Chapter 4

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

Jun Zhu

Purpose

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

Definitions

Mating Design

A set of inbred lines is sampled from a reference population. Parents are used to produce F_1 crosses and their F_2. Experiments with parents, F_1s, and F_2s are conducted in multiple environments using a randomized complete block design.

Genetic Model

The genetic model for genetic entry of the kth type of generation derived from parents i and j in the lth block within the hth environment is

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

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.

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

$$G_{ii0} + GE_{hii0} = 2A_i + D_{ii} + 4AA_{ii} + 2AE_{hi} + DE_{hii} + 4AAE_{hii}$$

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

$$\begin{aligned} G_{ij1} + GE_{hij1} &= A_i + A_j + D_{ij} + AA_{ii} + AA_{jj} + 2AA_{ij} + AE_{hi} \\ &\quad + AE_{hj} + DE_{hij} + AAE_{hii} + AAE_{hjj} + 2AAE_{hij} \end{aligned}$$

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

$$\begin{aligned} G_{ij2} + GE_{hij2} &= A_i + A_j + \tfrac{1}{4}D_{ij} + \tfrac{1}{4}D_{ii} + \tfrac{1}{2}D_{jj} + AA_{ii} + AA_{jj} + 2AA_{ij} \\ &\quad + AE_{hi} + AE_{hj} + \tfrac{1}{4}DE_{hii} + \tfrac{1}{4}DE_{hjj} + \tfrac{1}{2}DE_{hij} \\ &\quad + AAE_{hii} + AAE_{hjj} + 2AAE_{hij} \end{aligned}$$

where A = additive effect, D = dominance effect, AA = additive by additive epistatic effect, AE = additive by environment interaction effect, DE = dominance by environment interaction effect, and AAE = epistasis 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

$$\begin{aligned} y &= Xb + U_A e_A + U_D e_D + U_{AA} e_{AA} + U_{AE} e_{AE} + U_{DE} e_{DE} + U_{AAE} e_{AAE} + U_B e_B + e_e \\ &= Xb + \sum_u^8 U_u e_u \end{aligned}$$

with variance-covariance matrix

$$\begin{aligned} \mathrm{var}(y) &= \sigma_A^2 U_A U_A^T + \sigma_D^2 U_D U_D^T + \sigma_{AA}^2 U_{AA} U_{AA}^T + \sigma_{AE}^2 U_{AE} U_{AE}^T \\ &\quad + \sigma_{DE}^2 U_{DE} U_{DE}^T + \sigma_{AAE}^2 U_{AAE} U_{AAE}^T + \sigma_B^2 U_B U_B^T + \sigma_e^2 I \\ &= \sum_{u=1}^8 \sigma_u^2 U_u U_u^T. \end{aligned}$$

Variance Components

Unbiased estimation of variances can be obtained by restricted maximum likelihood (REML) or MINQUE(1) approaches. When experimental variances (σ_u^2) are estimated, genetic variance components can be obtained by $V_A = 2\sigma_A^2$, $V_D = \sigma_D^2$, $V_{AA} = 4\sigma_{AA}^2$, $V_{AE} = 2\sigma_{AE}^2$, $V_{DE} = \sigma_{DE}^2$, $V_{AAE} = 4\sigma_{AAE}^2$, $V_e = \sigma_e^2$. The total phenotypic variance is $V_P = V_A + V_D + V_{AA} + V_{AE} + V_{DE} + V_{AAE} + V_e$.

Covariance Components and Correlation

Unbiased estimation of covariances can be obtained by MINQUE(1) approaches (Zhu, 1992; Zhu and Weir, 1996). When experimental covariances ($\sigma_{u/u}$) are estimated, genetic covariance components can be obtained by $C_A = 2\sigma_{A/A}$, $C_D = \sigma_{D/D}$, $C_{AA} = 4\sigma_{AA/AA}$, $C_{AE} = 2\sigma_{AE/AE}$, $C_{DE} = \sigma_{DE/DE}$, $C_{AAE} = 4\sigma_{AAE/AAE}$, $C_e = \sigma_{e/e}$. The total phenotypic covariance is $C_P = C_A + C_D + C_{AA} + C_{AE} + C_{DE} + C_{AAE} + C_e$. For trait 1 and trait 2, correlation coefficients of genetic components can be estimated by $r_A = C_A / \sqrt{V_{A(1)} V_{A(2)}}$, $r_D = C_D / \sqrt{V_{D(1)} V_{D(2)}}$, $r_{AA} = C_{AA} / \sqrt{V_{AA(1)} V_{AA(2)}}$, $r_{AE} = C_{AE} / \sqrt{V_{AE(1)} V_{AE(2)}}$, $r_{DE} = C_{DE} / \sqrt{V_{DE(1)} V_{DE(2)}}$, $r_{AAE} = C_{AAE} / \sqrt{V_{AAE(1)} V_{AAE(2)}}$, and $r_e = C_e / \sqrt{V_{e(1)} V_{e(2)}}$.

Heritability Components

The total heritability (h^2) can be partitioned into two components ($h^2 = h_G^2 + h_{GE}^2$), where $h_G^2 = (V_A + V_{AA})/V_P$ is general heritability and $h_{GE}^2 = (V_{AE} + V_{AAE})/V_P$ is interaction heritability (Zhu, 1997).

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 use of the linear unbiased prediction (LUP) method (Zhu, 1992; Zhu and Weir, 1996) or the 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 relative to midparent or relative to better parent can be calculated as follows:

General heterosis of F_n relative to midparent:
$$H_M(F_n) = (\tfrac{1}{2})^{n-1} \Delta_D + 2\Delta_{AA}$$
Interaction heterosis of F_n relative to midparent:
$$H_{ME}(F_n) = (\tfrac{1}{2})^{n-1} \Delta_{DE} + 2\Delta_{AAE}$$
General heterosis of F_n relative to better parent (P_i):
$$H_B(F_n) = H_M(F_n) - \tfrac{1}{2}\varpi_G$$
Interaction heterosis of F_n relative to better parent (P_i):
$$H_{BE}(F_n) = H_{ME}(F_n) - \tfrac{1}{2}\varpi_{GE}$$

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

Heterosis based on population mean ($H_{PM} = \tfrac{1}{\mu}H_M$, $H_{PME} = \tfrac{1}{\mu}H_{ME}$, $H_{PB} = \tfrac{1}{\mu}H_B$, or $H_{PBE} = \tfrac{1}{\mu}H_{BE}$) 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 (COTADAA.TXT) to be analyzed (Parent = 10, Year = 2, Generation = P, F_1, F_2, Blk = 1):

Year	Male	Fem	Gen	Blk	Bolls	Lint%
1	1	1	0	1	10.39	37.16
1	1	6	1	1	16.69	39.29
1	1	6	2	1	15.05	37.68
1	1	7	1	1	18.27	40.92
1	1	7	2	1	14.44	38.35
1	1	9	1	1	13.36	36.43
1	1	9	2	1	12.37	36.1
1	1	10	1	1	14.57	33.45
1	1	10	2	1	11.52	34.81
1	2	2	0	1	18.06	34.95
1	2	6	1	1	16.65	38.28
1	2	6	2	1	15.43	39.5
1	2	7	1	1	17.67	39.27
1	2	7	2	1	18.82	38.43
1	2	8	1	1	19.89	38.22
1	2	8	2	1	12.65	35.44
1	2	9	1	1	18.03	34.57
1	2	9	2	1	15.45	35.51
1	2	10	1	1	17.08	33.69
1	2	10	2	1	16.1	29.89
1	3	3	0	1	11.03	39.53
1	3	7	1	1	17.52	42.46
1	3	7	2	1	13.99	39.38
1	3	9	1	1	14.56	37.04
1	3	9	2	1	12.28	38.27
1	3	10	1	1	13.27	37.83
1	3	10	2	1	16.42	39.14
1	4	4	0	1	16.54	40.8
1	4	6	1	1	17.11	40.34
1	4	6	2	1	14.58	40.77
1	4	8	1	1	16.7	40.92
1	4	8	2	1	14.7	39.72
1	4	9	1	1	17.1	38.7
1	4	9	2	1	17.34	38.41

1	4	10	1	1	14.14	36.54
1	4	10	2	1	13.86	36.99
1	5	5	0	1	13.89	40.49
1	5	7	1	1	18.57	41.6
1	5	7	2	1	14.53	41.53
1	5	8	1	1	17.27	40.33
1	5	8	2	1	16.1	39.9
1	5	9	1	1	16.31	39.16
1	5	9	2	1	14.82	39.92
1	5	10	1	1	16.98	37.65
1	5	10	2	1	12.22	37.3
1	6	6	0	1	16.66	39.1
1	7	7	0	1	18.35	42.04
1	8	8	0	1	13.49	38.81
1	9	9	0	1	12.91	35.98
1	10	10	0	1	11.52	30.89
2	1	1	0	1	10.09	37.69
2	1	6	1	1	10.82	41.92
2	1	6	2	1	11.13	38.06
2	1	7	1	1	7.97	40.53
2	1	7	2	1	11.08	41.2
2	1	9	1	1	8.22	37.49
2	1	9	2	1	9.85	37.45
2	1	10	1	1	7.26	33.81
2	1	10	2	1	8.52	33.53
2	2	2	0	1	9.87	39.3
2	2	6	1	1	12.31	40.64
2	2	6	2	1	11.95	41.35
2	2	7	1	1	11.3	42.04
2	2	7	2	1	9.98	40.17
2	2	8	1	1	13.5	39.85
2	2	8	2	1	11.47	37.64
2	2	9	1	1	11.93	37.71
2	2	9	2	1	10.83	37.45
2	2	10	1	1	8.23	34.59
2	2	10	2	1	11.1	34.01
2	3	3	0	1	6.4	39.44
2	3	7	1	1	8	42.68
2	3	7	2	1	9.09	43.29
2	3	9	1	1	11.49	37.92
2	3	9	2	1	10.78	38.9
2	3	10	1	1	7.32	34.76
2	3	10	2	1	10.9	38.42
2	4	4	0	1	8.83	42.65
2	4	6	1	1	11.37	42.67
2	4	6	2	1	11.77	41.45
2	4	8	1	1	13.07	41.84
2	4	8	2	1	11.18	42.27
2	4	9	1	1	10.63	38.12
2	4	9	2	1	11.47	41.08
2	4	10	1	1	10.43	39.06
2	4	10	2	1	11.84	37.58
2	5	5	0	1	11.37	42.86
2	5	7	1	1	12.03	42.65
2	5	7	2	1	10.69	44.69
2	5	8	1	1	10.2	40.36
2	5	8	2	1	10.09	39.53

2	5	9	1	1	10.47	40.31
2	— 5	9	2	1	10.89	40.03
2	5	10	1	1	10.33	38.78
2	5	10	2	1	8.95	39.09
2	6	6	0	1	11.24	38.6
2	7	7	0	1	10.67	43.22
2	8	8	0	1	10.77	40.74
2	9	9	0	1	6.87	37.43
2	.10	10	0	1	11.69	35.05

1. Run GENADE.EXE to create mating design matrix files and data for additive-dominance-epistasis (AD+AA) models. The data files (COTADAA.TXT) should have five columns: (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 under the name COTADAA.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. The two programs in Step 2 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. All results are automatically stored in text files for later use or printing. Examples of output files are provided with the names COTADAA.VAR for analysis of variance and genetic effects, COTADAA.PRE for heterosis, and COTADAA.COR for analysis of covariances and correlation.

Output 1 for Variance Analysis

```
Traits =, 2
Variance components = , 7
Degree of freedom = , 99
File name is COTADAA.VAR
Date and Time for Analysis: Fri Jun 23 08:33:02 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 Contrast Test:
+<1>   +<2>   +<3>   +<4>   +<5>   -<6>   -<7>   -<8>   -<9>   -<10>

Diallel Analysis of Trait, Bolls, for Public Users.

Var Comp              Estimate      S. E.       P-value
(1): Additive Var     2.36714       0.474734    1.31e-006      S**
(2): Dominance Var    12.4508       2.25708     1.39e-007      S**
(3): Add.*Add. Var    3.48369    .  0.502654    1.9e-010       S**
(4): Add. * Env. Var  3.59761       0.745664    2.55e-006      S**
(5): Dom. * Env. Var  16.8931       2.83894     2.03e-008      S**
(6): (AA) * Env. Var  0             0           1              NS
(7): Residual Var     3.12779       0.712819    1.43e-005      S**
(8): Var(Pheno.)      41.9202       4.31614     2.55e-011      S**

Proportion of Var(G)/Var(T)Estimate       S. E.          P-value
(1): Additive Var/Vp        0.0564678      0.0211358      0.00441      S**
(2): Dominance Var/Vp       0.297013       0.0369701      2.44e-011    S**
(3): Add.*Add. Var/Vp       0.0831029      0.0214262      9.46e-005    S**
(4): Add. * Env. Var/Vp     0.0858205      0.0120405      5.86e-011    S**
(5): Dom. * Env. Var/Vp     0.402983       0.0341788      2.55e-011    S**
(6): (AA) * Env. Var/Vp     0              0              1            NS
(7): Residual Var/Vp        0.0746131      0.0151876      1.78e-006    S**

Heritability                Estimate    '  S. E.          P-value

(8): Heritability(N)        0.139571       0.0266373      4.55e-007    S**
(9): Heritability(B)        0.436584       0.0348678      2.55e-011    S**
(10): Heritability(NE)      0.0858205      0.0120405      5.86e-011    S**
(11): Heritability(BE)      0.488803       0.03613        -2.55e-011   S**

Genetic Predictor, S.E., P-value for Two-tail t-test
(1): Random Effect is Additive Effects
A1                 0.020391       1.046932   0.984         NS
A2                -0.172118       0.865219   0.843         NS
A3                 0.243015       0.933404   0.795         NS
A4                 0.024512       0.610581   0.968         NS
A5                -0.198413       0.284266   0.487         NS
A6                -0.045113       0.559257   0.936         NS
A7                -0.006029       0.525715   0.991         NS
```

A8	-0.242755	0.336519	0.472	NS
A9	0.177528	0.247130	0.474	NS
A10	0.197105	0.780527	0.801	NS
Linear Contrast	-0.237404	11.14	0.983	NS

(2): Random Effect is Dominance Effects

D1*1	-1.985631	1.605723	0.219	NS
D2*2	-4.853828	3.095245	0.12	NS
D3*3	-0.293169	0.924650	0.752	NS
D4*4	-1.707263	1.061605	0.111	NS
D5*5	-7.790652	3.617237	0.0337	S*
D6*6	-2.681446	1.218021	0.03	S*
D7*7	-4.154995	2.393013	0.0856	S+
D8*8	-7.236830	3.889634	0.0658	S+
D9*9	-3.026015	1.713898	0.0806	S+
D10*10	1.364409	1.417177	0.338	NS
D1*6	1.844893	1.020188	0.0736	S+
D1*7	0.088293	2.692258	0.974	NS
D1*9	-2.270995	1.155729	0.0522	S+
D1*10	2.668295	1.548696	0.088	S+
D2*6	1.351880	0.655828	0.0419	S*
D2*7	-1.297874	1.003310	0.199	NS
D2*8	9.815433	5.523754	0.0786	S+
D2*9	5.188726	2.350358	0.0296	S*
D2*10	-4.090970	1.895508	0.0333	S*
D3*7	3.495850	2.000000	0.0836	S+
D3*9	4.970930	2.262232	0.0303	S*
D3*10	-9.112045	4.458072	0.0436	S*
D4*6	2.946256	1.541041	0.0588	S+
D4*8	5.140935	2.364873	0.0321	S*
D4*9	-1.798652	0.660681	0.00766	S**
D4*10	-1.958099	0.910923	0.034	S*
D5*7	6.710816	3.253640	0.0418	S*
D5*8	-0.368711	0.290930	0.208	NS
D5*9	0.235750	0.576913	0.684	NS
D5*10	8.804042	3.903617	0.0263	S*
Heterosis <Delta>	2.90056	12.8407	0.822	NS

(3): Random Effect is Add.*Add. Effects

AA1*1	-1.827866	0.885620	0.0416	S*
AA2*2	1.857440	0.692252	0.00855	S**
AA3*3	-3.923112	1.819274	0.0335	S*
AA4*4	-0.427958	0.372799	0.254	NS
AA5*5	1.095843	0.431401	0.0126	S*
AA6*6	1.074095	0.485307	0.0292	S*
AA7*7	2.010456	0.866196	0.0223	S*
AA8*8	0.866474	0.254778	0.00097	S**
AA9*9	-2.618613	1.297275	0.0462	S*
AA10*10	-1.434506	0.678498	0.037	S*
AA1*6	1.127468	0.554236	0.0446	S*
AA1*7	0.260405	0.142121	0.0699	S+
AA1*9	-0.626353	0.353682	0.0796	S+
AA1*10	-2.892538	1.389233	0.0399	S*
AA2*6	-0.039485	0.150785	0.794	NS
AA2*7	0.997226	0.482695	0.0414	S*
AA2*8	-2.373975	1.062655	0.0277	S*
AA2*9	0.916657	0.551207	0.0995	S+

AA2*10	0.966337	0.475264	0.0447	S*
AA3*7	-1.240906	0.602029	0.0419	S*
AA3*9	0.736135	0.560053	0.192	NS
AA3*10	3.882660	1.687257	0.0235	S*
AA4*6	-0.333696	0.292460	0.257	NS
AA4*8	0.232070	0.281352	0.411	NS
AA4*9	3.758026	1.714850	0.0308	S*
AA4*10	0.453800	0.251847	0.0746	S+
AA5*7	-1.360470	0.556477	0.0163	S*
AA5*8	0.698657	0.311950	0.0274	S*
AA5*9	1.219364	0.571954	0.0355	S*
AA5*10	-3.054544	1.399209	0.0314	S*
Heterosis <Delta>	1.12761	5.66678	0.843	NS

(4): Random Effect is Add. * Env. Effects

AE1 in E1	-1.871303	1.336265	0.165	NS
AE2 in E1	1.679535	1.500118	0.266	NS
AE3 in E1	-0.899398	0.974282	0.358	NS
AE4 in E1	0.355846	0.398988	0.375	NS
AE5 in E1	0.613201	0.505110	0.228	NS
AE6 in E1	-0.319194	0.433700	0.463	NS
AE7 in E1	3.154071	2.503520	0.211	NS
AE8 in E1	-1.709535	0.955588	0.0767	S+
AE9 in E1	-1.004626	0.705371	0.158	NS
AE10 in E1	0.000037	0.749113	1	NS
AE1 in E2	-0.687704	0.654509	0.296	NS
AE2 in E2	0.130732	0.339243	0.701	NS
AE3 in E2	-1.165105	0.703354	0.101	NS
AE4 in E2	1.212089	0.914817	0.188	NS
AE5 in E2	-0.818562	0.501433	0.106	NS
AE6 in E2	1.647312	1.146417	0.154	NS
AE7 in E2	-2.111514	1.652810	0.204	NS
AE8 in E2	1.666313	1.018155	0.105	NS
AE9 in E2	1.460007	0.882265	0.101	NS
AE10 in E2	-1.334250	0.692084	0.0567	S+
Linear Contrast	-0.000322198	0.00010415	0.00257	S**

(5): Random Effect is Dom. * Env. Effects

DE11 in E1	-7.339941	3.362180	0.0314	S*
DE22 in E1	-5.544965	3.293144	0.0954	S+
DE33 in E1	-1.685938	2.763209	0.543	NS
DE44 in E1	-1.592941	1.468080	0.281	NS
DE55 in E1	-6.919656	3.156330	0.0307	S*
DE66 in E1	-2.769618	1.534016	0.074	S+
DE77 in E1	-5.708889	3.470978	0.103	NS
DE88 in E1	-6.906281	3.149161	0.0306	S*
DE99 in E1	-3.155495	1.695257	0.0657	S+
DE1010 in E1	-4.448080	3.583114	0.217	NS
DE16 in E1	1.945276	1.444322	0.181	NS
DE17 in E1	6.019940	4.117258	0.147	NS
DE19 in E1	0.953192	0.789965	0.23	NS
DE110 in E1	5.306395	3.178059	0.0981	S+
DE26 in E1	0.018365	0.840712	0.983	NS
DE27 in E1	-4.879109	2.046507	0.019	S*
DE28 in E1	11.874683	6.855778	0.0864	S+
DE29 in E1	2.481694	2.213078	0.265	NS
DE210 in E1	1.704185	1.338270	0.206	NS

DE37 in E1	5.935123	3.679177	0.11	NS
DE39 in E1	2.916905	2.004578	0.149	NS
DE310 in E1	-5.481360	3.413565	0.112	NS
DE46 in E1	3.541911	2.501341	0.16	NS
DE48 in E1	1.163906	1.499863	0.44	NS
DE49 in E1	-1.462106	0.664229	0.03	S*
DE410 in E1	0.093319	0.547534	0.865	NS
DE57 in E1	5.091230	3.513362	0.15	NS
DE58 in E1	0.249648	0.907277	0.784	NS
DE59 in E1	1.192191	1.072943	0.269	NS
DE510 in E1	7.405446	4.610249	0.111	NS
DE11 in E2	6.233934	2.649984	0.0206	S*
DE22 in E2	0.070564	1.631085	0.966	NS
DE33 in E2	2.860760	1.834532	0.122	NS
DE44 in E2	0.496960	1.260403	0.694	NS
DE55 in E2	0.762586	0.976264	0.437	NS
DE66 in E2	0.750042	0.589078	0.206	NS
DE77 in E2	2.513161	1.959827	0.203	NS
DE88 in E2	-0.681558	1.133328	0.549	NS
DE99 in E2	1.396232	1.222769	0.256	NS
DE1010 in E2	6.754486	3.043240	0.0287	S*
DE16 in E2	-0.782136	0.571314	0.174	NS
DE17 in E2	-6.286620	3.932846	0.113	NS
DE19 in E2	-2.727444	1.812851	0.136	NS
DE110 in E2	-2.626815	1.660283	0.117	NS'
DE26 in E2	0.500294	0.497259	0.317	NS
DE27 in E2	2.695619	1.378225	0.0533	S+
DE28 in E2	0.710618	1.939384	0.715	NS
DE29 in E2	1.408633	0.928007	0.132	NS
DE210 in E2	-5.416844	3.370826	0.111	NS
DE37 in E2	-2.775914	1.748225	0.116	NS
DE39 in E2	1.697015	1.049894	0.109	NS
DE310 in E2	-4.892908	3.552561	0.172	NS
DE46 in E2	-0.956358	0.906075	0.294	NS
DE48 in E2	2.794023	1.735292	0.111	NS
DE49 in E2	-1.011061	1.141284	0.378	NS
DE410 in E2	-1.635955	1.322434	0.219	NS
DE57 in E2	0.749728	1.094644	0.495	NS
DE58 in E2	-1.851171	0.743874	0.0145	S*
DE59 in E2	-1.672750	0.952113	0.082	S+
DE510 in E2	0.922233	1.377869	0.505	NS

(6): Random Effect is (AA) * Env. Effects
No Significant Effects.

Fixed Effect <1>, 15.345
Fixed Effect <2>, 10.3648

Results of Lint% are not presented.

Time Used (Hour) = 0.004722

Output 2 for Covariance Analysis

Traits =, 2

```
Covariance components = , 7
Degree of freedom = , 99
File name is COTADAA.COV
Date and Time for Analysis: Fri Jun 23 08:33:35 2000

Covariance Components Estimated by MINQUE(1) with GENCOV1C.EXE.
Jackknifing Over Cell Mean 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, , &, Lint%, for Public
     Users.:
```

Covariances	Estimates	S.E.	P-value	
Additive Cov	-0.165704	0.968417	0.864	NS
Dominance Cov	0.802175	2.31849	0.73	NS
Add.*Add. Cov	0.52236	0.79344	0.512	NS
Add. * Env. Cov	-0.585695	0.668664	0.383	NS
Dom. * Env. Cov	1.44656	2.09928	0.492	NS
(AA) * Env. Cov	-0.116658	1.07689	0.914	NS
Residual Cov	0.192467	0.376523	0.61	NS

Cov<1=Genotypic> Cov <2=Phenotypic>	Estimates	S.E.	P-value	
Cov 2	2.09551	1.35407	0.125	NS
Cov 1	1.90304	1.35435	0.163	NS

Correlation	Estimates	S.E.	P-value	
Additive Cor	-0.043057	0.0498808	0.39	NS
Dominance Cor	0.100186	0.0495757	0.046	S *
Add.*Add. Cor	0.174520	0.0516629	0.00104	S **
Add. * Env. Cor	-0.207088	0.0362769	1.19e-007	S **
Dom. * Env. Cor	0.000000	0	1	NS
(AA) * Env. Cor	0.000000	0	1	NS
Residual Cor	0.079717	0.0377952	0.0375	S *

Cor <1=Genotypic> Cor <2=Phenotypic>	Estimates	S.E.	P-value	
Cor 2	0.073183	0.0448333	0.106	NS
Cor 1	0.072636	0.0500355	0.15	NS

```
Time Used (Hour) = 0.003056
```

Output 3 for Heterosis Analysis

```
Traits =, 2
Variance components = , 7
Degree of freedom = , 99
File name is COTADJM.PRE
Date and Time for Analysis: Fri Jun 23 08:34:07 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.

Var Comp, Estimate, S. E. , P-value of One Tail t-test of, Bolls, for Public Users.

	Estimate	S. E.	P-value	Sig.
Additive Var	2.36728	0.474749	1.31e-006	S **
Dominance Var	12.4508	2.25708	1.39e-007	S **
Add.*Add. Var	3.48381	0.502665	1.9e-010	S **
Add. * Env. Var	3.59769	0.745673	2.54e-006	S **
Dom. * Env. Var	16.893	2.83894	2.03e-008	S **
(AA) * Env. Var	0	0	0.5	NS
Residual Var	3.12783	0.712823	1.43e-005	S **

Heterosis Analysis of Trait, Bolls, for F_2 Seeds with total mean =, 12.854884

No.		Cross	F1 (GE)	S.E.	P-value	Sig.	F2 (GE)	S.E.	P-value	Sig.
Cro 1	<E1>	<1 * 6>	-0.25	1.85	0.90	NS	-3.75	1.57	0.02	S *
Cro 2	<E1>	<1 * 7>	7.30	4.14	0.08	S +	1.03	1.39	0.46	NS
Cro 3	<E1>	<1 * 9>	-1.92	1.60	0.23	NS	-5.02	1.88	0.01	S **
Cro 4	<E1>	<1 * 10>	3.44	3.50	0.33	NS	-2.17	2.05	0.29	NS
Cro 5	<E1>	<2 * 6>	1.38	1.17	0.24	NS	-0.71	1.26	0.57	NS
Cro 6	<E1>	<2 * 7>	-0.04	3.21	0.99	NS	-0.42	2.55	0.87	NS
Cro 7	<E1>	<2 * 8>	11.84	6.84	0.09	S +	2.79	2.30	0.23	NS
Cro 8	<E1>	<2 * 9>	3.16	2.41	0.19	NS	-0.26	1.40	0.85	NS
Cro 9	<E1>	<2 * 10>	3.38	1.63	0.04	S *	0.03	1.43	0.98	NS
Cro 10	<E1>	<3 * 7>	8.19	4.09	0.05	S *	3.37	1.89	0.08	S +
Cro 11	<E1>	<3 * 9>	1.01	2.25	0.65	NS	-1.66	1.67	0.32	NS
Cro 12	<E1>	<3 * 10>	-6.38	3.52	0.07	S +	-5.17	2.04	0.01	S *
Cro 13	<E1>	<4 * 6>	3.58	2.53	0.16	NS	0.72	0.98	0.47	NS
Cro 14	<E1>	<4 * 8>	-0.19	1.73	0.91	NS	-2.90	1.47	0.05	S +
Cro 15	<E1>	<4 * 9>	-2.11	0.82	0.01	S *	-2.57	0.89	0.00	S **
Cro 16	<E1>	<4 * 10>	0.45	0.81	0.58	NS	-1.11	1.39	0.43	NS
Cro 17	<E1>	<5 * 7>	8.86	4.38	0.05	S *	3.16	2.50	0.21	NS
Cro 18	<E1>	<5 * 8>	-0.85	1.20	0.48	NS	-4.43	1.51	0.00	S **
Cro 19	<E1>	<5 * 9>	0.80	1.22	0.51	NS	-2.31	1.20	0.06	S +
Cro 20	<E1>	<5 * 10>	8.02	4.80	0.10	S +	1.47	1.73	0.40	NS
Cro 21	<E2>	<1 * 6>	0.18	0.77	0.82	NS	2.31	0.92	0.01	S *
Cro 22	<E2>	<1 * 7>	-9.09	4.23	0.03	S *	-3.76	1.82	0.04	S *
Cro 23	<E2>	<1 * 9>	-1.95	1.88	0.30	NS	1.32	0.89	0.14	NS
Cro 24	<E2>	<1 * 10>	-4.65	1.97	0.02	S *	-0.09	1.17	0.94	NS
Cro 25	<E2>	<2 * 6>	2.28	0.97	0.02	S *	2.23	1.05	0.04	S *
Cro 26	<E2>	<2 * 7>	0.72	1.80	0.69	NS	0.01	1.27	0.99	NS
Cro 27	<E2>	<2 * 8>	2.51	1.99	0.21	NS	2.00	1.12	0.08	S +
Cro 28	<E2>	<2 * 9>	3.00	1.18	0.01	S *	2.66	1.00	0.01	S **
Cro 29	<E2>	<2 * 10>	-6.62	3.59	0.07	S +	-2.21	1.30	0.09	S +
Cro 30	<E2>	<3 * 7>	-6.05	2.55	0.02	S *	-3.32	1.71	0.05	S +
Cro 31	<E2>	<3 * 9>	1.99	1.19	0.10	S +	2.21	0.94	0.02	S *
Cro 32	<E2>	<3 * 10>	-7.39	3.97	0.07	S +	-2.54	1.53	0.10	NS
Cro 33	<E2>	<4 * 6>	1.90	1.64	0.25	NS	2.69	1.44	0.06	S +
Cro 34	<E2>	<4 * 8>	5.67	2.21	0.01	S *	4.23	1.49	0.01	S **
Cro 35	<E2>	<4 * 9>	1.66	1.61	0.31	NS	2.64	1.29	0.04	S *
Cro 36	<E2>	<4 * 10>	-1.76	1.31	0.18	NS	0.87	0.94	0.35	NS
Cro 37	<E2>	<5 * 7>	-2.18	2.04	0.29	NS	-1.74	1.67	0.30	NS
Cro 38	<E2>	<5 * 8>	-1.00	0.91	0.27	NS	-0.06	0.76	0.94	NS
Cro 39	<E2>	<5 * 9>	-1.03	1.05	0.33	NS	0.35	0.65	0.60	NS

```
Cro 40 <E2>   <5 * 10> -1.23   1.67 0.46      NS   0.19  1.10   0.87      NS
```

Significance of F1 or F2 is over Population Mean 12.854884

Number	Cross	F1(G)	S.E.	P-value	Sig.		F2(G)	S.E.	P-value	Sig.
Cro 1	<1 * 6>	16.18	1.01	0.00	S	**	14.09	0.98	0.21	NS
Cro 2	<1 * 7>	13.66	2.81	0.78	NS		12.08	1.30	0.55	NS
Cro 3	<1 * 9>	5.08	1.77	0.00	S	**	4.96	1.64	0.00	S **
Cro 4	<1 * 10>	6.69	3.39	0.07	S	+	5.20	2.95	0.01	S *
Cro 5	<2 * 6>	16.84	1.27	0.00	S	**	14.28	1.52	0.35	NS
Cro 6	<2 * 7>	17.24	1.85	0.02	S	*	15.64	2.33	0.24	NS
Cro 7	<2 * 8>	20.23	5.09	0.15	NS		12.30	2.58	0.83	NS
Cro 8	<2 * 9>	19.12	2.07	0.00	S	**	14.56	1.07	0.12	NS
Cro 9	<2 * 10>	11.15	1.91	0.37	NS		12.32	1.42	0.71	NS
Cro 10	<3 * 7>	12.19	2.39	0.78	NS		9.33	1.62	0.03	S *
Cro 11	<3 * 9>	13.18	2.73	0.91	NS		9.86	1.89	0.12	NS
Cro 12	<3 * 10>	6.59	4.32	0.15	NS		11.41	2.81	0.61	NS
Cro 13	<4 * 6>	15.76	1.80	0.11	NS		13.19	1.32	0.80	NS
Cro 14	<4 * 8>	18.68	1.98	0.00	S	**	13.87	0.86	0.24	NS
Cro 15	<4 * 9>	15.73	1.49	0.06	S	+	15.45	1.71	0.13	NS
Cro 16	<4 * 10>	10.16	0.76	0.00	S	**	11.06	0.67	0.01	S **
Cro 17	<5 * 7>	19.75	2.59	0.01	S	**	13.41	0.98	0.58	NS
Cro 18	<5 * 8>	15.40	0.84	0.00	S	**	11.83	1.97	0.61	NS
Cro 19	<5 * 9>	13.99	0.64	0.08	S	+	11.16	1.12	0.13	NS
Cro 20	<5 * 10>	15.21	4.39	0.59	NS		9.20	2.55	0.16	NS

No.	Cross		$H_{pm}(F_1)$ (GE)	S.E.	P-value	Sig.	$H_{pm}(F_2)$ (GE)	S.E.	P-value	Sig.
Cro 1 <E1>	<1 * 6>		0.54	0.25	0.03	S *	0.27	0.12	0.03	S *
Cro 2 <E1>	<1 * 7>		0.98	0.54	0.07	S +	0.49	0.27	0.07	S +
Cro 3 <E1>	<1 * 9>		0.48	0.19	0.01	S *	0.24	0.10	0.01	S *
Cro 4 <E1>	<1 * 10>		0.87	0.45	0.06	S +	0.44	0.23	0.06	S +
Cro 5 <E1>	<2 * 6>		0.32	0.15	0.03	S *	0.16	0.07	0.03	S *
Cro 6 <E1>	<2 * 7>		0.06	0.28	0.84	NS	0.03	0.14	0.84	NS
Cro 7 <E1>	<2 * 8>		1.41	0.77	0.07	S +	0.70	0.38	0.07	S +
Cro 8 <E1>	<2 * 9>		0.53	0.27	0.05	S +	0.27	0.13	0.05	S +
Cro 9 <E1>	<2 * 10>		0.52	0.24	0.04	S *	0.26	0.12	0.04	S *
Cro 10 <E1>	<3 * 7>		0.75	0.46	0.11	NS	0.37	0.23	0.11	NS
Cro 11 <E1>	<3 * 9>		0.42	0.26	0.12	NS	0.21	0.13	0.12	NS
Cro 12 <E1>	<3 * 10>		-0.19	0.43	0.67	NS	-0.09	0.22	0.67	NS
Cro 13 <E1>	<4 * 6>		0.45	0.29	0.13	NS	0.22	0.15	0.13	NS
Cro 14 <E1>	<4 * 8>		0.42	0.20	0.03	S *	0.21	0.10	0.03	S *
Cro 15 <E1>	<4 * 9>		0.07	0.12	0.55	S	0.04	0.06	0.55	NS
Cro 16 <E1>	<4 * 10>		0.24	0.15	0.10	S +	0.12	0.07	0.10	S +
Cro 17 <E1>	<5 * 7>		0.89	0.46	0.06	S +	0.44	0.23	0.06	S +
Cro 18 <E1>	<5 * 8>		0.56	0.19	0.00	S **	0.28	0.10	0.00	S **
Cro 19 <E1>	<5 * 9>		0.48	0.20	0.02	S *	0.24	0.10	0.02	S *
Cro 20 <E1>	<5 * 10>		1.02	0.57	0.08	S +	0.51	0.29	0.08	S +
Cro 21 <E2>	<1 * 6>		-0.33	0.13	0.01	S *	-0.17	0.06	0.01	S *
Cro 22 <E2>	<1 * 7>		-0.83	0.46	0.08	S +	-0.41	0.23	0.08	S +
Cro 23 <E2>	<1 * 9>		-0.51	0.24	0.04	S *	-0.25	0.12	0.04	S *
Cro 24 <E2>	<1 * 10>		-0.71	0.30	0.02	S *	-0.35	0.15	0.02	S *
Cro 25 <E2>	<2 * 6>		0.01	0.08	0.93	NS	0.00	0.04	0.93	NS
Cro 26 <E2>	<2 * 7>		0.11	0.16	0.51	NS	0.05	0.08	0.51	NS
Cro 27 <E2>	<2 * 8>		0.08	0.22	0.72	NS	0.04	0.11	0.72	NS
Cro 28 <E2>	<2 * 9>		0.05	0.12	0.66	NS	0.03	0.06	0.66	NS
Cro 29 <E2>	<2 * 10>		-0.69	0.39	0.08	S +	-0.34	0.19	0.08	S +
Cro 30 <E2>	<3 * 7>		-0.42	0.23	0.06	S +	-0.21	0.11	0.06	S +

```
Cro 31 <E2> <3 * 9>    -0.03   0.12 0.77   NS    -0.02  0.06  0.77  NS
Cro 32 <E2> <3 * 10>   -0.75   0.43 0.08   S +   -0.38  0.22  0.08  S +
Cro 33 <E2> <4 * 6>    -0.12   0.12 0.29   NS    -0.06  0.06  0.29  NS
Cro 34 <E2> <4 * 8>     0.22   0.20 0.26   NS     0.11  0.10  0.26  NS
Cro 35 <E2> <4 * 9>    -0.15   0.14 0.29   NS    -0.08  0.07  0.29  NS
Cro 36 <E2> <4 * 10>   -0.41   0.20 0.04   S *   -0.20  0.10  0.04  S *
Cro 37 <E2> <5 * 7>    -0.07   0.13 0.59   NS    -0.03  0.06  0.59  NS
Cro 38 <E2> <5 * 8>    -0.15   0.09 0.09   S +   -0.07  0.04  0.09  S +
Cro 39 <E2> <5 * 9>    -0.21   0.12 0.08   S +   -0.11  0.06  0.08  S +
Cro 40 <E2> <5 * 10>   -0.22   0.20 0.26   NS    -0.11  0.10  0.26  NS
```

Significance of F1 or F2 is over Population Mean 12.854884

No.	Cro	$H_{pm}(F_1)$ (G)	S.E.	P-value	Sig.	$H_{pm}(F_2)$ (G)	S.E.	P-value	Sig.
Cro 1	<1 * 6>	0.56	0.12	0.00	S **	0.40	0.08	0.00	S **
Cro 2	<1 * 7>	0.27	0.31	0.39	NS	0.15	0.16	0.35	NS
Cro 3	<1 * 9>	0.27	0.10	0.01	S *	0.26	0.08	0.00	S **
Cro 4	<1 * 10>	0.04	0.19	0.85	NS	-0.08	0.12	0.50	NS
Cro 5	<2 * 6>	0.16	0.20	0.42	NS	-0.04	0.13	0.78	NS
Cro 6	<2 * 7>	0.10	0.18	0.56	NS	-0.02	0.10	0.84	NS
Cro 7	<2 * 8>	0.65	0.62	0.30	NS	0.04	0.37	0.92	NS
Cro 8	<2 * 9>	0.91	0.26	0.00	S **	0.56	0.13	0.00	S **
Cro 9	<2 * 10>	-0.07	0.17	0.70	NS	0.03	0.10	0.80	NS
Cro 10	<3 * 7>	0.40	0.21	0.06	S +	0.18	0.11	0.09	S +
Cro 11	<3 * 9>	1.14	0.21	0.00	S **	0.88	0.19	0.00	S **
Cro 12	<3 * 10>	0.27	0.52	0.61	NS	0.65	0.40	0.11	NS
Cro 13	<4 * 6>	0.30	0.18	0.10	NS	0.10	0.11	0.36	NS
Cro 14	<4 * 8>	0.75	0.28	0.01	S **	0.38	0.14	0.01	S *
Cro 15	<4 * 9>	0.87	0.24	0.00	S **	0.84	0.25	0.00	S **
Cro 16	<4 * 10>	0.08	0.12	0.53	NS	0.15	0.10	0.14	NS
Cro 17	<5 * 7>	0.53	0.43	0.22	NS	0.04	0.26	0.88	NS
Cro 18	<5 * 8>	0.51	0.23	0.03	S *	0.23	0.11	0.04	S *
Cro 19	<5 * 9>	0.75	0.16	0.00	S **	0.53	0.10	0.00	S **
Cro 20	<5 * 10>	0.49	0.42	0.25	NS	0.02	0.26	0.94	NS

No.	Cross	$H_{pb}(F_1)$ (GE)	S.E.	P-value	Sig.	$H_{pb}(F_2)$ (GE)	S.E.	P-value	Sig.
Cro 1	<E1> <1 * 6>	0.25	0.23	0.28	NS	-0.03	0.13	0.85	NS
Cro 2	<E1> <1 * 7>	0.52	0.56	0.35	NS	0.03	0.31	0.91	NS
Cro 3	<E1> <1 * 9>	0.25	0.16	0.13	NS	0.01	0.10	0.92	NS
Cro 4	<E1> <1 * 10>	0.61	0.45	0.17	NS	0.18	0.23	0.45	NS
Cro 5	<E1> <2 * 6>	0.28	0.18	0.13	NS	0.11	0.15	0.44	NS
Cro 6	<E1> <2 * 7>	-0.05	0.27	0.86	NS	-0.08	0.19	0.68	NS
Cro 7	<E1> <2 * 8>	1.09	0.75	0.15	NS	0.39	0.37	0.30	NS
Cro 8	<E1> <2 * 9>	0.42	0.31	0.18	NS	0.15	0.20	0.46	NS
Cro 9	<E1> <2 * 10>	0.43	0.31	0.17	NS	0.17	0.23	0.45	NS
Cro 10	<E1> <3 * 7>	0.59	0.50	0.24	NS	0.22	0.29	0.46	NS
Cro 11	<E1> <3 * 9>	0.35	0.30	0.25	NS	0.14	0.19	0.45	NS
Cro 12	<E1> <3 * 10>	-0.23	0.42	0.60	NS	-0.13	0.22	0.56	NS
Cro 13	<E1> <4 * 6>	0.35	0.31	0.27	NS	0.12	0.17	0.46	NS
Cro 14	<E1> <4 * 8>	0.05	0.22	0.81	NS	-0.16	0.17	0.36	NS
Cro 15	<E1> <4 * 9>	-0.10	0.13	0.46	NS	-0.13	0.09	0.16	NS
Cro 16	<E1> <4 * 10>	0.10	0.20	0.60	NS	-0.02	0.15	0.91	NS
Cro 17	<E1> <5 * 7>	0.64	0.44	0.15	NS	0.20	0.22	0.38	NS
Cro 18	<E1> <5 * 8>	0.38	0.23	0.11	NS	0.10	0.19	0.61	NS
Cro 19	<E1> <5 * 9>	0.46	0.20	0.02	S *	0.22	0.13	0.08	S +
Cro 20	<E1> <5 * 10>	0.97	0.59	0.11	NS	0.46	0.32	0.15	NS
Cro 21	<E2> <1 * 6>	-0.36	0.19	0.06	S +	-0.20	0.14	0.16	NS

```
Cro 22 <E2><1 * 7>    -1.08   0.48 0.03   S *    -0.67  0.25  0.01  S **
Cro 23 <E2><1 * 9>    -0.53   0.27 0.05   S +    -0.28  0.17  0.10  S +
Cro 24 <E2><1 * 10>   -0.74   0.34 0.03   S *    -0.38  0.21  0.07  S +
Cro 25 <E2><2 * 6>    -0.14   0.11 0.21   NS     -0.14  0.08  0.08  S +
Cro 26 <E2><2 * 7>     0.03   0.23 0.90   NS     -0.02  0.16  0.88  NS
Cro 27 <E2><2 * 8>    -0.01   0.24 0.96   NS     -0.05  0.14  0.71  NS
Cro 28 <E2><2 * 9>    -0.10   0.14 0.48   NS     -0.13  0.10  0.19  NS
Cro 29 <E2><2 * 10>   -0.83   0.40 0.04   S *    -0.49  0.22  0.03  S *
Cro 30 <E2><3 * 7>    -0.51   0.26 0.05   S +    -0.30  0.16  0.06  S +
Cro 31 <E2><3 * 9>    -0.18   0.14 0.21   NS     -0.16  0.10  0.11  NS
Cro 32 <E2><3 * 10>   -0.89   0.44 0.05   S *    -0.52  0.23  0.03  S *
Cro 33 <E2><4 * 6>    -0.17   0.11 0.13   NS     -0.11  0.07  0.13  NS
Cro 34 <E2><4 * 8>     0.21   0.22 0.33   NS      0.10  0.13  0.43  NS
Cro 35 <E2><4 * 9>    -0.21   0.14 0.15   NS     -0.13  0.09  0.14  NS
Cro 36 <E2><4 * 10>   -0.45   0.22 0.04   S *    -0.25  0.14  0.07  S +
Cro 37 <E2><5 * 7>    -0.10   0.18 0.57   NS     -0.07  0.13  0.60  NS
Cro 38 <E2><5 * 8>    -0.28   0.12 0.02   S *    -0.21  0.09  0.03  S *
Cro 39 <E2><5 * 9>    -0.42   0.13 0.00   S **   -0.31  0.09  0.00  S **
Cro 40 <E2><5 * 10>   -0.41   0.24 0.09   S +    -0.30  0.15  0.05  S +
```

Significance of F1 or F2 is over Population Mean 12.854884

No.	Cro	$H_{pb}(F_1)$ (G)	S.E.	P-value	Sig.	$H_{pb}(F_2)$ (G)	S.E.	P-value	Sig.
Cro 1	<1 * 6>	0.14	0.17	0.43	NS	-0.02	0.15	0.88	NS
Cro 2	<1 * 7>	-0.24	0.31	0.44	NS	-0.36	0.18	0.05	S *
Cro 3	<1 * 9>	0.12	0.14	0.42	NS	0.11	0.13	0.42	NS
Cro 4	<1 * 10>	-0.17	0.21	0.42	NS	-0.29	0.15	0.05	S +
Cro 5	<2 * 6>	0.14	0.20	0.49	NS	-0.06	0.13	0.63	NS
Cro 6	<2 * 7>	0.04	0.20	0.85	NS	-0.08	0.13	0.53	NS
Cro 7	<2 * 8>	0.40	0.64	0.53	NS	-0.22	0.39	0.58	NS
Cro 8	<2 * 9>	0.31	0.24	0.19	NS	-0.04	0.16	0.80	NS
Cro 9	<2 * 10>	-0.31	0.25	0.22	NS	-0.22	0.20	0.28	NS
Cro 10	<3 * 7>	-0.35	0.23	0.14	NS	-0.58	0.20	0.00	S **
Cro 11	<3 * 9>	1.05	0.21	0.00	S **	0.79	0.21	0.00	S **
Cro 12	<3 * 10>	-0.18	0.53	0.74	NS	0.20	0.40	0.63	NS
Cro 13	<4 * 6>	0.11	0.18	0.55	NS	-0.09	0.11	0.41	NS
Cro 14	<4 * 8>	0.72	0.27	0.01	S **	0.34	0.15	0.03	S *
Cro 15	<4 * 9>	0.49	0.25	0.05	S +	0.46	0.26	0.08	S +
Cro 16	<4 * 10>	0.05	0.17	0.76	NS	0.12	0.16	0.44	NS
Cro 17	<5 * 7>	0.23	0.44	0.60	NS	-0.26	0.27	0.34	NS
Cro 18	<5 * 8>	0.49	0.23	0.04	S *	0.22	0.13	0.10	S +
Cro 19	<5 * 9>	0.38	0.19	0.05	S *	0.16	0.18	0.36	NS
Cro 20	<5 * 10>	0.48	0.39	0.23	NS	0.01	0.25	0.96	NS

Significance of Heterosis is over Population Mean 12.854884

```
Pre(F1)          13.987        0.730276    0.124        NS
Pre(F2)          12.6895       0.306025    0.59         NS
Hpm(F1)          0.147004      0.136824    0.285        NS
Hpm(F2)          0.0457101     0.0706352   0.519        NS
Hpb(F1)         -0.837894      0.143119    6.23e-008    S **
Hpb(F2)         -0.939187      0.0983169  -5.09e-011    S **
Generation n     0.569721      0.0534007  -5.09e-011    S **
0.5 Omiga(AA)    0.673029      0.0727739  -5.09e-011    S **
2Delta(AA)      -0.0555835     0.0447671   0.217        NS
```

Results of Lint% are not presented.
Time Used (Hour) = 0.003056