24	0.99	0.22	NS
Env.<2>	<1*3>	-2.12	1.11	0.06	S+	0.86	1.17	0.47	NS	-1.44	0.65	0.03	S*	-1.54	0.85	0.08	S+
Env.<2>	<1*4>	-2.63	1.41	0.07	S+	0.05	0.83	0.96	NS	-1.44	0.65	0.03	S*	-1.23	0.61	0.05	S+
Env.<2>	<2*3>	-2.47	1.47	0.10	NS	1.00	0.70	0.16	NS	-1.57	1.03	0.14	NS	-1.90	0.84	0.03	S*
Env.<2>	<2*4>	-2.88	1.55	0.07	S+	0.28	0.73	0.70	NS	-1.57	1.03	0.14	NS	-1.59	0.84	0.07	S+
Env.<2>	<3*5>	1.27	1.24	0.31	NS	-1.01	0.69	0.15	NS	-0.54	0.39	0.17	NS	2.82	1.24	0.03	S*
Env.<2>	<4*5>	2.24	1.67	0.19	NS	-1.48	0.83	0.08	S+	0.59	0.80	0.46	NS	3.12	1.48	0.04	S*

No.	Cro	HmE(T)	S.E.	Pv	Sig	HmE(O)	S.E.	Pv	Sig	HmE(C)	S.E.	Pv	Sig	HmE(M)	S.E.	Pv	Sig
Env.<1>	<1*3>	-0.03	0.01	0.02	S*	0.00	0.00	0.37	NS	0.03	0.01	0.01	S*	0.00	0.00	2.00	NS

Env.<1><1*4>	0.02	0.04	0.59	NS	-0.01	0.03	0.81	NS	0.03	0.01	0.02	S*	0.00	0.00	2.00	NS
Env.<1><2*3>	0.04	0.05	0.49	NS	-0.01	0.01	0.53	NS	0.04	0.04	0.28	NS	0.00	0.00	2.00	NS
Env.<1><2*4>	0.05	0.03	0.18	NS	0.00	0.02	0.94	NS	0.05	0.03	0.13	NS	0.00	0.00	2.00	NS
Env.<1><3*5>	-0.01	0.02	0.54	NS	0.00	0.01	0.85	NS	-0.01	0.02	0.38	NS	0.00	0.00	2.00	NS
Env.<1><4*5>	-0.01	0.03	0.79	NS	0.01	0.02	0.62	NS	-0.02	0.01	0.11	NS	0.00	0.00	2.00	NS
Env.<2><1*3>	-0.02	0.01	0.10	S+	-0.01	0.01	0.06	S+	-0.01	0.01	0.28	NS	0.00	0.00	2.00	NS
Env.<2><1*4>	-0.04	0.05	0.48	NS	-0.01	0.04	0.78	NS	-0.03	0.02	0.14	NS	0.00	0.00	2.00	NS
Env.<2><1*5>	-0.03	0.05	0.53	NS	-0.02	0.04	0.71	NS	-0.01	0.02	0.41	NS	0.00	0.00	2.00	NS
Env.<2><2*4>	-0.04	0.05	0.47	NS	-0.01	0.03	0.71	NS	-0.03	0.02	0.24	NS	0.00	0.00	2.00	NS
Env.<2><3*5>	-0.06	0.06	0.29	NS	-0.02	0.04	0.67	NS	-0.05	0.01	0.00	S**	0.00	0.00	2.00	NS
Env.<2><4*5>	-0.04	0.05	0.45	NS	-0.01	0.03	0.84	NS	-0.03	0.01	0.00	S**	0.00	0.00	2.00	NS

No.	Cro HfE(T)	S.E.	Pv	Sig	HfE(O)	S.E.	Pv	Sig	HfE(C)	S.E.	Pv	Sig	HfE	S.E.	Pv	Sig
Env.<1><1*3>	0.04	0.02	0.07	S+	0.01	0.02	0.47	NS	0.03	0.01	0.05	S+	0.00	0.00	2.00	NS
Env.<1><1*4>	0.00	0.08	0.97	NS	0.07	0.09	0.47	NS	-0.07	0.04	0.09	S+	0.00	0.00	2.00	NS
Env.<1><2*3>	-0.04	0.07	0.58	NS	-0.07	0.04	0.06	S+	0.03	0.05	0.50	NS	0.00	0.00	2.00	NS
Env.<1><2*4>	-0.07	0.05	0.21	NS	-0.01	0.04	0.79	NS	-0.06	0.05	0.23	NS	0.00	0.00	2.00	NS
Env.<1><3*5>	0.13	0.04	0.00	S**	0.13	0.04	0.00	S**	0.00	0.02	0.98	NS	-4.88	0.27	0.00	S**
Env.<1><4*5>	0.17	0.04	0.00	S**	0.08	0.03	0.01	S**	0.10	0.05	0.09	S+	-2.54	0.25	0.00	S**
Env.<2><1*3>	0.00	0.04	1.00	NS	-0.02	0.03	0.42	NS	0.02	0.02	0.23	NS	0.00	0.00	2.00	NS
Env.<2><1*4>	-0.01	0.04	0.77	NS	-0.04	0.05	0.41	NS	0.03	0.03	0.24	NS	0.00	0.00	2.00	NS
Env.<2><2*3>	0.00	0.05	0.97	NS	-0.04	0.06	0.55	NS	0.03	0.02	0.14	NS	0.00	0.00	2.00	NS
Env.<2><2*4>	-0.01	0.05	0.80	NS	-0.05	0.06	0.36	NS	0.04	0.02	0.11	NS	0.00	0.00	2.00	NS
Env.<2><3*5>	0.04	0.05	0.44	NS	-0.05	0.04	0.24	NS	0.09	0.04	0.04	S*	0.00	0.00	2.00	NS
Env.<2><4*5>	0.07	0.05	0.19	NS	-0.02	0.02	0.53	NS	0.08	0.04	0.04	S*	0.00	0.00	2.00	NS

Results of Oil% are not presented.

Time Used (Hour) = 0.000278