



Concurrent dynamic model in stability analysis

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Abstract. Concurrent dynamic model can be used to predict the performance of an untried genotype grown in a hypothetical environment at any growth time, when all the genotypes, growth periods and environments are selected randomly from the breeding population and from the full spectrum of time and environments, respectively. This involves the development of regressions of interaction components onto both genotypic and time-space effects, when the positive correlation between regression coefficient and phenotypic mean exists. The data on fresh weight of twenty-four lines of *Arabidopsis thaliana* grown under twelve different environmental conditions in seven growth periods were used to demonstrate the proposed model and to test its applicability.

Key words: *Arabidopsis thaliana*; Concurrence; Concurrent dynamic model; Genotype-time-environment interaction; Stability index.

Introduction

The importance of genotype \times environment ($G \times E$) interaction is well known to plant breeders and geneticists. Linear regression method of measuring $G \times E$ interaction developed by Finlay and Wilkinson (1963) and later improved by Eberhart and Russell (1966) as well as Perkins and Jinks (1968a, b) has been extensively used in many crop plants to evaluate the stability of a set of genotypes to varying environments. In their model, an environmental index was measured by mean performance of all genotypes grown in an environment, and the regression coefficient was estimated by regressing the $G \times E$ interaction (Finlay and Wilkinson, 1963; Perkins and Jinks, 1968a, b) or the mean performance (Eberhart and Russell, 1966) of individual genotype in different environments on the environmental index. The estimated regression coefficient (b) in Finlay-Wilkinson's method plus 1 is equal to that in Eberhart-Russell's method. The value of $(1+b)$ is often called the stability index in plant breeding. Both the regres-

sion coefficient and phenotypic mean are the parameters for evaluating the relative degree of adaptation among genotypes. A genotype having a stability index near 1.0 and a high mean yield is regarded as being well adapted to environments.

Lu and Wu (1987) showed that the stability of a genotype often varies with different developmental stages, and they proposed a dynamic model by integrating time factor into the linear model to elucidate the stability of genotypes of *Arabidopsis thaliana* tested in different environmental conditions and growth periods. The model provides three kinds of stability indices, namely, growth stability index, environment stability index and growth \times environment stability index. The main advantage of using the dynamic model is that both genotype-time and genotype-environment can be studied simultaneously. Hence, a criterion of selection can be determined according to the breeding objective and it provides a direct and easy method of screening genotypes in different time and space. The results also indicated independence between growth and environ-

ment stability, and significant positive correlations between the phenotypic mean and stability indices.

The positive correlation between the phenotypic mean and the regression coefficient has been found in a number of previous studies (Eberhart and Russell, 1966; Perkins and Jinks, 1968a, b; Westerman, 1971; Wright, 1971; Connolly and Jinks, 1975; Phillips *et al.*, 1979; Lu and Wu, 1987). Wright (1971, 1976) has pointed out that the correlation indicates that all regression lines in the Finlay-Wilkinson's method tend to intersect at a common point (i. e. regression is concurrent). That is, the regression lines will converge at some small region in the environmental space and radiate out from this region with varying slopes. Thus, another approach is to regress the interaction components onto genotypes and environments jointly, as suggested by Wright (1971) and, in a rather different context, Mandel (1969). It can be detected by fitting a single parameter which is common to the entire set of data, and then it may be possible to predict the performance of an untried genotype grown in a hypothetical environment, when both genotypes and environments are selected randomly from larger populations.

The aim of this study is to extend the dynamic model in our previous paper (Lu and Wu, 1987) to the condition that individual regression and phenotypic mean are correlated. Twenty-four inbred lines of *Arabidopsis thaliana* were used to demonstrate the proposed model and to test its applicability and reliability of prediction.

Statistical Model

If Y_{tjkk} represents the observed value of the i -th genotype in the j -th environment for the k -th plant at the t -th growth time ($t=1\dots m$, $i=1\dots n$, $j=1\dots p$, $k=1\dots q$), then the basic model is

$$Y_{tjkk} = \mu + G_i + T_t + E_j + \alpha_{ti} + \beta_{tj} + I_{ij} + \gamma_{tij} + e_{tjkk} \quad (1)$$

where μ is the grand mean; G_i , T_t and E_j are the effects of genotype, growth time and environment, respectively; α_{ti} , β_{tj} , I_{ij} and γ_{tij} are the interaction effects between genotype \times growth time, growth time \times environment, genotype \times environment, and genotype \times growth time \times environment, respectively; e_{tjkk} is the error term and independently normally distributed with mean zero and variance σ^2 . All the genotypes, environments and

growth periods included are assumed to be randomly selected from the breeding population and from the full spectrum of environments and time, respectively; that is, all the main effects are random, and conventional analysis of variance will therefore allow the estimation of the associated variance components.

In the previous study (Lu and Wu, 1987), the dynamic model was established by regressing the interaction components (α_{ti} , I_{ij} and γ_{tij}) onto the effects of time (T_t), environment (E_j) and time \times environment (β_{tj}), respectively. That is, we can obtain

$$\begin{cases} \alpha_{ti} = \xi_i T_t + \eta_{ti} \\ I_{ij} = b_j E_j + \delta_{ij} \\ \gamma_{tij} = \phi_i \beta_{tj} + \theta_{tij} \end{cases} \quad (2)$$

where ξ_i , b_j and ϕ_i are the regression coefficients, and η_{ti} , δ_{ij} and θ_{tij} represent the residual deviations from the three fitted regressions, respectively. Such regression analyses are expressed in a way analogous to Finlay-Wilkinson (1963) type of analysis, thus, equation (1) may be rewritten as:

$$Y_{tjkk} = \mu + G_i + T_t + E_j + \beta_{tj} + \xi_i T_t + b_j E_j + \phi_i \beta_{tj} + \eta_{ti} + \delta_{ij} + \theta_{tij} + e_{tjkk} \quad (3)$$

If the positive correlation between regression coefficient and phenotypic mean ($\bar{Y}_{i..}$) exists, there may be a regression of the regression coefficient onto genotypic effect (G_i) as:

$$\begin{cases} \xi_i = c_1 G_i \\ b_j = c_2 G_i \\ \phi_i = c_3 G_i \end{cases} \quad (4)$$

where the coefficient of concurrence c_1 , c_2 , c_3 adequately describe the situation where the ξ_i , b_j , ϕ_i are correlated, that is, all regressions lines in the analysis of dynamic model have a common point of intersection. Hence, the concurrent dynamic model may be expressed as:

$$Y_{tjkk} = \mu + T_t + G_i + E_j + \beta_{tj} + c_1 G_i T_t + c_2 G_i E_j + c_3 G_i \beta_{tj} + \eta'_{ti} + \delta'_{ij} + \theta'_{tij} + e_{tjkk} \quad (5)$$

where η'_{ti} , δ'_{ij} and θ'_{tij} are the residual deviations from the regressions, respectively. c_1 , c_2 and c_3 can be alternatively considered as the regression of the interaction effect (α_{ti} , I_{ij} , γ_{tij}) onto both genotypic effect (G_i) and time-space effects (T_t , E_j , β_{tj}) respectively.

The dynamic model of equation (3) involves regression of interaction effects onto time-space effects, therefore it concerns with assessment of adaptation for

a set of genotypes grown under varying environments in different growth periods. A second expansion of equation (1) is in a sense the converse of (3) in which interaction effects (α_{ti} , I_{ij} , γ_{tij}) are regressed onto genotypic effect (G_i):

$$Y_{tij} = \mu + T_t + G_i + E_j + \beta_{ij} + \xi G_i + a_j G_i + \psi_{ij} G_i + \alpha_{ti} + \rho_{ij} + \nu_{tij} + e_{tij} \quad (6)$$

(Wright, 1971; Utz, 1972; Moav and Wohlfarth, 1974), where ξ , a_j and ψ_{ij} are regression coefficients, and α_{ti} , ρ_{ij} and ν_{tij} represent the residual deviations from the three fitted regressions, respectively. This model is often used in the choice of particularly useful screening environments. The parameters (c_1 , c_2 , c_3) of model (5) can be alternatively estimated by regressing the regression coefficients (ξ , a_j , ψ_{ij}) onto time-space effects (T_t , E_j , β_{ij}) respectively. That is, the two models involving regression onto time-space effects (3) or genotypic effects (6) are equivalent when regression lines are concurrent, but they are not when concurrence is absent.

However, the condition for all regression lines being complete concurrent is not always met in practice. If deviations do exist, the relationship between deviation components and time-space effects of model (5) can be further examined as:

$$\begin{cases} \eta'_{ti} = \xi'_i T_t + \xi'_t G_i + d_{ti} \\ \delta'_{ij} = b'_i E_j + a'_j G_i + s_{ij} \\ \theta'_{tij} = \phi'_i \beta_{ij} + \psi'_{ij} G_i + \gamma_{tij} \end{cases} \quad (7)$$

where the values of the independent, partial coefficients (ξ'_i and ξ'_t , b'_i and a'_j , ϕ'_i and ψ'_{ij}) are the residual regressions after removal of independence on corresponding indices, respectively. d_{ti} , s_{ij} and γ_{tij} are the deviation components which is independent of regression onto time-space effects. Thus model (5) can be further expanded to

$$Y_{tij} = \mu + T_t + G_i + E_j + \beta_{ij} + c_1 G_i T_t + c_2 G_i E_j + c_3 G_i \beta_{ij} + \xi'_i T_t + \xi'_t G_i + b'_i E_j + a'_j G_i + \phi'_i \beta_{ij} + \psi'_{ij} G_i + d_{ti} + s_{ij} + \gamma_{tij} \quad (8)$$

The ANOVA and estimated value of all items are shown in Table 1. Tests of significance for all sources of variation in the joint regression analysis are based on F test assuming a random effects model. If equation (7) exists, it indicates that concurrence is poor. The partial coefficients can be estimated by using simultaneous equations, as suggested by Wright (1971), or obtained from the relationship between model (5) and model (6), as suggested by Wright (1976). The formulas

modified by Lu (1989) to compute the estimated values of partial coefficients are given as follow.

$$\begin{cases} \xi'_t = \xi_t - c_1 T_t \\ a'_j = a_j - c_2 E_j \\ \psi'_{ij} = \psi_{ij} - c_3 \beta_{ij} \\ \xi'_i = \xi_i - c_1 G_i \\ b'_i = b_i - c_2 G_i \\ \phi'_i = \phi_i - c_3 G_i \end{cases} \quad (9)$$

At the point of convergence the mean values \bar{Y}_{tij} are all the same; i.e. difference in performance between genotypes disappear (Hardwick, 1981), which occurred at $T_t = -1/c_1$, $E_j = -1/c_2$ and $\beta_{ij} = 1/c_3$. Such a relation is

$$\bar{Y}_{tij} = \mu + T_t + E_j + \beta_{ij} = \mu - 1/c_1 - 1/c_2 + 1/c_3 \quad (10)$$

where \bar{Y}_{tij} is the mean value of the i -th genotype in the j -th environment at the t -th growth time.

If all regression lines have a common point, i.e. relationship of equation (4) exists, it is apparent that c_1 , c_2 and c_3 provide a useful guide to prediction, as it is common to the entire set of data. Hence, if all the time, environment and the genotype are reasonable to be assumed as random effects, the coefficients of concurrence can be used in the prediction of the performance of untried genotype-time-environment combinations. It has been pointed out by Breese (1969) that the broad sense heritability is appropriate to represent the degree of reliability of prediction. The familiar broad sense heritability is

$$h^2 = \sigma_G^2 / \sigma_P^2 \quad (11)$$

where σ_G^2 is the variance of genotypic effects, and σ_P^2 the total variance. Where the time and environment are assumed to be random effects, then the prediction of the performance of an untried genotype grown in a hypothetical environment at any growth time can be made with a reliability of

$$(\sigma_G^2 + \sigma_T^2 + \sigma_E^2 + \sigma_\beta^2) / \sigma_P^2 \quad (12)$$

where σ_T^2 , σ_E^2 and σ_β^2 are the variance of the components of time-space effects, respectively. Hence, if c_1 , c_2 and c_3 provide a useful guide to prediction, its reliability can be estimated as:

$$(\sigma_G^2 + \sigma_T^2 + \sigma_E^2 + \sigma_\beta^2 + \sigma_{c_1}^2 + \sigma_{c_2}^2 + \sigma_{c_3}^2) / \sigma_P^2 \quad (13)$$

where $\sigma_{c_i}^2$ ($i=1, 2, 3$) is the variance of the component of interaction variation attributable to concurrence, and the total variance

Table 1. Analysis of variance on the assumption of random effects model

Source	D. F.	S. S.	Expectation of MS
Time (T)	m-1	$S1 = npq \sum_{t=1}^m \hat{T}_t^2$	$\sigma^2 + q\sigma_\omega^2 + nq\sigma_\beta^2 + pq\sigma_\alpha^2 + npq\sigma_T^2$
Environment (E)	p-1	$S2 = mnq \sum_{j=1}^p \hat{E}_j^2$	$\sigma^2 + q\sigma_\omega^2 + mq\sigma_i^2 + nq\sigma_\beta^2 + mnq\sigma_E^2$
Genotype (G)	n-1	$S3 = mpq \sum_{i=1}^n \hat{G}_i^2$	$\sigma^2 + q\sigma_\omega^2 + mq\sigma_i^2 + pq\sigma_\alpha^2 + mpq\sigma_G^2$
T × E (β)	(m-1)(p-1)	$S4 = nq \sum_{t=1}^m \sum_{j=1}^p \hat{\beta}_{tj}^2$	$\sigma^2 + q\sigma_\omega^2 + nq\sigma_\beta^2$
G × T (α)	(n-1)(m-1)	$S5 = pq \sum_{t=1}^m \sum_{i=1}^n \hat{\alpha}_{ti}^2$	$\sigma^2 + q\sigma_\omega^2 + pq\sigma_\alpha^2$
Concurrence (c ₁)	1	$S6 = pq\hat{c}_1^2 \sum_{j=1}^n \hat{G}_j^2 \sum_{t=1}^m \hat{T}_t^2$	$\sigma^2 + q\sigma_\eta^2 + mnpq\sigma_{c_1}^2$
Residual (η')	(n-1)(m-1)-1	S5-S6	$\sigma^2 + q\sigma_\eta^2$
Residual regr. onto:			
T (ξ')	n-2	$S7 = pq \sum_{t=1}^n \hat{\xi}_t^2 \sum_{i=1}^m \hat{T}_i^2 - S6$	$\sigma^2 + q\sigma_d^2 + mpq\sigma_\xi^2$
G (ζ')	m-2	$S8 = pq \sum_{j=1}^m \hat{\zeta}_j^2 \sum_{i=1}^n \hat{G}_i^2 - S6$	$\sigma^2 + q\sigma_d^2 + npq\sigma_\zeta^2$
Residual (d)	(n-2)(m-2)	S5-S6-S7-S8	$\sigma^2 + q\sigma_d^2$
G × E (l)	(n-1)(p-1)	$S9 = mq \sum_{i=1}^n \sum_{j=1}^p \hat{l}_{ij}^2$	$\sigma^2 + q\sigma_\omega^2 + mq\sigma_l^2$
Concurrence (c ₂)	1	$S10 = mq\hat{c}_2^2 \sum_{i=1}^n \hat{G}_i^2 \sum_{j=1}^p \hat{E}_j^2$	$\sigma^2 + q\sigma_\delta^2 + mnpq\sigma_{c_2}^2$
Residual (δ')	(n-1)(p-1)-1	S9-S10	$\sigma^2 + q\sigma_\delta^2$
Residual regr. onto:			
E (b')	n-2	$S11 = mq \sum_{i=1}^n \hat{b}_i^2 \sum_{j=1}^p \hat{E}_j^2 - S10$	$\sigma^2 + q\sigma_s^2 + mpq\sigma_b^2$
G (a')	p-2	$S12 = mq \sum_{j=1}^p \hat{a}_j^2 \sum_{i=1}^n \hat{G}_i^2 - S10$	$\sigma^2 + q\sigma_s^2 + mnq\sigma_a^2$
Residual (s)	(n-2)(p-2)	S9-S10-S11-S12	$\sigma^2 + q\sigma_s^2$
G × T × E (ω)	(n-1)(m-1)(p-1)	$S13 = q \sum_{t=1}^m \sum_{i=1}^n \sum_{j=1}^p \hat{\omega}_{tij}^2$	$\sigma^2 + q\sigma_\omega^2$
Concurrence (c ₃)	1	$S14 = q\hat{c}_3^2 \sum_{i=1}^n \hat{G}_i^2 \sum_{t=1}^m \sum_{j=1}^p \hat{\beta}_{tj}^2$	$\sigma^2 + q\sigma_\theta^2 + mnpq\sigma_{c_3}^2$
Residual (θ')	(n-1)(m-1)(p-1)-1	S13-S14	$\sigma^2 + q\sigma_\theta^2$
Residual regr. onto:			
T × E (φ')	n-2	$S15 = q \sum_{i=1}^n \hat{\phi}_i^2 \sum_{t=1}^m \sum_{j=1}^p \hat{\beta}_{tj}^2 - S14$	$\sigma^2 + q\sigma_T^2 + mpq\sigma_\phi^2$
G (ψ')	(m-1)(p-1)-1	$S16 = pq \sum_{t=1}^m \hat{\psi}_t^2 \sum_{i=1}^n \hat{G}_i^2 - S14$	$\sigma^2 + q\sigma_T^2 + nq\sigma_\psi^2$
Residual (γ)	(n-2)(mp-m-p)	S13-S14-S15-S16	$\sigma^2 + q\sigma_T^2$
Error (e)	q(mnp-1)	$\sum_{t=1}^m \sum_{i=1}^n \sum_{j=1}^p (Y_{tijk} - \bar{Y}_{tij})^2$	σ^2

where

$$\hat{\xi}_t = \sum_{i=1}^m \hat{G}_i \hat{T}_t / \sum_{t=1}^m \hat{T}_t^2, \hat{b}_i = \sum_{j=1}^p \hat{G}_i \hat{E}_j / \sum_{j=1}^p \hat{E}_j^2, \hat{\phi}_i = \sum_{t=1}^m \sum_{j=1}^p \hat{G}_i \hat{\beta}_{tj} / \sum_{t=1}^m \sum_{j=1}^p \hat{\beta}_{tj}^2$$

$$\hat{\zeta}_j = \sum_{i=1}^n \hat{G}_i \hat{T}_j / \sum_{i=1}^n \hat{G}_i^2, \hat{a}_j = \sum_{i=1}^n \hat{G}_i \hat{E}_j / \sum_{i=1}^n \hat{G}_i^2, \hat{\psi}_j = \sum_{i=1}^n \hat{G}_i \hat{\beta}_{ij} / \sum_{i=1}^n \hat{G}_i^2$$

$$\hat{c}_1 = \sum_{i=1}^n \hat{\xi}_i \hat{G}_i / \sum_{i=1}^n \hat{G}_i^2, \hat{c}_2 = \sum_{i=1}^n \hat{b}_i \hat{G}_i / \sum_{i=1}^n \hat{G}_i^2, \hat{c}_3 = \sum_{i=1}^n \hat{G}_i \hat{\phi}_i / \sum_{i=1}^n \hat{G}_i^2$$

$$\sigma_p^2 = \sigma_G^2 + \sigma_T^2 + \sigma_E^2 + \sigma_{GT}^2 + \sigma_{GE}^2 + \sigma_{TE}^2 + \sigma_r^2 + \sigma^2$$

(σ^2 is the error variance).

Materials and Methods

The data on plant fresh weight of twenty-four lines of *Arabidopsis thaliana* grown under twelve different environmental conditions in seven growth periods were used in this study (Wu, 1972).

Results and Discussion

In our previous results of stability analysis (Lu and Wu, 1987), the response of each genotype across environments for different growth periods can be represented approximately by a straight line, the dynamic model was appropriate to assess the relative degree of adaptation among genotypes. The results also indicated significant positive correlations between the phenotypic mean and stability indices. Thus the concurrent dynamic model may be further considered here.

The result of ANOVA and the estimates of variance components were shown in Table 2. $G \times T$, $G \times E$, and $G \times T \times E$ interactions were highly significant. This means that when inbred lines of *A. thaliana* were grown in different environments throughout the whole growth periods, the $G \times E$ interaction could be partitioned into: $G \times T$, $G \times E$, and $G \times T \times E$ interactions. Further, similarly as found in the regression analyses for all interactions, both the concurrence and residual components were highly significant, indicating that the regression lines of different genotypes would tend to intersect at a common point. The mean squares for partial coefficients (ϕ') showed significant, indicating that the regression of $G \times T \times E$ interaction both onto time-space effects and genotypic effects may not give a perfect fit to the concurrence of an effect; that is, the two models involving regression onto time-space effects or genotypic effects can not equally be applied to the data. The values of "linear proportion (l.p.)" for dynamic model has been previously estimated as 96.79%, 79.61% and 93.11% for the $G \times T$, $G \times E$ and $G \times T \times E$ interactions, respectively, by Lu and Wu (1987). From the result of ANOVA based on regression model with respect to selection for environments, all sources were highly significant and the values of linear

proportion of three interactions were 99.20%, 85.00% and 72.67%, respectively (Table 3). Evidently, the linear proportion values of regression of $G \times T \times E$ interaction onto genotypic effects is significantly lower than that of regressing interaction onto time-space effects. However, the source of concurrence accounted for a large proportion of the interaction sum of squares, thus, the coefficients of concurrence can adequately describe the situation where the phenotypic mean (genotypic mean) and stability indices (regression coefficients) are correlated, that is, all regressions lines may tend to intersect at a common point.

The estimated values of c_1 , c_2 and c_3 were 0.0457, 0.0578 and 0.0604, respectively. At the point of convergence, $(T_i, E_j, \beta_{ij}, \bar{Y}_{ij}) = (-21.8818, -17.3010, 16.5563, -0.0865)$, genotypic differences in performance tends to be the smallest. Calculation of a concurrence mean square and the estimation of the point of convergence will provide a convenient method for investigating the form of the $G \times T \times E$ interaction, and is specially useful in the situation where the regression method is used as a selection criterion for stability. Eagles *et al.* (1977) pointed out that the most successful use of the regression method for stability is that the criterion can help breeders select genotypes having mean performance and high stability. This situation occurs either (a) when the heterogeneity among regressions is large and significant, but variation due to concurrence is small and nonsignificant, or (b) when the heterogeneity among regressions and variation due to concurrence are both large and significant, but the point of convergence lies within the range of normal production environments. In this study, the uniform performance was -0.0865, a value below the mean production level of *A. thaliana* ($\mu = 22.54$ g) and outside the range of our growth stages ($T_i = -21.64 \sim 25.19$) as well as environments ($E_j = -10.52 \sim 17.01$). Obviously, the point of convergence lies outside the range of normal production environments. Therefore, genotypes superior at high yield levels will be inferior at low levels and vice versa. Selection with use of mean yields alone would save genotypes that are superior at all yield levels.

Assuming the *A. thaliana* genotypes adopted here are randomly selected from a large population, and range of growth periods and environments is similarly representative of certain seasonal and locational difference, the coefficient of concurrence can be used in the prediction of the performance of untried genotype

Table 2. ANOVA of the data for 24 inbred lines of *Arabidopsis thaliana* based on the dynamic concurrent model

Source	D. F.	M. S.	Variance components
Time (T)	6	530914.37**	$\sigma_T^2 = 360.8$
Environment (E)	11	52198.67**	$\sigma_E^2 = 50.1$
Genotype (G)	23	35760.45**	$\sigma_G^2 = 67.0$
T × E (β)	66	7535.56**	$\sigma_\beta^2 = 52.1$
G × T (α)	138	5050.98**	$\sigma_\alpha^2 = 62.9$
Concurrence (c_1)	1	45237.28**	$\sigma_{c_1}^2 = 4.0$
Residual (η')	137	4757.65**	
Residual regr. onto:			
T (ξ')	22	53.86	
G (ζ')	5	24.71	
Residual (d)	110	5913.55**	
G × E (I)	253	3840.15**	$\sigma_I^2 = 73.2$
Concurrence (c_2)	1	22360.42*	$\sigma_{c_2}^2 = 1.8$
Residual (δ')	252	3766.66**	
Residual regr. onto:			
E (b')	22	621.87	
G (a')	10	357.21	
Residual (s)	220	4236.11**	
G × T × E (ω)	1518	1279.31**	$\sigma_\omega^2 = 170.4$
Concurrence (c_3)	1	157693.08**	$\sigma_{c_3}^2 = 15.5$
Residual (θ')	1517	1176.21**	
Residual regr. onto:			
T × E (ϕ')	22	4081.60**	$\sigma_{\phi'}^2 = 7.0$
G (ψ')	65	772.45	
Residual (γ)	1430	1149.86**	
Error (e)	8064	427.29	

** , * : Significant at 1% and 5% level, respectively.

Table 3. Analysis of variance based on the model of regression onto genotypic effects

Source	D. F.	M. S.	l. p. (%)
Time (T)	6	530914.37**	
Environment (E)	11	52198.67**	
Genotype (G)	23	35760.45**	
T × E (β)	66	7535.56**	
G × T (α)	138	5050.98**	
Het. bet. reg. 's (ξ)	6	90721.69**	99.20
Residual (o)	132	1156.86**	
G × E (I)	253	3840.15**	
Het. bet. reg. 's (a)	11	16502.53**	85.00
Residual (ρ)	242	3264.59**	
G × T × E (ω)	1518	1279.31**	
Het. bet. reg. 's (ψ)	83	2504.85**	72.67
Residual (ν)	1435	1208.43**	
Error (e)	8064	427.29	

Het. bet. reg. 's : Heterogeneity between regression's.

l. p. (%): Linear proportion.

** : Significant at 1% level.

-time-environment combinations which are members of the joint population. The prediction can be made with a reliability of 44.17%. In fact, the sample of genotypes here is not a typical member of the population of interest. Thus, such prediction has a low reliability. The use of a larger, more representative sample of genotypes might well yield a more accurate estimation of concurrence with a consequent increase in reliability of prediction.

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共點動態模式在穩定性分析之應用

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共點動態模式在各試因均為逢機效應之前提下，可對同一族群其他未受試基因型在未受試環境下其生長過程中任一階段的反應表現進行預測。該模式係在各基因型之迴歸係數與表型平均值間呈正相關關係時，以共點之觀念引入評價適應性的動態模式中，而將交感成分同時隨基因型效應及環境效應作迴歸分析。該共點動態模式之建立，曾藉 *Arabidopsis thaliana* 之24個自交系在12種相異環境下7種不同生長時期所測得的鮮重資料，作為應用上之分析，配合所擬定的理論模式，以說明動態共點模式在穩定性分析之研究上的應用情形。