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Diallel analysis for sex-linked and maternal effects

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Abstract Genetic models including sex-linked and maternal effects as well as autosomal gene effects are described. Monte Carlo simulations were conducted to compare efficiencies of estimation by minimum norm quadratic unbiased estimation (MINQUE) and restricted maximum likelihood (REML) methods. MINQUE(1), which has 1 for all prior values, has a similar efficiency to MINQUE(θ), which requires prior estimates of parameter values. MINQUE(1) has the advantage over REML of unbiased estimation and convenient computation. An adjusted unbiased prediction (AUP) method is developed for predicting random genetic effects. AUP is desirable for its easy computation and unbiasedness of both mean and variance of predictors. The jackknife procedure is appropriate for estimating the sampling variances of estimated variances (or covariances) and of predicted genetic effects. A t-test based on jackknife variances is applicable for detecting significance of variation. Worked examples from mice and silkworm data are given in order to demonstrate variance and covariance estimation and genetic effect prediction.

Key words Diallel analysis · Sex-linked and maternal effects · Variance and covariance components · Genetic prediction

Introduction

Diallel crosses with reciprocal F_1s provide a way for analyzing reciprocal effects. Henderson (1948) and Griffing (1956) proposed diallel models for estimating reciprocal effects and associated variance components. In animal breeding experiments, sex-linked and maternal effects are the primary sources of reciprocal effects. Eisen et al. (1966) presented a model containing parameters for sex-linked and maternal effects as well as autosomal genetic effects. Since sex-linked and maternal effects are confounded in that model, variance components can not be estimated directly by the analysis of variance (ANOVA) method. Cockerham and Weir (1977) suggested a bio-model that included parameters for maternal and paternal effects assuming no sex-linked effects. The ANOVA method can not give distinct estimates of maternal and paternal variance components. Carbonell et al. (1983) extended the model of Eberhard and Gardner (1966) to include sex-linked and maternal effects. Jakubec et al. (1988) proposed a genetic model by which gene effects can be estimated for both autosomal and sex-chromosomal inheritance. All the gene effects are fixed in the models proposed by Carbonell et al. (1983) and Jakubec et al. (1988), and variance components of these effects are not estimable by the standard least squares procedures. In the present study, genetic models with random sex-linked and maternal effects as well as environment interactions are proposed. Methods of directly estimating genetic variances for one trait and covariances between two traits are presented. Monte Carlo simulations are used to evaluate estimation methods of minimum norm quadratic unbiased estimation (MINQUE) (Rao 1970, 1971) and restricted maximum likelihood (REML) (Patterson and Thompson 1971). A method of adjusted unbiased prediction (AUP) for random genetic effects is compared to the best linear unbiased prediction (BLUP) procedure. Mouse data from 7×7 diallel crosses for body weight and tail length at 28 days of age provided by W.R. Atchley (personal communication) are analyzed, as are data for cocoon weight and fibroin content of silkworm diallel experiments in two seasons (Zhong 1992). These analyses are conducted as demonstrations for estimating variance and covariance components and for predicting genetic effects.

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Genetic models

A full diallel crossing system consists of all possible crosses among a set of parents. On the basis of Griffing's (1956) definition for diallel mating methods, method 1 includes parents, F_1s and reciprocal F_1s, and method 3 consists of F_1s and reciprocal F_1s. The general assumptions for our genetic models are (1) regular diploid segregation; (2) inbred parents randomly sampled from a reference population; (3) no epistatic effects; (4) X (or Z) chromosome dosage compensation; and (5) inert Y (or W) chromosome in XY (or ZW) cells. If there is no genotype-by-environment interaction, the general model for the phenotypic mean of sex s in block k from the cross between maternal line i and paternal line j is

$$y_{ijsk} = \mu + G_{ijs} + b_k + \epsilon_{ijsk} \tag{1}$$

where y_{ijsk} is the average phenotypic value of genetic entry G_{ijs} in block k, μ is a fixed population mean, b_k is the random effect of block k, $b_k \sim (0,\sigma_b^2)$, ϵ_{ijsk} is a residual effect, $\epsilon_{ijsk} \sim (0, \sigma_e^2)$.

When the genetic notation of Eisen et al. (1966) is used the genotypic effects G_{ijs} for heterogametic progeny (XY or ZW, $s = 1$) and for homogametic progeny (XX or ZZ, $s = 2$) from dam $i \times$ sire j can be partitioned as

$$\begin{aligned} G_{ij1}^{XY} &= A_i + A_j + D_{ij} + L_{i1} + M_i \\ G_{ij1}^{ZW} &= A_i + A_j + D_{ij} + L_{j1} + M_i \\ G_{ij2}^{XX/ZZ} &= A_i + A_j + D_{ij} + \frac{1}{2}L_{i2} + \frac{1}{2}L_{j2} + M_i \end{aligned} \tag{2}$$

where A_i (or A_j) is the additive effect of autosomal genes from dam i (or sire j), A_i (or A_j) $\sim (0, \sigma_A^2)$, D_{ij} is the dominance effect of autosomal genes from the cross of dam $i \times$ sire j, $D_{ij} \sim (0, \sigma_D^2)$, L_{i1} (or L_{j1}) is the additive effect of sex-linked genes in heterogametic offspring from parent i (or j), L_{i2} (or L_{j2}) is the additive effect of sex-linked genes in homogametic offspring from parent i (or j), L_{i1} (or L_{j1}), L_{j2} (or L_{j2}) $\sim (0, \sigma_L^2)$, M_i is the maternal effect of dam i, $M_i \sim (0, \sigma_M^2)$.

The phenotypic variance V_P can be partitioned into genetic variance components,

$$\begin{aligned} V_P &= 2\sigma_A^2 + \sigma_D^2 + \sigma_L^2 + \sigma_M^2 + \sigma_e^2 \\ &= V_A + V_D + V_L + V_M + V_e \end{aligned} \tag{3}$$

When genotype-by-environment interactions do exist, genetic experiments should be conducted in different environments. The genetic model including genotype-by-environment interactions is an extension of Eq. 1. The phenotypic mean of sex s from the cross between maternal line i and paternal line j in the kth block within environment h can be expressed as

$$y_{hijsk} = \mu_h + G_{ijs} + GE_{hijs} + b_{hk} + \epsilon_{hijsk} \tag{4}$$

where y_{hijsk} is the average phenotypic value of genetic entry G_{ijs} in the kth block within environment h; μ_h is the fixed mean of population in environment h; b_{hk} is the random effect of block k within the hth environment, $b_{hk} \sim (0, \sigma_b^2)$; ϵ_{hijsk} residual effect, $\epsilon_{hijsk} \sim (0, \sigma_e^2)$.

The genotypic effect G_{ijs} is defined as in Eq. 2. The effect of genotype-by-environment interaction GE_{hijs} is defined as

$$\begin{aligned} GE_{hij1}^{XY} &= AE_{hi} + AE_{hj} + DE_{hij} + LE_{hi1} + ME_{hi} \\ GE_{hij1}^{ZW} &= AE_{hi} + AE_{hj} + DE_{hij} + LE_{hj1} + ME_{hi} \\ GE_{hij2}^{XX/ZZ} &= AE_{hi} + AE_{hj} + DE_{hij} + \frac{1}{2}LE_{hi2} \\ &\quad + \frac{1}{2}LE_{hj2} + ME_{hi} \end{aligned}$$

where the interaction terms are defined in a way similar to the main effects, with

$$AE_{hi}, AE_{hj} \sim (0, \sigma_{AE}^2)$$

$$DE_{hij} \sim (0, \sigma_{DE}^2)$$

$$LE_{hi1}, LE_{hj1}, LE_{hi2}, LE_{hj2} \sim (0, \sigma_{LE}^2)$$

$$ME_{hi} \sim (0, \sigma_{ME}^2)$$

Partitioning of phenotypic variance V_P in this genetic model is

$$\begin{aligned} V_P &= 2\sigma_A^2 + \sigma_D^2 + \sigma_L^2 + \sigma_M^2 + 2\sigma_{AE}^2 \\ &\quad + \sigma_{DE}^2 + \sigma_{LE}^2 + \sigma_{ME}^2 + \sigma_e^2 \\ &= V_A + V_D + V_L + V_M + V_{AE} + V_{DE} + V_{LE} + V_{ME} + V_e \end{aligned} \tag{6}$$

These two genetic models can be written in the matrix form of a mixed linear model for all the entries in the mating design,

$$\mathbf{y} = \mathbf{Xb} + \sum_{u=1}^{q+1} \mathbf{U}_u \mathbf{e}_u \tag{7}$$

with the variance-covariance matrix

$$\mathrm{Var}(\mathbf{y}) = \sum_{u=1}^{q+1} \sigma_u^2 \mathbf{U}_u \mathbf{U}_u'$$

where **b** is the vector of population means; **X** is the known incidence matrix relating to the fixed vector **b**; $\mathbf{U}_x$ is the known incidence matrix relating to the random vector $\mathbf{e}_u$, $\mathbf{e}_u \sim (0, \sigma_u^2\mathbf{I})$; $\mathbf{U}'_u$ is the transpose of $\mathbf{U}_u$; $\mathbf{U}_{q+1} = \mathbf{I}$ is an identity matrix; q is the number of random effects other than the residuals ($q = 5$ for Eq. 1 and $q = 9$ for Eq. 4).

Analysis methodology

Methods 1 and 3 for diallel crosses can be analyzed by the methods of MINQUE (Rao 1970, 1971) for mixed linear models. Variance components of the mixed linear model in Eq. 7 can be estimated by solving the following MINQUE equations for $u, v = 1,2,\ldots q-1$:

$$[\mathrm{tr}(\mathbf{U}'_u\mathbf{Q}_\alpha\mathbf{U}_v\mathbf{U}'_v\mathbf{Q}_\alpha\mathbf{U}_u)][\sigma_u^2] = [\mathbf{y}'\mathbf{Q}_\alpha\mathbf{U}_u\mathbf{U}'_u\mathbf{Q}_\alpha\mathbf{y}] \quad (8)$$

where

$$\mathbf{V}_\alpha = \sum_{u=1}^{q+1} \alpha_u\mathbf{U}_u\mathbf{U}'_u, \text{ with inverse } \mathbf{V}_\alpha^{-1}$$

$$\mathbf{Q}_\alpha = \mathbf{V}_\alpha^{-1} - \mathbf{V}_\alpha^{-1}\mathbf{X}(\mathbf{X}'\mathbf{V}_\alpha^{-1}\mathbf{X})^{-1}\mathbf{X}'\mathbf{V}_\alpha^{-1}$$

and the trace of a matrix, denoted by tr, is the sum of its diagonal elements. α_u are prior values of variances (or covariances) for variance (or covariance) estimation. For two random variables, $\mathbf{y}_a$ and $\mathbf{y}_b$ with equal design matrices, invariant and unbiased estimators of covariance components can be obtained by solving the following system of equations ($u, v = 1, 2, \ldots q+1$):

$$[\mathrm{tr}(\mathbf{U}'_u\mathbf{Q}_\alpha\mathbf{U}_v\mathbf{U}'_v\mathbf{Q}_\alpha\mathbf{U}_u)][\sigma^2_{a_u/b_u}] = [\mathbf{y}'_a\mathbf{Q}_\alpha\mathbf{U}_u\mathbf{U}'_u\mathbf{Q}_\alpha\mathbf{y}_b] \quad (9)$$

The matrices $[\mathrm{tr}(\mathbf{U}'_u\mathbf{Q}_\alpha\mathbf{U}_v\mathbf{U}'_v\mathbf{Q}_\alpha\mathbf{U}_u]$ and $\mathbf{Q}_\alpha\mathbf{U}_u\mathbf{U}'_u\mathbf{Q}_\alpha$ in Eq. 9 are the same as those in Eq. 8. Therefore, they can be storeed for later recall to estimate variances and covariances for multiple traits. The prior values for variances or covariances may be chosen from prior experiments, from iterations or from theoretical considerations. The estimators are unbiased, provided the choice of prior values does not depend on the data. If the parameter values are known and used for $[\alpha_u]$ ($\alpha_u = \sigma_u^2$ or $\sigma_{1u/2u}$), this is the MINQUE(θ) that will give the minimum variance, invariant, unbiased estimators for linear functions of variance components under the normality assumption (Rao 1972). If the user has no basis for selecting α, MINQUE(1) with $\alpha = 1$ suggested by Giesbrecht (1985) can be used. If α_u are replaced by the iterated estimates with the restriction that they are within parameter space, REML estimates can be obtained by iteration until convergence.

The uth vector of random genetic effects in Eqs. 2 or 5 can be predicted by

$$\hat{\mathbf{e}}_{u(\alpha)} = \alpha_u\mathbf{U}'_u\mathbf{Q}_\alpha\mathbf{y} \quad (10)$$

If the prior values are replaced by the true parameter values, the best linear unbiased prediction (BLUP) (Henderson 1963) can be obtained. Since the true variances are unknown in practice, estimated variances are usually used in prediction. With such prediction-using estimates ("BLUP"), the linearity and unbiasedness of BLUP may be lost. The genetic effects can also be predicted by choosing prior values α as in the case of the MINQUE method. It will give a linear unbiased prediction (LUP). The LUP can be accommodated by the estimated variance to give an adjusted unbiased prediction (AUP),

$$\hat{\mathbf{e}}^A_{u(\alpha)} = \kappa\hat{\mathbf{e}}_{u(\alpha)}$$

where $\kappa = \sqrt{[(df_u\sigma_u^2)/(\hat{\mathbf{e}}'_{u(\alpha)}\hat{\mathbf{e}}_{u(\alpha)})]}$, with constraint $\hat{\sigma}_u^2 \geq 0$, and df the uth vector size minus 1.

The predicted genetic effects can be further used for testing hypotheses about gene effects. Since the sum of all the dominance effects is zero

$$\sum_i D_{ii} + \sum_{i<j} D_{ij} = 0$$

it follows that

$$-\sum_i D_{ii} = \sum_{i<j} D_{ij}$$

where D_{ii} is a homozygote dominance effect and D_{ij} a heterozygote dominance effect.

Under the null hypothesis of no heterosis for the trait analyzed,

$$\sum_{i<j} D_{ij} = \sum_i D_{ii} = 0$$

If there are p parents involved in the diallel mating, a significant positive value of $(-\Sigma_i\hat{D}_{ii})/p$ would indicate positive heterosis, and the reverse is true for negative heterosis.

Under the null hypothesis of no average difference between males and females for the trait analyzed,

$$\left(\sum_i L_{i1}\right)\Big/p = \left(\sum_i L_{i2}\right)\Big/p = 0$$

Since $\Sigma_i L_{i1} + \Sigma_i L_{i2} = 0$, the average difference between males and females can be tested by the statistic $(2\Sigma_i\hat{L}_{i1})/p$. XY males or ZW females will have larger values if there is significant positive $(2\Sigma_i\hat{L}_{i1})/p$.

Sampling variances for estimated variances and covariances as well as for predicted genetic effects can be estimated by the jackknife procedure (Miller 1974; Efron 1982). For diallel analysis, genetic entries can serve as resampling units, deleting one genotype in all replicates at a time. When jackknife estimates and their standard errors are obtained, the null hypotheses of zero parameter values can then be tested by a t-test.

Simulation results

Monte Carlo simulations were performed for cell means of seven-parent diallel crosses to evaluate the estimation of variances by MINQUE(θ), MINQUE(1), and REML. The unbiasedness and efficiency of prediction with BLUP, AUP, and "BLUP" methods were also compared by Monte Carlo simulations. Pseudo-random normal deviates with zero mean and unit variance were generated by the method of Kinderman and Monahan (1977). For each case, 500 simulations were run to obtain sample means of estimates, bias, and Mean Squared Error (MSE). If the absolute value of bias approached zero, the estimate was considered to be unbiased for the parameter. In cases where the parameter value of variance or covariance component is zero, bias < 1% of the sum of variances was considered to be negligible.

Simulation results for bias and MSE are summarized in Table 1 for variance components. Variance of residual effects can always be efficiently estimated without bias by MINQUE(θ), MINQUE(1), and REML methods. Both MINQUE(θ) and MINQUE(1) gave unbiased estimates for variance components no matter what values were set for the parameters. There were no apparent differences of bias and MSE between these two MINQUE methods. Unbiased estimates were also ob-

Table 1 Bias and MSE of variance components estimated by MINQUE(θ), MINQUE(1), and REML for 7 × 7 diallel crosses.

Parameter	Value	MINQUE(θ)		MINQUE(1)		REML	
		Bias	MSE	Bias	MSE	Bias	MSE
σ_A^2	50	−0.12	991	−0.22	987	−0.17	999
σ_D^2	30	−0.47	135	−0.47	135	−0.50	135
σ_D^2	20	−0.11	162	−0.09	167	0.21	178
σ_M^2	20	−0.06	231	−0.04	235	−0.05	232
σ_e^2	30	−0.35	34	−0.35	34	−0.33	35
σ_A^2	50	0.05	993	0.33	976	−0.04	1000
σ_D^2	30	0.48	134	−0.48	134	−0.50	135
σ_L^2	0	−0.10	11	0.01	30	1.30	8
σ_M^2	20	0.11	208	0.04	230	0.11	213
σ_e^2	30	−0.32	32	−0.32	34	−0.32	33
σ_A^2	50	−0.11	931	−0.38	973	−0.14	943
σ_D^2	30	−0.47	133	−0.49	134	−0.48	135
σ_L^2	0	−0.07	8	−0.04	26	1.09	5
σ_M^2	0	0.11	7	0.09	10	1.10	5
σ_e^2	30	−0.34	31	−0.31	34	−0.38	31

tainable by the REML method for non-zero variances. If there was no variation for sex-linked effects and/or maternal effects, variance components for these effects tended to be slightly over-estimated by the REML method. Since REML requires enormous computations due to iterations, there is no apparent advantage of REML over MINQUE(1). With the MINQUE(1) method, the sex-linked models were quite robust for estimating variance components even when there were no sex-linked and maternal effects.

Five hundred simulation runs were conducted for estimating bias in predicted effects and distance between predictor vector $\hat{\mathbf{e}}_u$ and sampling vector $\tilde{\mathbf{e}}_u$. The distance was defined as $\|\hat{\mathbf{e}} - \tilde{\mathbf{e}}\| = \sqrt{[\Sigma_u(\hat{\mathbf{e}} - \tilde{\mathbf{e}}_u]^2}$. Two prediction methods, "BLUP" $\hat{\mathbf{e}}_{u(\hat{\theta})}$ using REML estimates and AUP $\tilde{\mathbf{e}}^A_{u(1)}$ with $\alpha = 1$, were compared with BLUP $\hat{\mathbf{e}}_{u(\theta)}$ using parameter values.

All these prediction methods gave extremely low bias for predicted mean genetic effects (Table 2). Hence these predictors were essentially unbiased for random genetic effects. The variances of predicted random genetic effects were always smaller than the true variances for both the BLUP and "BLUP" method. These two methods gave prediction with unbiased means but under-estimated

Table 2 Prediction of genetic effects by BLUP, AUP, and "BLUP" for 7 × 7 diallel crosses[a]

Parameter[b]	BLUP $\hat{\mathbf{e}}_{u(\theta)}$		AUP $\hat{\mathbf{e}}^A_{(1)}$		"BLUP" $\hat{\mathbf{e}}_{u(\hat{\theta})}$	
	Variance	Distance	Variance	Distance	Variance	Distance
$\sigma_L^2 = \sigma_M^2 = 20$						
A	44.3	8.3	49.8	8.5	45.0	8.5
D	18.1	18.3	29.5	19.4	18.6	18.7
L	11.4	11.1	20.0	12.2	13.0	11.8
M	15.3	6.5	20.0	6.8	16.1	6.8
$\sigma_L^2 = 0, \sigma_M^2 = 20$						
A	45.1	8.1	49.7	8.4	45.5	8.2
D	18.2	18.3	29.5	19.4	18.6	18.7
L	0.0	0.0	2.2	3.2	0.4	1.2
M	16.5	5.9	20.0	6.6	16.7	6.2
$\sigma_L^2 = \sigma_M^2 = 0$						
A	45.7	7.8	49.6	8.3	45.6	8.0
D	18.2	18.3	29.5	19.3	18.6	18.7
L	0.0	0.0	2.0	3.1	0.3	1.1
M	0.0	0.0	1.3	1.7	0.5	0.9

[a] Absolute bias for mean prediction of genetic effects was $10^{-5} \sim 10^{-7}$ for these three predictions
[b] Parameter values were set to $\sigma_A^2 = 50$ for additive effects and $\sigma_D^2 = 30$ for dominance effects

variances for all the random effects. In animal breeding, "BLUP" is used by breeders mostly for evaluating breeding values. Under-estimated variances of "BLUP" predictors indicate that the absolute values of predicted genetic effects will be smaller than the real values. When adjusted by estimated variances, AUP gave predictors with unbiased means as well as variances for random genetic effects. Since adjustor κ needs the constraint of $\hat{\sigma}_u^2 \geqslant 0$, variances of AUP predictors are slightly over-estimated if there are no random effects.

The BLUP $\hat{\mathbf{e}}_{u(\theta)}$ should give the smallest distance for the predicted genetic effects among all unbiased linear predictions (Henderson 1979). The distances of "BLUP" $\hat{\mathbf{e}}_{u(\hat{\theta})}$ and AUP $\hat{\mathbf{e}}^A_{u(1)}$ were a little larger than those of BLUP $\hat{\mathbf{e}}_{u(\theta)}$. Distance tended to be slightly greater for AUP. It is concluded that AUP can be used for predicting genetic effects.

Examples of diallel analyses for mice and silkworm

For half-diallel crosses, eight to ten parents are preferred for unbiased estimations (Pederson 1971). Since full diallel crosses measuring two sexes were employed in the present study, the experiment size was four times larger than the general analysis for half-diallel crosses with the same number of parents and replications. Diallel crosses with seven or more parents are suggested for unbiased estimation of genetic parameters in these genetic models. As a demonstration of using the new methods, we analyzed cell means of a 7×7 diallel cross for mice (Appendix A) and of 5×5 diallel crosses in two seasons for silkworm (Appendix B). Variance and covariance components were estimated by MINQUE(1) approaches, and genetic effects predicted by the AUP method. Each genetic entry with two sex means served as the resampling unit in the jackknife procedure. A one-tail t-test was conducted for testing variance components while a two-tail t-test was utilized for testing covariances or genetic effects.

The mouse genetic experiment was conducted by W.R. Atchley, Department of Genetics, North Carolina State University. A total of 2970 mice (1478 males and 1492 females) resulting from a 7×7 diallel cross of the inbred strains A/J, BALB/cByJ, C57BL/6ByJ, C3He/FeJ, SEA/GnJ, SEC/1ReJ, and SWR/J were employed. Body weight (g) and tail length (mm) were measured at 28 days of age. The mean for each cell was the average of approximately 30 individuals. Since there were 49 genetic entries (seven parents and 42 F_1 hybrids), the degrees of freedom for the t-test were 48.

Means of 28-day body weights were 23.14 ($\pm$ 0.22) and 19.43 ($\pm$ 0.19) for male and female mice, respectively. No apparent difference was found for average tail length between male mice (85.93 $\pm$ 0.50) and female mice (84.17 $\pm$ 0.43). The estimated variance and covariance components for body weight and tail length are presented in Table 3. Additive variance was most important for both body weight and tail length. Dominance variance was not significant for either of these two traits. Sex-linked variance and maternal variance were important for body weight but not for tail length. There was a significant positive covariance of additive effects between body weight and tail length. Highly significant covariance was also obtained for residual errors. Covariance components were not significant for other gene effects.

Predicted genetic effects and their standard errors for body weight and tail length are presented in Table 4 for those with positive values of estimated variances. The breeding values of the inbred strains can be evaluated by additive and maternal effects as well as by sex-linked effects for body weight. Strain 6 (SEC/1ReJ) had positive additive effects but negative maternal effects for body weight, the reverse was true for strain 3 (C57BL/6ByJ). Male mice tended to be bigger than female mice. This was due to the larger sex-linked effects for males. The predicted genetic difference between males and females was $(2\Sigma_i \hat{L}_{i1})/7 = 2.60(\pm 0.08)$ for body weight. Significant sex-linked and maternal effects indicated that there might have been some reciprocal effects for body weight of mice. The reciprocal effect can be predicted by $(\hat{L}_{i1} - \hat{L}_{j1}) + (\hat{M}_i - \hat{M}_j)$ for male offspring and $(\hat{M}_i - \hat{M}_j)$ for female offspring. Since strain 6 had a relatively small sex-linked effect ($\hat{L}_{61} = 0.20$) and the smallest maternal effect ($\hat{M}_6 = -3.02$), paternal strain 6 mating to other dams gave offspring with much higher body weights than their reciprocal crosses. For tail length, significant additive effects were predicted with negative values for strain 2 (BALB/cByJ) and strain 5 (SEA/GnJ) but with

Table 3 Estimates of variance and covariance components for body weight (g) and tail length (mm) of mice at 28 days of age

Variance	Body weight	Tail length	Covariance	Weight vs. length
	Estimate $\pm$ SE	Estimate $\pm$ SE		Estimate $\pm$ SE
V_A	3.74** $\pm$ 0.89	6.02* $\pm$ 3.43	C_A	3.13* $\pm$ 1.51
V_D	-0.07 ± 0.27	0.32 ± 2.75	C_D	-0.17 ± 0.81
V_L	2.53** $\pm$ 0.36	-1.03 ± 0.93	C_L	0.36 ± 0.93
V_M	2.15** $\pm$ 0.75	4.22 ± 4.16	C_M	1.49 ± 1.57
V_e	0.68** $\pm$ 0.23	6.55** $\pm$ 2.01	C_e	1.75 ± 0.65

* $P < 0.05$, ** $P < 0.01$, one-sided alternative for variance components

Table 4 Predicted genetic effects and standard errors for body weight and tail length of mice at 28 days of age

	$i=1$	$i=2$	$i=3$	$i=4$	$i=5$	$i=6$	$i=7$
Body weight (mg)							
A_i	$-0.96^{*} \pm 0.32$	$-1.77^{**} \pm 0.41$	-0.75 ± 0.34	$0.74^{**} \pm 0.28$	-0.22 ± 0.40	$2.82^{**} \pm 0.51$	0.13 ± 0.35
$\hat{L}_{i1}$	$1.00^{**} \pm 0.22$	$1.37^{**} \pm 0.38$	$1.47^{**} \pm 0.32$	2.06 ± 0.26	$0.82^{*} \pm 0.33$	0.20 ± 0.39	2.17 ± 0.39
$\hat{L}_{i2}$	$-0.45^{**} \pm 0.17$	0.25 ± 0.22	$-1.75^{**} \pm 0.36$	$-0.99^{**} \pm 0.30$	$-1.23^{**} \pm 0.51$	$-3.64^{**} \pm 0.51$	$-1.30^{**} \pm 0.24$
$\hat{M}_i$	0.32 ± 0.18	$1.20^{*} \pm 0.59$	$1.83^{**} \pm 0.48$	-0.57 ± 0.33	0.46 ± 0.49	$-3.02^{**} \pm 0.61$	-0.22 ± 0.48
Tail length (mm)							
$\hat{A}_i$	-1.45 ± 1.18	$-3.09^{**} \pm 1.19$	$2.01^{*} \pm 0.90$	2.14 ± 1.11	$-2.07^{**} \pm 0.88$	1.80 ± 0.93	0.65 ± 0.86
$\hat{D}_{i1}$	-6.65 ± 4.18						
$\hat{D}_{i2}$	2.64 ± 1.45	-1.47 ± 1.52					
$\hat{D}_{i3}$	3.75 ± 2.22	2.62 ± 1.40	0.67 ± 0.87				
$\hat{D}_{i4}$	0.72 ± 1.32	-2.62 ± 3.84	0.17 ± 0.78	1.58 ± 1.42			
$\hat{D}_{i5}$	0.48 ± 2.00	0.32 ± 0.88	$-4.38^{*} \pm 1.99$	1.39 ± 2.59	0.66 ± 1.01		
$\hat{D}_{i6}$	1.82 ± 1.63	-2.34 ± 4.82	0.46 ± 0.84	-2.50 ± 2.66	2.00 ± 1.12	1.10 ± 1.33	
$\hat{D}_{i7}$	2.56 ± 1.55	-0.09 ± 1.01	-2.39 ± 2.90	1.35 ± 1.08	-2.60 ± 3.12	-0.10 ± 1.42	0.86 ± 1.06
$\hat{M}_i$	-0.57 ± 0.80	3.42 ± 1.91	-1.34 ± 1.16	-2.83 ± 1.62	2.87 ± 1.52	-3.06 ± 1.77	1.50 ± 1.36

$^{*} P < 0.05$, $^{**} P < 0.01$, one-sided alternative for variance components

positive value for strain 3. No significant maternal effects were found for tail length. The estimates of dominance variance were negative for body weight and not significantly positive for tail length. None of the dominance effects of tail length, except for D_{35}, were significantly different from zero.

Data for cocoon weight and fibroin content (Zhong 1992) for a 5×5 diallel cross in summer and fall, 1991 were analyzed for evaluating interaction variance components as well as genetic variance components. Silkworm is a heterogametic female species with ZZ sex chromosomes for males and ZW sex chromosomes for females. Instead of estimating variance and covariance components, we can estimate the ratio of variance components to phenotypic variance and genetic correlations. In order to estimate ratios of variance components, we set all of the negative estimates of variance components to zero. the jackknife estimates and standard errors for ratio of variance components and correlations are listed in Table 5. Since there were a total of 50 genetic entries in two seasons, the degrees of freedom for a t-test were 49. The most important contribution to phenotypic variation of cocoon weight was sex-linked effects followed by additive and dominance effects. For fibroin content, additive and dominance effects were the major sources of variation. No variation was detected for maternal effects of cocoon weight or for sex-linked by environment interaction effects of fibroin content. Additive-by-environment interaction variance contributed about 5% of the total variation for cocoon weight and fibroin content. The other variance ratios of environment interaction were relatively small. The ratio of residual errors was around 5% for these two traits. All these detectable variance ratios were highly significant ($P < 0.01$). Except for maternal effects and sex-linked-by-environment interaction effects, significant positive correlations were observed for all the genetic effects and residual errors between cocoon weight and fibroin content. There were positive correlations of sex-linked effects, dominance effects, additive effects, and residual effects. Negative correlations were observed for interactions of dominance and maternal effects.

Table 5 Estimation of variance and covariance components for cocoon weight and fibroin content of silkworm (summer and fall 1991)

Ratio	Cocoon weight	Fibroin content	Covariance	Cocoon vs. fibroin
	Estimate $\pm$ SE	Estimate $\pm$ SE		Estimate $\pm$ SE
V_A/V_P	$0.196^{**} \pm 0.022$	$0.453^{**} \pm 0.043$	r_A	$0.640^{**} \pm 0.066$
V_D/V_P	$0.196^{**} \pm 0.025$	$0.330^{**} \pm 0.035$	r_D	$0.847^{**} \pm 0.063$
V_L/V_P	$0.403^{**} \pm 0.024$	$0.034^{**} \pm 0.011$	r_L	$0.867^{**} \pm 0.061$
V_M/V_P	0.000 ± 0.000	$0.044^{**} \pm 0.012$	r_M	0.000 ± 0.000
V_{AE}/V_P	$0.058^{**} \pm 0.011$	$0.044^{**} \pm 0.015$	r_{AE}	0.032 ± 0.063
V_{DE}/V_P	$0.038^{**} \pm 0.010$	$0.028^{**} \pm 0.010$	r_{DE}	$-1.000^{**} \pm 0.065$
V_{LE}/V_P	$0.031^{**} \pm 0.006$	0.000 ± 0.000	r_{LE}	0.000 ± 0.000
V_{ME}/V_P	$0.022^{**} \pm 0.005$	$0.022^{**} \pm 0.006$	r_{ME}	$-0.480^{**} \pm 0.070$
V_e/V_P	$0.056^{**} \pm 0.010$	$0.046^{**} \pm 0.013$	r_e	$0.652^{**} \pm 0.073$

$^{*} P < 0.05$, $^{**} P < 0.01$, one-sided alternative

Discussion

Variance components for sex-linked and maternal effects, as well as for additive and dominance effects, can be estimated by the MINQUE(1) method for diallel crosses. When the jackknife procedure is used for estimating the sampling variances of estimated variances and covariances or of predicted genetic effects, a *t*-test can be performed for the null hypothesis of no variation. There are several ways of resampling the diallel crosses for the jackknife procedure. For genetic experiments conducted in multiple environments with randomized complete block design, blocks within each environment can be used for resampling. For experiments without blocks, the block effect in Eq. (1) or (4) should be dropped. The genetic entry with cell means can then be used as the resampling unit.

In animal breeding practice, parent and hybrid genetic merit are sometimes of more concern to the breeder. The random genetic effects are predictable by the "BLUP" procedure using estimates of variance components (Henderson 1963). In the present study Monte Carlo simulation has shown that "BLUP" gives unbiased means but smaller variation for predictors. Therefore, genetic merit for some parents and their offspring could be predicted by "BLUP" with smaller absolute values than they should be. Since AUP can give an unbiased mean and variance for predicted genetic effects, comparison of genetic merit among genetic entries studied should be more reliable by AUP than by "BLUP". Another advantage of using AUP is its easy computation. If variance components are estimated by the MINQUE(1) method, $\hat{\mathbf{e}}^{A}_{u(1)}$ can be obtained by $\mathbf{U}'_u\mathbf{Q}_{\alpha=1}\mathbf{y}$ without uch more computation since the calculation of $\mathbf{U}'_u\mathbf{Q}_{\alpha=1}\mathbf{y}$ has already been finished before the estimation of variances by Eq. 8. In order to obtain "BLUP", $\mathbf{Q}_{\alpha_u=\hat{\sigma}^2_u}$ should be recalculated after variance estimation.

Due to the random inactivation of one X-chromosome in the primitive ectoderm lineage of female mammals, the genetic activity of only one X-chromosome is expressed in somatic cells (Lyon 1988). On the assumption of X-chromosome dosage compensation, heterozygous females are mosaic with half-chance inactivation of maternal or paternal X-chromosome. The model of Eisen et al. (1966) was modified by considering X-chromosome dosage compensation (Zhu 1989). Those two models can be analyzed by the statistical methods proposed in this paper. When we analyzed the mouse data by the same procedures with those two models, we could not find any significant variance of sex-linked effects even for body weight. Since an underlying assumption for those two models is of no difference between males and females, those models are of low efficiency in detecting sex-linked variation. For some domestic animals, there may be no dosage compensation of sex-linked genes (Cock and Morton 1963). In those situations, the coefficients before L_{i2} and L_{j2} in Eqs. 2 or before LE_{hi2} and LE_{hj2} in Eqs. 5 should be dropped.

The sex-linked models proposed in this paper can be analyzed by several mixed model approaches but not by ANOVA methods (Searle et al. 1992). Maximum likelihood (ML) (Hartley and Rao 1967) and REML (Patterson and Thompson 1971) are two methods that can be applied for estimating variance components in the models. Since these two methods need iterations, there are enormous computations involved with the jackknife procedure. We suggest the use of the MINQUE(1) method for its unbiased estimation and non-iterative computation. MINQUE estimation will not guarantee positive estimates for variances. If negative estimates are set to be zero, over-estimated variances can then be expected.

Appendix A Cell mean of body weight (gm) and tail length (mm) for mice at 28 days of age from a 7 × 7 diallel cross (WR Atchley, personal communication)

Parents		Body weight		Tail length	
Maternal	Paternal	Male	Female	Male	Female
1	1	16.763	15.531	71.500	70.852
1	2	17.843	17.039	76.455	75.968
1	3	17.639	15.987	83.515	80.370
1	4	19.569	18.088	78.387	78.273
1	5	18.379	16.561	73.621	73.433
1	6	21.491	18.304	78.677	77.571
1	7	18.234	16.543	80.222	78.697
2	1	19.088	17.298	79.533	78.821
2	2	16.660	16.162	75.133	75.367
2	3	18.266	15.839	83.931	81.400
2	4	17.765	17.361	73.545	75.645
2	5	18.466	16.369	77.800	76.433
2	6	22.130	18.796	80.633	80.300
2	7	18.387	16.849	79.379	78.871
3	1	20.000	17.617	79.438	77.700
3	2	19.420	17.276	76.839	77.586
3	3	20.264	17.295	79.185	78.690
3	4	20.887	18.357	79.500	79.700

Appendix A (Continued)

Parents		Body weight		Tail length	
Maternal	Paternal	Male	Female	Male	Female
3	5	17.245	15.617	70.567	70.382
3	6	22.532	18.547	79.448	78.581
3	7	20.819	18.013	78.357	77.344
4	1	19.590	17.707	77.080	76.600
4	2	18.601	16.237	76.129	74.759
4	3	19.927	16.531	80.419	77.483
4	4	20.961	17.904	80.333	79.839
4	5	19.373	16.095	76.194	75.229
4	6	20.754	17.418	74.742	74.031
4	7	20.518	17.459	79.405	79.226
5	1	17.914	16.371	77.483	78.867
5	2	16.946	16.449	74.846	76.939
5	3	17.361	15.240	75.778	75.800
5	4	19.953	18.336	82.600	83.735
5	5	19.523	17.165	77.118	76.528
5	6	21.900	18.352	81.333	80.556
5	7	17.642	16.371	73.448	74.029
6	1	17.465	16.221	77.697	77.237
6	2	14.806	13.142	68.875	67.680
6	3	17.826	14.202	80.069	76.581
6	4	17.977	15.711	77.938	77.464
6	5	18.478	16.058	77.966	76.636
6	6	20.878	17.530	78.033	78.214
6	7	17.614	15.608	76.500	75.800
7	1	18.553	15.716	82.143	79.100
7	2	17.898	15.718	78.394	76.077
7	3	17.388	15.070	76.519	76.909
7	4	21.017	17.747	84.297	82.963
7	5	20.010	17.179	78.133	78.233
7	6	22.548	17.499	82.844	81.281
7	7	20.454	16.987	82.280	79.710

Appendix B Cell mean of cocoon weight (mg) and fibroin content (mg) in two seasons for silkworm from a 5 × 5 diallel cross (Zhong 1992)

Season	Parents		Cocoon weight		Fibroin content	
	Maternal	Paternal	Female	Male	Female	Male
1	1	1	1348	1004	125	112
1	1	2	1452	1147	174	163
1	1	3	1529	1225	201	191
1	1	4	1650	1303	207	182
1	1	5	1648	1313	208	191
1	2	1	1647	1206	226	200
1	2	2	1651	1271	239	216
1	2	3	1700	1280	268	243
1	2	4	1604	1245	260	243
1	2	5	1788	1377	280	268
1	3	1	1595	1209	210	187
1	3	2	1550	1226	256	234
1	3	3	1562	1304	228	218
1	3	4	1773	1425	275	268
1	3	5	1875	1460	291	267
1	4	1	1639	1266	183	173
1	4	2	1545	1249	239	236
1	4	3	1785	1400	282	269
1	4	4	1289	1030	175	171
1	4	5	1691	1363	259	252
1	5	1	1657	1294	216	197
1	5	2	1748	1445	260	247
1	5	3	1641	1260	246	225
1	5	4	1888	1485	276	258
1	5	5	1689	1316	245	221
2	1	1	1439	1016	134	118
2	1	2	1750	1366	248	224

Appendix B (Continued)

Season	Parents		Cocoon weight		Fibroin content	
	Maternal	Paternal	Female	Male	Female	Male
2	1	3	1757	1330	240	213
2	1	4	1775	1375	229	209
2	1	5	1794	1386	237	217
2	2	1	1847	1400	257	230
2	2	2	1970	1545	292	277
2	2	3	1795	1446	304	301
2	2	4	1880	1464	303	286
2	2	5	2180	1672	315	299
2	3	1	1804	1359	244	227
2	3	2	1923	1501	316	298
2	3	3	1640	1403	254	251
2	3	4	2172	1713	341	325
2	3	5	2218	1727	346	324
2	4	1	1832	1433	243	225
2	4	2	1883	1533	291	282
2	4	3	2048	1664	315	310
2	4	4	1775	1361	228	208
2	4	5	2082	1609	317	294
2	5	1	1947	1439	262	231
2	5	2	2097	1645	312	297
2	5	3	2190	1635	324	306
2	5	4	2215	1665	331	292
2	5	5	2059	1488	314	266

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