Invited Paper *Sri Lankan Journal of Applied Statistics, Vol.9, 2008, p53-73*

Multiplicative Structural Models for Analysis of Genotype-Environment Interaction

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ABSTRACT

Joint linear and bi linear models have been proposed for structuring interaction in two way tables. In this paper we propose to review some of these models under univariate set up. A model under two ways MANOVA set up was considered in the contest of genotype-environment interaction. A two stage procedure for structuring η_{ij} *.the interaction effect of the form*

$$\eta_{ij} = \sum_{t=1}^{q} P_t \left(\sum_{s=1}^{m} u_{si} v_{sj} s_s\right)_t \text{ and } \eta_{ij} = \sum_{t=1}^{q} C_t \left(\sum_{s=1}^{m} g_{si} h_{sj} d_s\right)_t$$

are considered using structural decomposition of interaction component matrix. A multiplicative component model is also proposed to structure the residuals from a regression model of the type $\eta_{ij} = (1+\beta_i)\gamma_j + \delta_{ij}$*.The models are illustrated with data from a multi-location trial.*

Key Words: Genotype-Environmental Interaction, Multiplicative component model, Structural decomposition

INTRODUCTION

The statistical examination of interaction in two-way tables has not been done specifically in the context of GE interaction. The development is mostly theoretical and independent of subject matter. The simplest model one can assume is an additive model. Estimation of parameters and testing certain hypothesis about them are relatively easy in additive model. But in practice, the data rarely obey a strictly additive model. A non-additive component of the factors can then be introduced in the model and represented in the form of a general two-way analysis of variance model with interaction. The main effects and interaction are tested against the experimental error. The hypothesis of no differences in the main effect is tested under the assumption of no interaction effect. Testing for main effects is no longer valid if the hypothesis of no interaction is rejected. However main effects are rarely

of direct concern in the presence of appreciable interaction. Interest then lies in studying the structure of interaction and testing for its dimension.

A general linear model with interaction is given by

$$Y_{ij} = \mu + \alpha_i + \gamma_j + \eta_{ij} + \varepsilon_{ij} \qquad (1)$$

where η_{ij} is the interaction or non-additive component. In the context of GE-interaction, we represent μ, α_i, γ_j and η_{ij} respectively the general mean, the ith genotype, j th environment and the interaction effect between them and ε_{ij} is the within environment random error normally and independently distributed with mean zero and common variance. If $\eta_{ij} = 0$, the model is known as additive model. If the interaction is significant, the Structure of η_{ij} assumes importance. The relationship between η_{ij} ,the interaction effect and γ_j ,the additive environment effect as considered by Yates and Cochron (1938), is of the type

$$\eta_{ij} = \beta_i \gamma_j + \delta_{ij} \qquad (2)$$

where β_i is the regression coefficicnt for the ith genotype and δ_{ij} is the deviation from regression. Using this relationship we can write the two way model in (1) as

$$Y_{ij} = \mu + \alpha_i + (1+\beta_i)\gamma_j + \delta_{ij} + \varepsilon_{ij}$$

This is known as the joint regression model of Yates and Cochron adopted by Finley and Wilkinson (1963) and Eberhart and Russel (1966) to describe the stability of genotypes.

The foregoing methods are used when the information on the environmental variables is obtained from the data by taking the deviation of environmental means from the grand mean. When independent observations on some external environmental variables are available, regression of these external environmental

variables may throw light on the factors responsible for interaction. Suppose that the information on few auxiliary variables x_{ij} (i=1,2,...,q) is available which remains same for all genotype in the jth environment.

Hardwick and Wood (1972), Shukla (1972), proposed a multiple regression model for structuring μ_{ij} in (2), when external environmental variables are available

$$Y_{ij} = \mu + \alpha_i + a_{i1}x_{1j} + a_{i2}x_{2j} + \ldots\ldots\ldots\ldots a_{iq}x_{qj} + \varepsilon_{ij} \qquad (3)$$

where a_{ik} (k=1,2,....q) is the regression coefficient of the i th genotype on k th auxiliary variate and ε_{ij} is the random error component.

When in the model (3) if x_{ij} is replaced by a linear function say E_{ij} (t<q) such that E_{1j} accounts for the largest variation, E_{2j} accounts for the second largest variation and so on of the environmental variable, then the model becomes

$$Y_{ij} = \mu + \alpha_i + a_{i1}E_{1j} + \ldots\ldots\ldots\ldots a_{it}E_{ij} + \varepsilon'_{ij} \qquad (4)$$

wnere $E_{ij} = P'x_{ij}$, is the linear function based on the first t (t<q) principal components.

The forgoing models are known as Bi linear or Bi additive models.

$\eta_{ij} = \lambda\alpha_i\gamma_j$, Then (1) becomes,

$$Y_{ij} = \mu + \alpha_i + \gamma_j + \lambda\alpha_i\gamma_j + \varepsilon_{ij} \qquad (5)$$

This is known as concurrent model.

Tukey (1949), suggested a test for λ=0 (1 df) known as test for non additivity. Williams (1952), obtained λ as the largest eigen root of the interaction matrix $\eta\eta'$ Fisher and Mackenzie (1923), used the least square technique to obtain λ Mandel (1961) proposed a "bundle of lines" model given by

$$Y_{ij} = \mu + (1 + C_j)\alpha_i + (1 + \beta_i)\gamma_j + \varepsilon_{ij} \qquad (6)$$

Tukey (1962), suggested a Vacuum Cleaner model incorporating the bundle of lines model and the concurrent model given by,

$$Y_{ij} = \mu + \alpha_i + \beta_j + C_j\alpha_i + \beta_i\gamma_j + \lambda\alpha_i\gamma_j \qquad (7)$$

The combination of concurrent and bundle of lines model can be obtained by restructuring η_{ij} as follows

$$\eta_{ij} = (\lambda\alpha_i + \beta_i)\gamma_j$$

These models are also bilinear models.

Multiplicative Component Models

Gollob (1968), used a step wise process to obtain both additive and multiplicative terms in model 1 and structured for η_{ij} given by

$$\eta = \theta_1 u_1 v_1' + \theta_2 u_2 v_2' + \ldots\ldots\ldots\ldots\ldots + \theta_c u_c v_c' \qquad (8)$$

where $\theta_1^2 > \theta_2^2 > \ldots\ldots\ldots\ldots > \theta_c^2$ are the eigen roots of $\eta\eta'$ or $\eta'\eta'$ and $u_i v_j$ are the corresponding vectors. Model (1) can now be written as,

$$Y_{ij} = \mu + \alpha_i + \gamma_j + \theta_1 u_1 v_1' + \theta_2 u_2 v_2' + \ldots\ldots\ldots\ldots + \theta_c u_c v_c' + \varepsilon_{ij}$$

He called this as **FANOVA** Model as it incorporates the benefit of data reduction from a factor decomposition of residuals and ease of analysis of variance for interpretation of results.

Mandel (1969) decomposed η_{ij} using singular value decomposition of the interaction matrix for estimation of the parameters which gives the same results as least square technique.

Gauch and Zobel (1988, 1989), Gauch (2002), Wright and Gauch (1989) used the Gollob's procedure and called their models as AMMI models (Additive main effect multiplicative interaction models)

Multivariate Structural Models:

In the analysis of GE-interaction, we have several variable measured on an individual genotype and most often these variables are inter- related. Although univariate analysis of data can provide valuable information, it often cannot discriminate between groups as it ignores the covariance existing between variables. The univariate treatment of data, separately for each variable is not justified because such correlated data in general lead to departures from the assumption of statistical independence and additivity of treatment effects. Many findings shows that the environment does not operate directly on individual characters but on the characters in stable groups. Keeping this in view, Sridhara (1988) proposed the general linear model under multivariate set up for structuring interaction.

$$Y_{ij} = \mu + \alpha_i + \gamma_j + \eta_{ij} + \varepsilon_{ij} \qquad (9)$$

where Y_{ij} is a pxl vector of means representing the p quantitative variables measured on genotype i (i=1,2,....g) in the environment j (j=1,2,....k) represented by a general mean vector μ, i th genotypic effect α_i, j th environmental effects γ_j. η_{ij} and ε_{ij} are the pxl vectors of interaction and within environmental error component.

A two stage procedure for structuring η_{ij} of the form

$$\eta_{ij} = \sum_{t=1}^{q} P_t (\sum_{s=1}^{m} u_{si} v_{sj} s_s)_t \qquad (10)$$

is considered.

In the first stage η_{ij} is represented as

$$\eta_{ij} = P' \xi_{ij}$$

where P = PxP matrix of orthogonal vectors and ξ_{ij} is a Px1 vector of orthogonal linear components of interaction means. Each of these orthogonal linear component is arranged in a g x k matrix $\xi = (\xi_{ij})$. The matrix ξ is decomposed in the form of $\xi = usv'$ by singular value decomposition to obtain the first m significant multiplicative components.

If the linear components of η_{ij} are obtained by maximizing the interaction covariance in the oblique space of within group covariance matrix, the analysis leads to the estimation of canonical variate means for interaction. Thus the structural model for η_{ij} is represented by

$$\eta_{ij} = \sum_{t=1}^{q} C_t (\sum_{s=1}^{m} g_{si} h_{sj} d_s) t \qquad (11)$$

In the first stage we obtain,

$$\eta_{ij} = C^{'}\xi_{ij}$$

where C is a PxP matrix of orthogonal vectors of Canonical variates, obtained such that

$$C^{'}\Sigma C = I$$

$$C^{'}\Gamma C = \Lambda$$

$$\Lambda = (\lambda_1 > \lambda_2 > \ldots \lambda_p)$$

$$\Gamma = \eta\eta^{'}$$

Analysis of Residuals from regression

In the joint regression models we have,

$$\eta_{ij} = (1+\beta_i)\gamma_j + \delta_{ij} \quad \text{or} \quad \eta_{ij} = b_i\gamma_j + \delta_{ij}$$

where $b_i = (1+\beta_i)$

Finley and Wilkinson (1963) defined the stability of the genotypes as bi=1. Eberhart and Russel (1966) proposed δ_{ij} as another parameter of stability in addition to bi. A variety is stable if bi=1 and $\sigma^2\delta_{ij}$=0 where $\sigma^2\delta_{ij}$ is the residual variance from the linear fit. In most situations, these conditions are not fulfilled and there is no way of identifying a stable genotype. We propose a structural model in the multivariate set up as a combination of joint regression and multiplicative models for the residuals.

In the univariate case the model is of the form

$$Y_{ij} = \mu + \alpha_i + (1+\beta_i)\gamma_j + \sum_{s=1}^{k}\theta_s u_s v_s^{'} \qquad (12)$$

In the multivariate case it is of the form

$$Y_{ij} = \mu + \alpha_i + \gamma_j + \beta_i X_j + e_{ij} + \varepsilon_{ij} \qquad (13)$$

where $e_{ij} = Z_{ij} - \beta_i \hat{X}_j$ or $E_{ij} = Z_i - \beta_i \hat{X}$

Let $Q_e = \sum_{i-1}^{q} E_i E_i^{'}$ be a PxP matrix of SSQCP due to residuals summed over all genotypes.

The spectral decomposition gives $Q_e = P^{'} \Lambda P$

We defined $W_{ij} = P^{'} e_{ij}$ and $W_{ij}^{(1)} = P_1^{'} e_{ij}$ which gives the linear function of the largest residual error. We arrange $W_{ij}^{(1)}$ is a gxk matrix representing g genotypes and k environments and obtain the SVD of W as

$$W = \sum_{s=1}^{k} u_s v_s^{'} s_s$$

u and v are gxk and kxk orthogonal matrices of $WW^{'}$ and $W^{'}W$ respectively and $S = (S_1 > S_2 > ..... S_k)$ are the square roots of the eigen values of $WW^{'}$.The ij^{th} element of W is , $W_{ij} = \sum^{k} u_{si} v_{sj} s_s$

The configuration of both genotypes and environments from this residual analysis in a biplot gives the information on the genotypes which are adaptable for a given environment

ILLUSTRATION OF THE RESULTS

The data set consists of 15 genotypes grown in 8 environments, with differing agro-climatic conditions. The experiment was laid out in a randomized block design with

three replications. To fulfill the objective of simultaneous study of several characters for plant characters are included. They are

1. Grain Yield (GY), Kg/5 sq.m
2. Productive number of tillers per plant (TP)
3. Main ear length (EL), cm
4. Number of fingers per ear (NF)

Table 1 represents the summary results of the principal component analysis of GE-interaction matrix. The first component accounts for about 53% of the total variability. The variable Main ear length (0.8926) characterizes the first component with a variable-component correlation of 0.9483. This variable accounts for about 98.54 percent of variation for the first two components .The number of fingers per ear also contributes substantially to the first principal component with correlation 0.6054. The contribution of this character to the second component (0.8310) has been revealed by the high correlation (0.7496). Thus the first two pc's are completely characterized by Main ear length and Number of fingers.

The variance of the first principal component means is 3.1081. The contribution to this from each environment can be obtained by the diagonal elements of the matrix x'x, , where X =(x_{ij}) and $x_{ij} = p_1' z_{ij}$. p_1 is the first component vector. It is observed that environments 8,4, and 2 are more variable and contribute more towards GE-interaction.

Similarly the results of canonical variate analysis are presented in table 2. The first two canonical variates account for about 64% of the variation in GE-interaction obtained in the metric of within group covariance matrix. The first variate is characterized by Grain yield (0.8788) with a substantial contribution from ear length (-0.3665). The second canonical vector is completely characterized by main ear length (0.8455), with contribution from grain yield (0.4206) and number of fingers per ear (0.4015). Most of the variation (65%) explained by the first two variate is due to these two variables.

Table 1: Principal component analysis of GE-interaction covariance matrix

GE-interaction covariance matrix:	GY	0.1676	0.0436	-0.0128	0.0448
	TP	0.09	1.1983	-0.0729	0.0497
	EL	-0.02	-0.04	2.7539	0.7001
	NF	0.08	0.03	0.32	1.7193
Eigen vectors:		P1	P2	P3	P4
	GY	0.0027	0.0477	0.0236	0.9986
	TP	-0.0217	0.3709	0.9272	-0.04
	EL	0.8926	-0.4117	0.1857	0.0128
	NF	0.4502	0.831	-0.3244	-0.0332
Eigen roots		3.1081	1.3989	1.1679	0.1642
Per cent of trace		53.23	23.95	20	2.82
Cm % trace		53.23	77.18	97.18	100
Standardized vectors:	GY	0.0004	*0.0073	0.0036	0.1537
	TP	-0.0106	0.1825	0.4564	-0.0198
	EL	0.6222	-0.2869	0.1294	0.0088
	NF	0.3274	0.6042	-0.2359	-0.0241
Structured correlations	GY	0.0115	0.1379	0.0623	0.9884
	TP	-0.035	0.4008	0.9154	-0.0148
	EL	0.9483	-0.2935	0.1209	0.0031
	NF	0.6054	0.7496	-0.2674	-0.0102
Cumulative percentages of variation explained by variable for each vector:					
	GY	0.0001	0.0191	0.023	1
	TP	0.0012	0.1618	0.9998	1
	EL	0.8992	0.9854	1	1
	NF	0.3665	0.9284	0.9999	1

Biplots

The data in Table-2 and Table-4 are presented in the form of generalized biplots for Principal component and Canonical variate respectively in Figures (1) to Figure (2).

The biplot for the first and second Principal components are displayed .The vertex of the point representing the environment is joined by a line from the origin. The environments (E2, E4) and (E2, E8) are almost at right angles to each other while E4 and E8 are in the opposite Quadrants indicating high negative correlation between them. The simultaneous display of both Genotypic and Environmental effects enable us to visualize and assess the performance of genotype in different environments. Thus one can see that for the first PC the genotypes 3,4,6,10,11,12,14, and 15 which are positioned on the right hand top Quadrant, perform well in E2 and E8 and may show poor performance in E3,E4,E6.

Table 2: Analysis of GE-interaction variability: Coordinates for genotypes and environments defined by the first two principle components

	PC1		PC2	
Genotype:	**s1u1**	**s2u2**	**s1*u1***	**s2*u2***
G1	-3.2679	-0.8608	0.2512	1.4277
G2	-1.5208	-2.5006	1.1746	0.9976
G3	0.1085	0.6492	-0.5723	0.0885
G4	2.0269	0.4055	-0.9763	-1.1405
G5	-0.5993	1.1093	-1.4917	0.042
G6	0.6364	0.3519	0.8051	-1.3022
G7	-3.4102	2.603	-0.2805	-1.2106
G8	-0.334	-2.9513	-0.9109	0.2947
G9	-1.6565	0.2432	-0.8965	0.7036
G10	1.4203	0.2637	2.5521	-0.4687
G11	1.3072	-0.0431	0.9354	-0.1973
G12	1.4269	0.0908	-0.8793	-0.3812
G13	1.7034	-0.7789	-0.1755	0.0564
G14	1.5321	1.5893	0.6761	-0.1042
G15	0.6251	-0.0099	-0.1711	1.7839
Environment:	**s1v1**	**s2v2**	**s1*v1***	**s2*v2***
E1	1.0339	-1.0856	0.3338	-0.8947
E2	-0.2236	4.2948	0.4059	2.0259
E3	-1.0888	-2.0384	2.0347	-0.1586
E4	-3.8369	-0.3682	-0.8677	0.4899
E5	-1.3958	1.0615	-2.8069	0.8236
E6	0.2064	-1.5426	0.7266	-0.6923
E7	0.342	-0.4002	1.1979	0.6342
E8	4.9628	0.0782	-1.0239	-2.2273

Similarly the biplots defined by the co-ordinates for the first two canonical variates are displayed in figures (3) and (4) .It can be seen that E1,E2,E4 and E7 are high response and E3 and E8 are low response environments. Genotypes 12, 15 performed better in E1,E2,E4 and E7, average in E5 and E6 performed poor in E3

Table-3. Canonical variate analysis of GE-Interaction covariate matrix

Canonical ratio matrix:				
GY	4.3789	1.7012	0.0621	-0.0872
TP	1.7012	4.4262	-0.2672	-0.6808
EL	0.0621	-0.2672	4.9606	-0.0375
NF	-0.0872	-0.6808	-0.0375	7.2645
Canonical vectors:	C1	C2	C3	C4
GY	-0.1932	0.6744	0.17	-0.6923
TP	-0.3115	0.6329	0.0228	0.7088
EL	0.0139	-0.1422	0.9848	0.0995
NF	0.9303	0.3528	0.0282	0.092
Normalized vectors:				
GY	6.1154	2.3391	0.282	0.6219
TP	-0.2629	-0.3973	1.985	0.2023
EL	-0.6493	1.1448	0.0936	0.5811
NF	-0.113	0.4907	0.2398	-1.2605
Canonocal roots	7.5127	5.9153	4.9639	2.6387
Per cent of trace	35.72	28.13	23.6	12.55
Cm % trace	35.72	63.58	87.45	100
Standardized vectors:				
GY	0.9417	0.3602	0.0434	0.0958
TP	-0.1294	-0.1956	0.977	0.0996
EL	-0.4526	0.798	0.0652	0.4051
NF	-0.0822	0.3568	0.1743	-0.9164
Structured correlations				
GY	0.8788	0.4206	0.1856	0.1207
TP	-0.0039	-0.1495	0.9805	0.1276
EL	-0.3665	0.8455	0.08	0.3787
NF	-0.0702	0.4015	0.1637	-0.8993

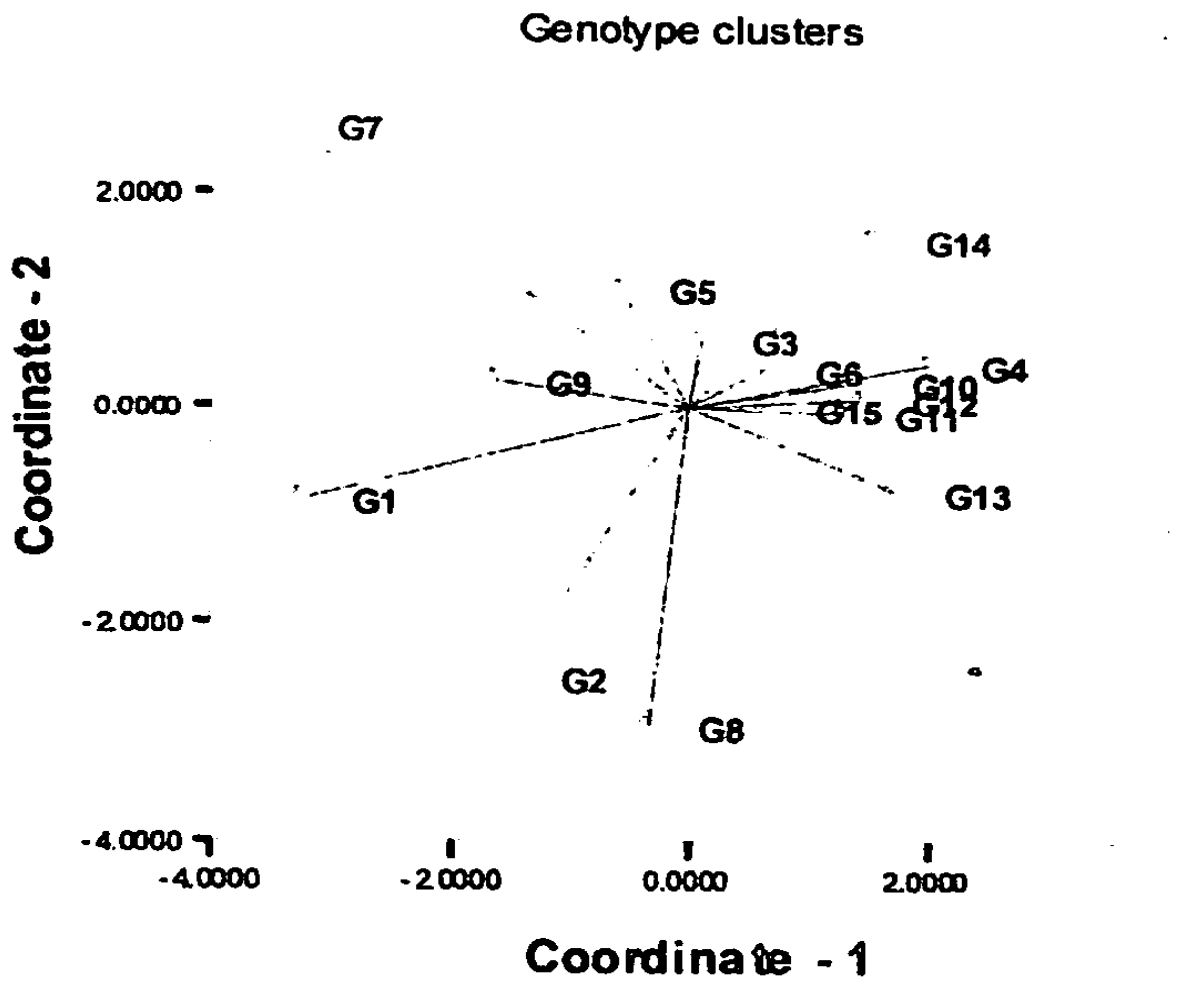
Cumulative percentages of variation explained by variable for each vector:

GY	77.22	94.92	98.36	99.82
TP	0	2.24	98.38	100
EL	13.43	84.93	85.57	99.91
NF	0.49	16.61	19.29	100

and E8. Genotypes 1, 2 and 3 performed well in low yielding environment E3 as well as in high yielding environment E1,E2 and E7.

Table 4: Analysis of GE-interaction variability: Coordinates for genotypes and environments defined by the first two Canonical variates.

	CV1		CV2	
Genotype:	**p1i1**	**p2i2**	**p1*i1***	**p2*i2***
G1	2.0774	-5.8591	3.3488	-1.1574
G2	1.6068	-2.5991	2.7164	-3.5056
G3	1.515	-0.5828	-0.5478	0.0617
G4	-4.9925	0.1873	-3.2022	-0.6598
G5	-0.9925	0.9262	-0.3794	0.9603
G6	-1.5266	0.588	-0.6684	0.6896
G7	0.5546	-1.1309	3.8707	3.3858
G8	-0.3044	0.3573	1.4801	-3.3588
G9	-0.3864	-1.0884	2.5037	1.5649
G10	-0.5488	-1.0771	-1.9232	0.1142
G11	-2.2078	0.0737	-1.2899	-0.9044
G12	4.9239	2.6598	-0.8276	0.9285
G13	-2.2068	1.2124	-2.8881	-1.3381
G14	-2.1392	2.7578	-1.4089	2.2844
G15	4.1519	3.4881	-0.784	0.9341
Environment:	**q1i1**	**q2i2**	**q1*i1***	**q2*i2***
E1	7.6583	-1.1361	0.6877	-0.8406
E2	2.6851	-1.1768	0.1943	5.264
E3	-2.1295	-4.7525	2.7181	-4.1243
E4	-0.8	5.1974	3.3354	-0.0779
E5	-2.6175	1.2367	1.6744	1.7542
E6	-2.0977	1.8282	-0.6249	-0.7116
E7	0.5778	2.3459	-1.1579	-0.1729
E8	-3.2774	-3.5436	-6.8267	-1.0908



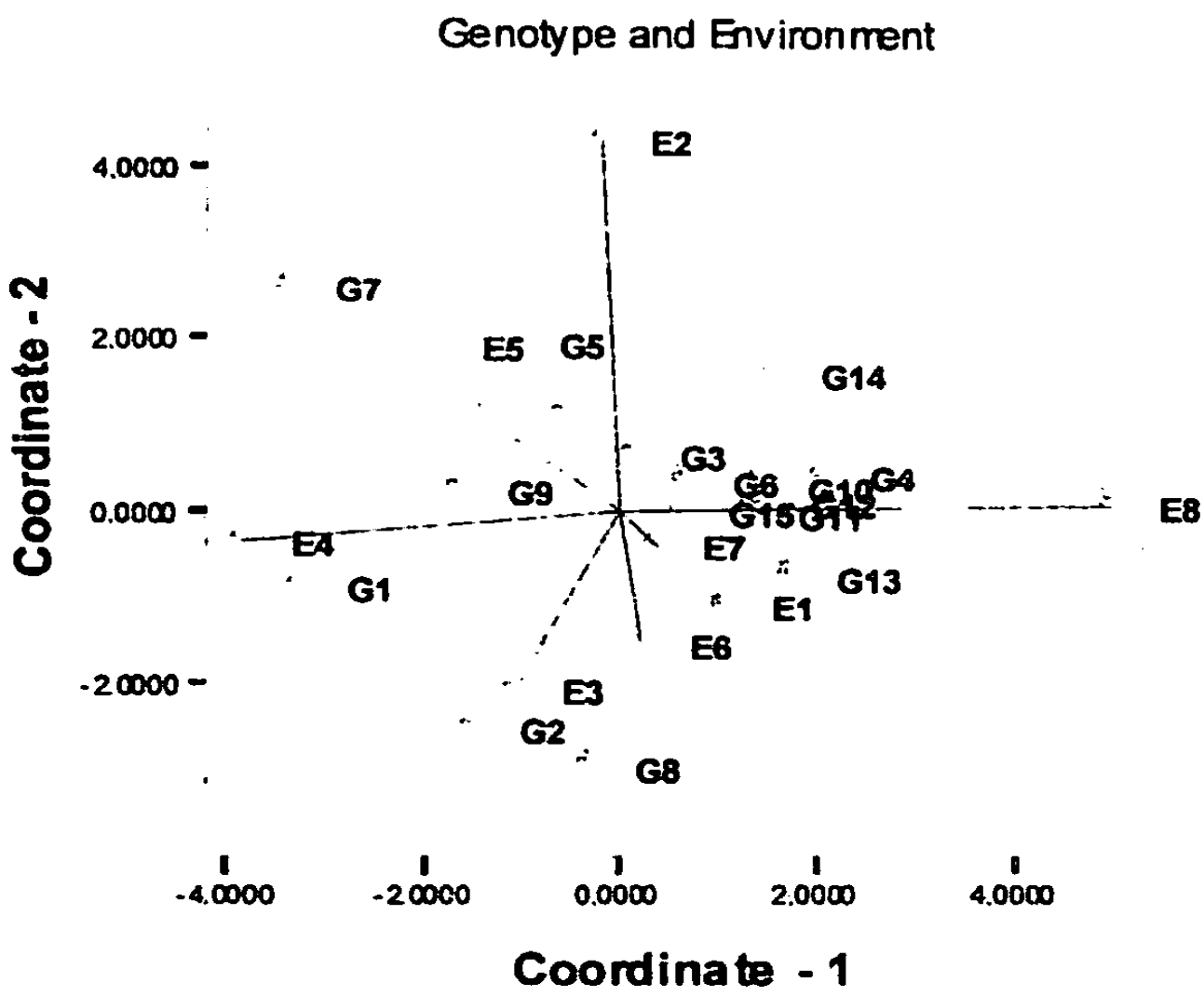
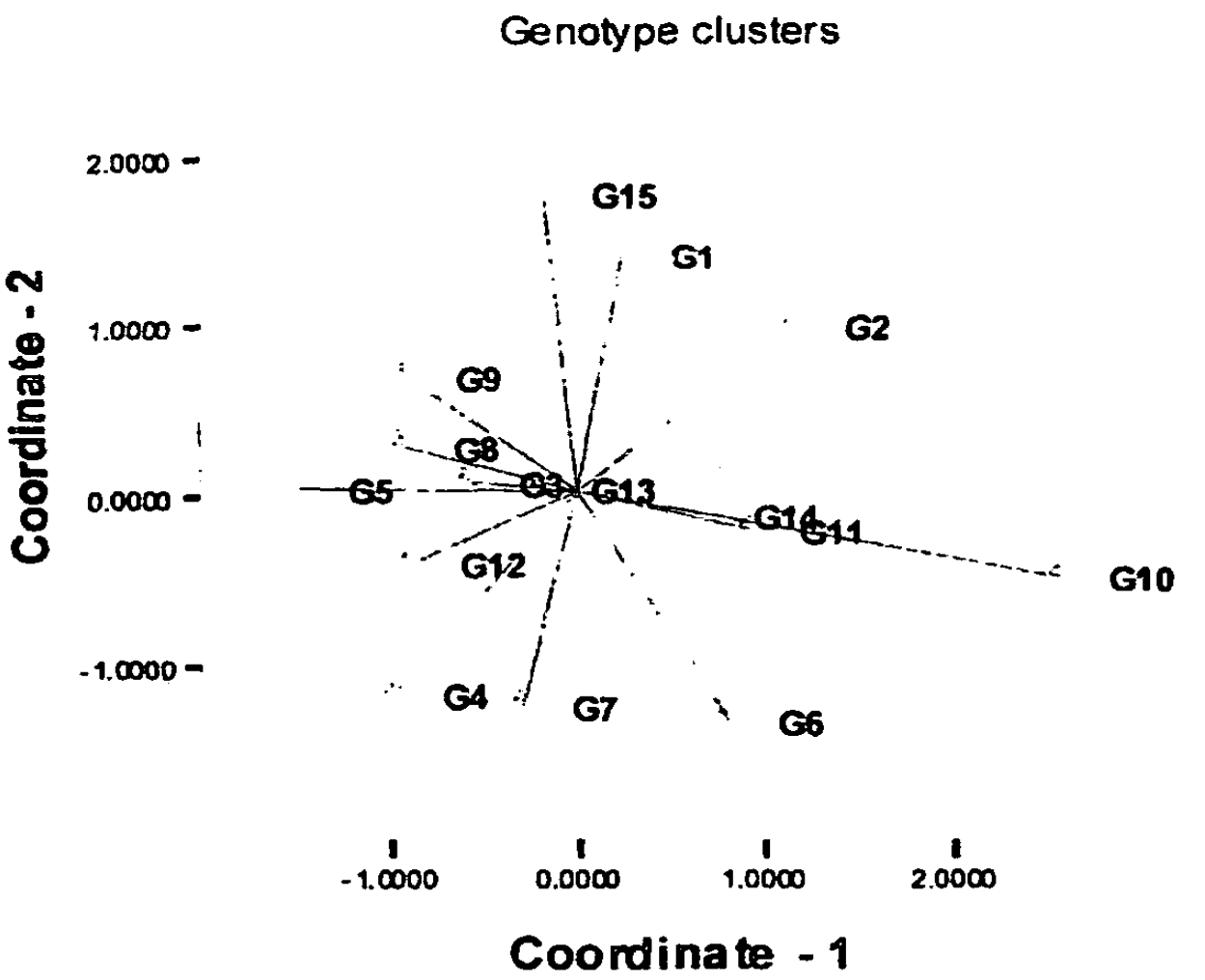


Figure 1: Biplots for Principal component – 1



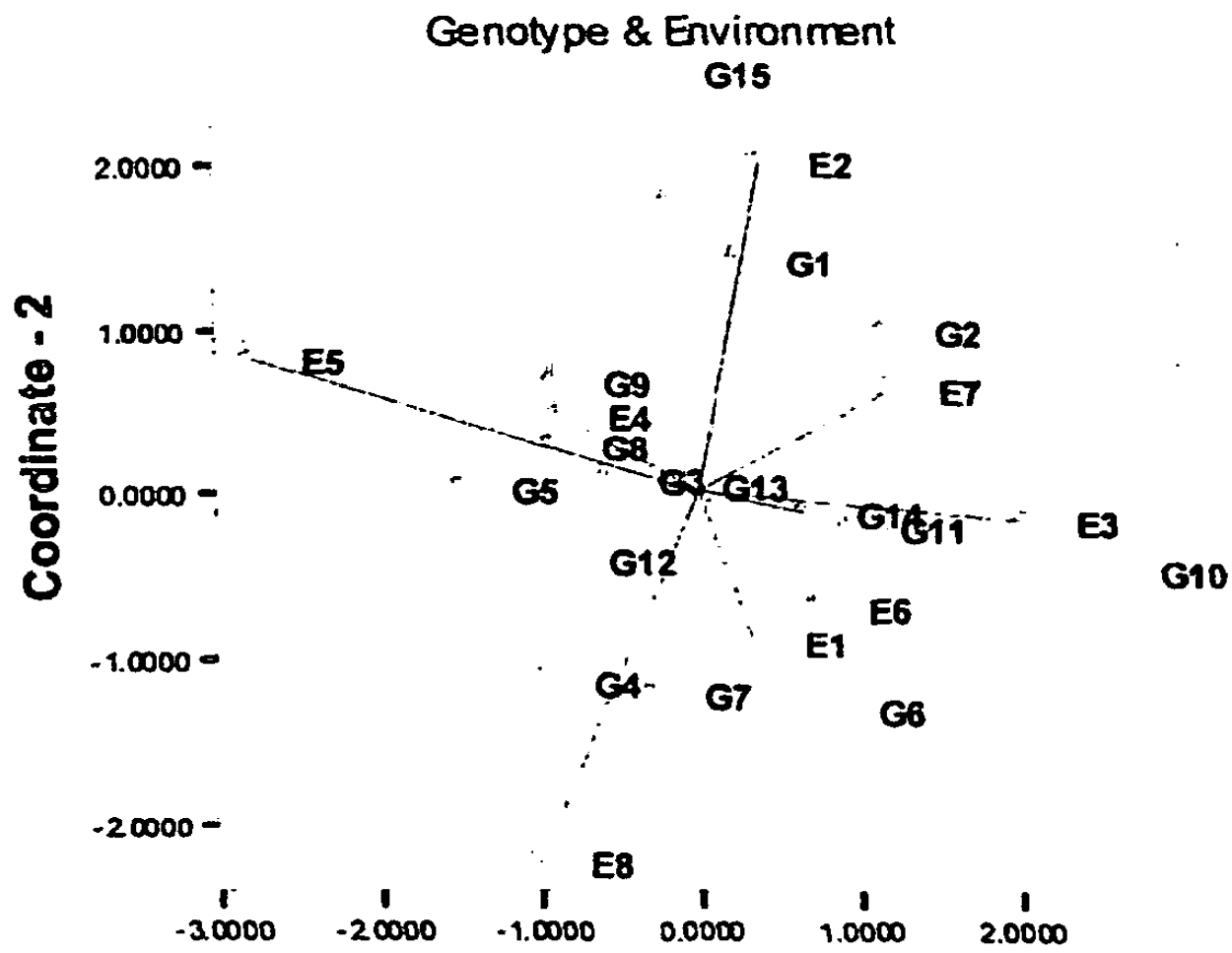
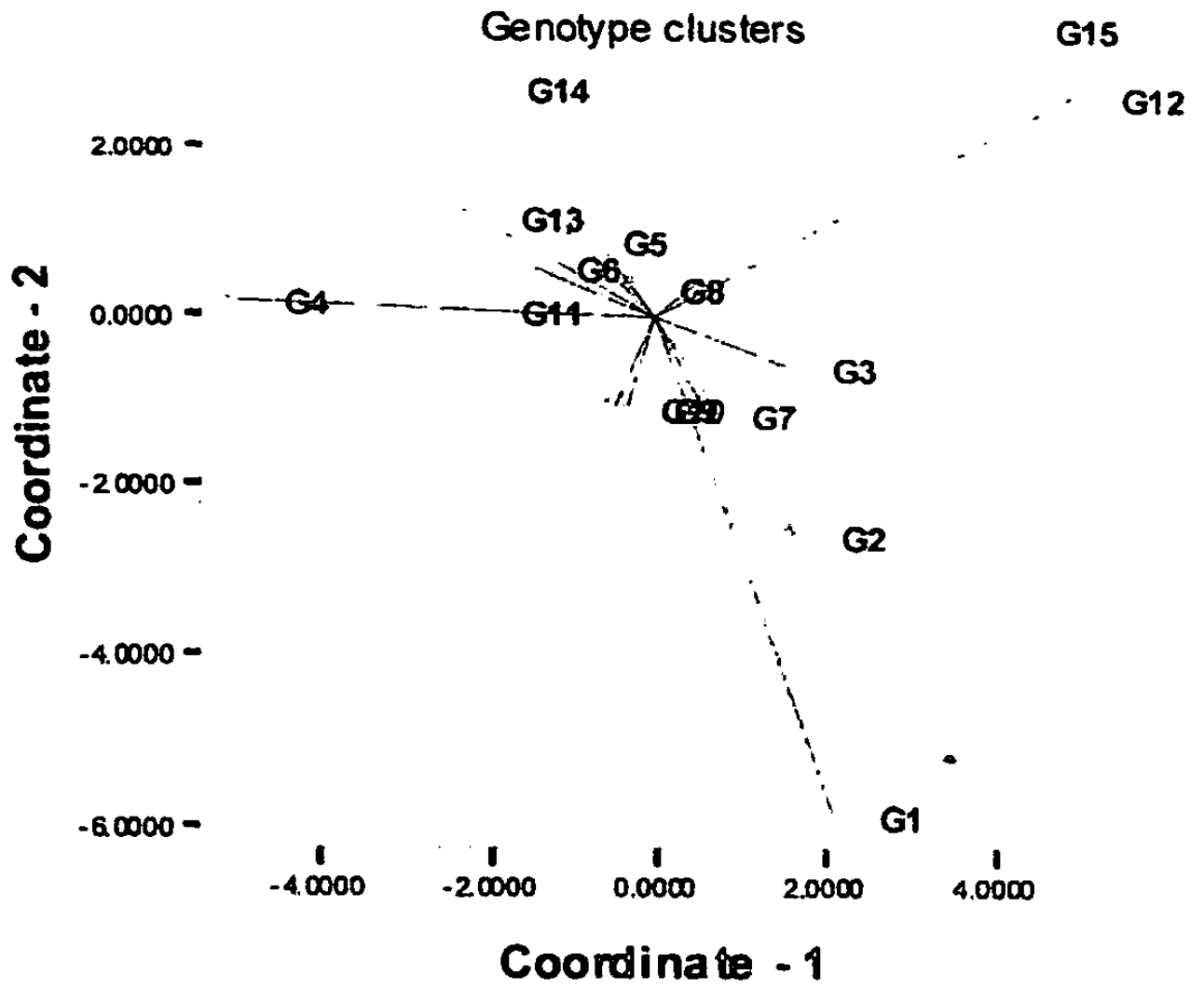


Figure 2: Biplots for Principal component – 2



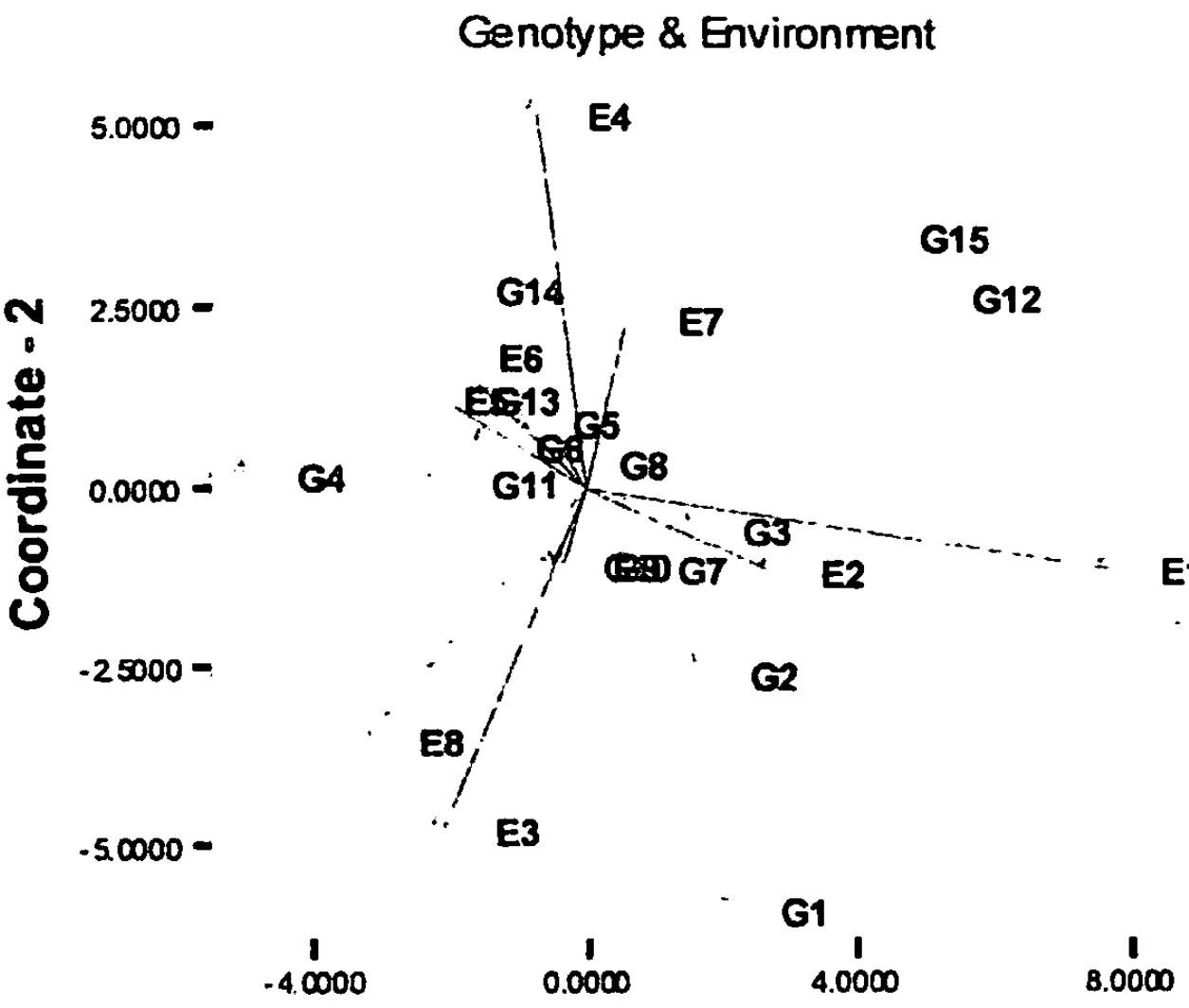


Figure 3: Biplots for Canonical variates – 1

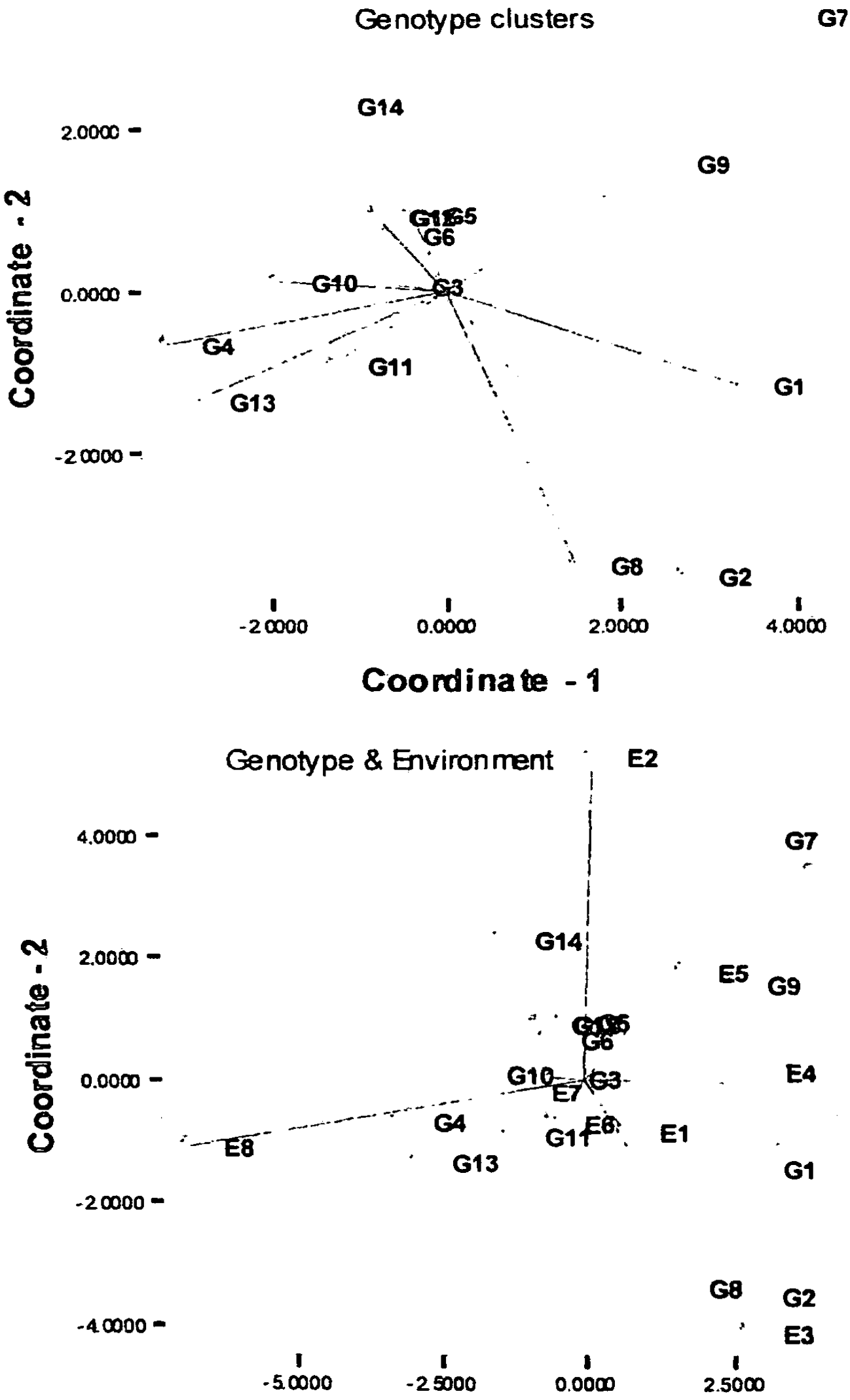


Figure 4: Biplots for Canonical variates – 2

Analysis of Residuals from Regression:

The results of the analysis based on the canonical variate analysis of residuals from regression are given in Tables (5) and Table (6) and a biplot in Figure (5). The data set consists of the 17 genotypes grown in 15 environments of finger millet crop spread over most of the states in India. Seven quantitative plant characters are included in the study.

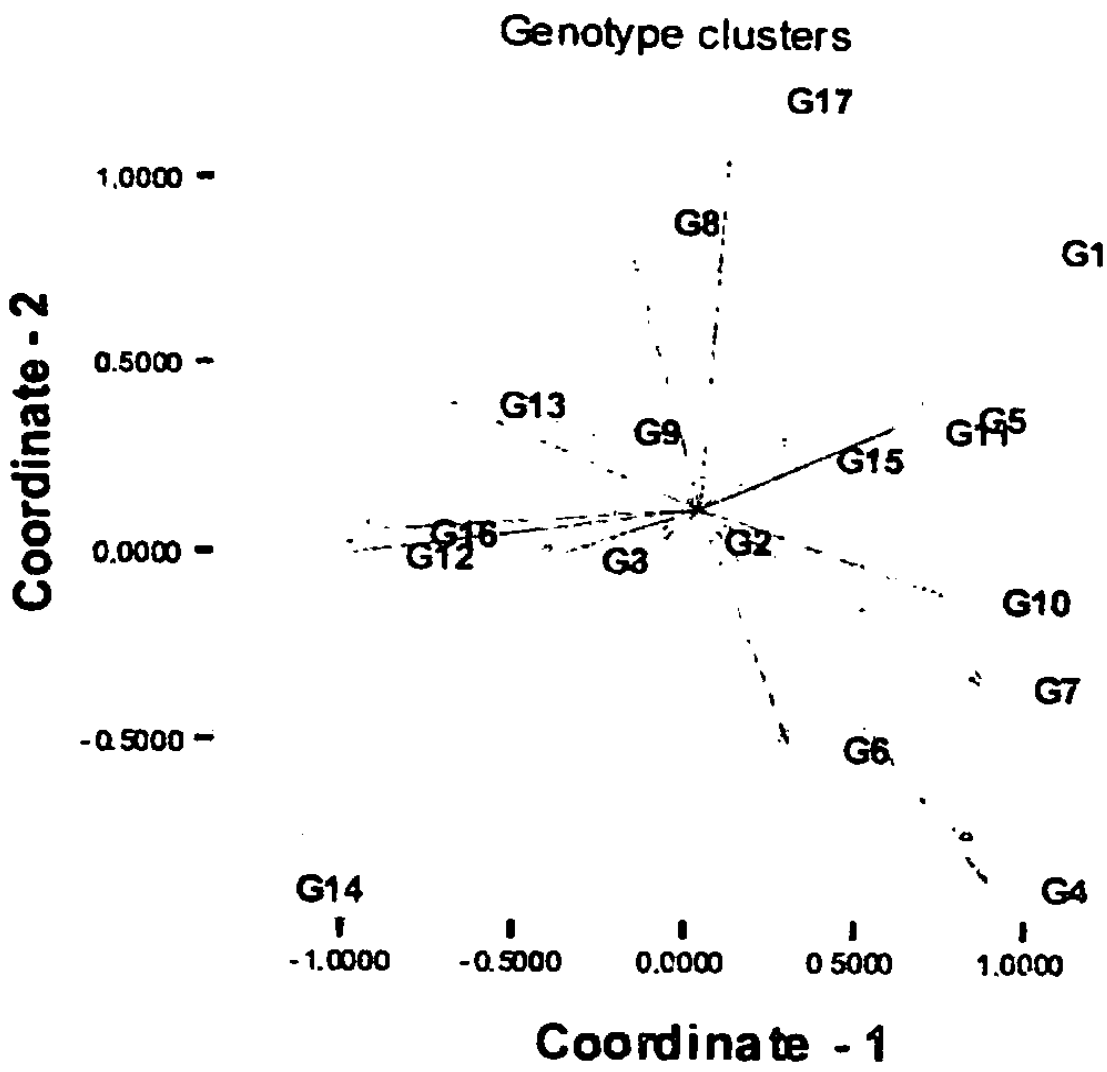
The first canonical component accounted for about 50% of variability and the first four for 91% variability. The coordinates for genotypes and the environments defined by the first canonical variate analysis of residuals from regression provide the configurations required for interpretation of inter relationship between Genotypes and Environment as could be seen from the biplot from Figure (5), the genotypes 1,5 and 11are highly adaptable in environments E4,E8 and E11.Genotypes 4,6,7 and 10 performed well in E1,E3,E10,E12 and E15.It could also be seen that E5 and E8 are high variable environments where as E2,E12 ,E14 and E15 are low variable environments. The performance of Genotypes grown in E6, E7, E9 and E13 are very low.

Table 5: Canonical Variate analysis of Residuals from regression Normalized vectors

	V1	V2	V3	V4	V5	V6	V7
X1	0.0437	-0.1498	0.2098	2.0191	1.5958	-0.5423	-0.4682
X2	-0.0013	0.0195	-0.0037	0.0355	-0.0598	0.0023	0.0244
X3	-0.2153	0.5005	0.3948	-0.1112	0.096	0.0327	-0.0159
X4	-0.0187	-0.1016	-0.0587	-0.1021	0.327	0.1132	0.394
X5	-0.1318	-0.0045	-0.071	-0.0057	0.0673	0.39	-0.1843
X6	-0.107	0.1164	-0.1464	0.0076	-0.0063	0.0019	0.0144
X7	0.3216	0.0019	0.0694	0.007	0.0099	0.0094	-0.0039
Canonical Roots	252.7036	99.9702	64.5144	43.9555	26.3489	11.1153	8.0093
% of Trace	49.88	19.73	12.73	8.68	5.2	2.19	1.5
Cumulative % Trace	49.88	69.61	82.34	91.02	96.22	98.41	100

Table 6: Coordinates for Genotypes and Environments defined by canonical variate analysis of residuals from regression

		CV1			
Canonical root:		252.7036			
% Trace:		49.88%			
Singular Values:	9.91	7.83			
Genotypes	**U1**	**U2**	**Environment**	**v1**	**v2**
1.GPU5	0.9591	0.8298	E1	1.1257	-0.5479
2.GPU6	-0.0277	0.0369	E2	-0.3955	-0.0761
3.GPU7	-0.3829	-0.0096	E3	1.441	-0.4909
4.GPU10	0.9017	-0.8774	E4	0.4982	0.8255
5.MR3	0.7159	0.3783	E5	-1.7602	1.0815
6.HR711	0.3167	-0.5153	E6	-0.4083	-0.4758
7.HR7302	0.8809	-0.345	E7	-0.6064	-0.8125
8.HR6-27	-0.1774	0.9029	E8	0.4979	1.6146
9.DPR1733	-0.2994	0.3285	E9	-0.6884	-0.8692
10.GRPE4	0.7933	-0.1151	E10	0.2948	-0.4441
11.HRRN30	0.6189	0.3433	E11	0.8847	0.8821
12.TNAU317	-0.961	-0.0067	E12	0.2483	-0.2008
13.TNAU3211	-0.6908	0.3967	E13	-0.9557	-0.1026
14.SR-SDG-82	-1.2771	-0.8914	E14	-0.1699	0.0173
15.PR202	0.2991	0.2614	E15	-0.006	-0.4012
16.PES110	-0.8956	0.053			
17.Local	0.1562	1.2314			



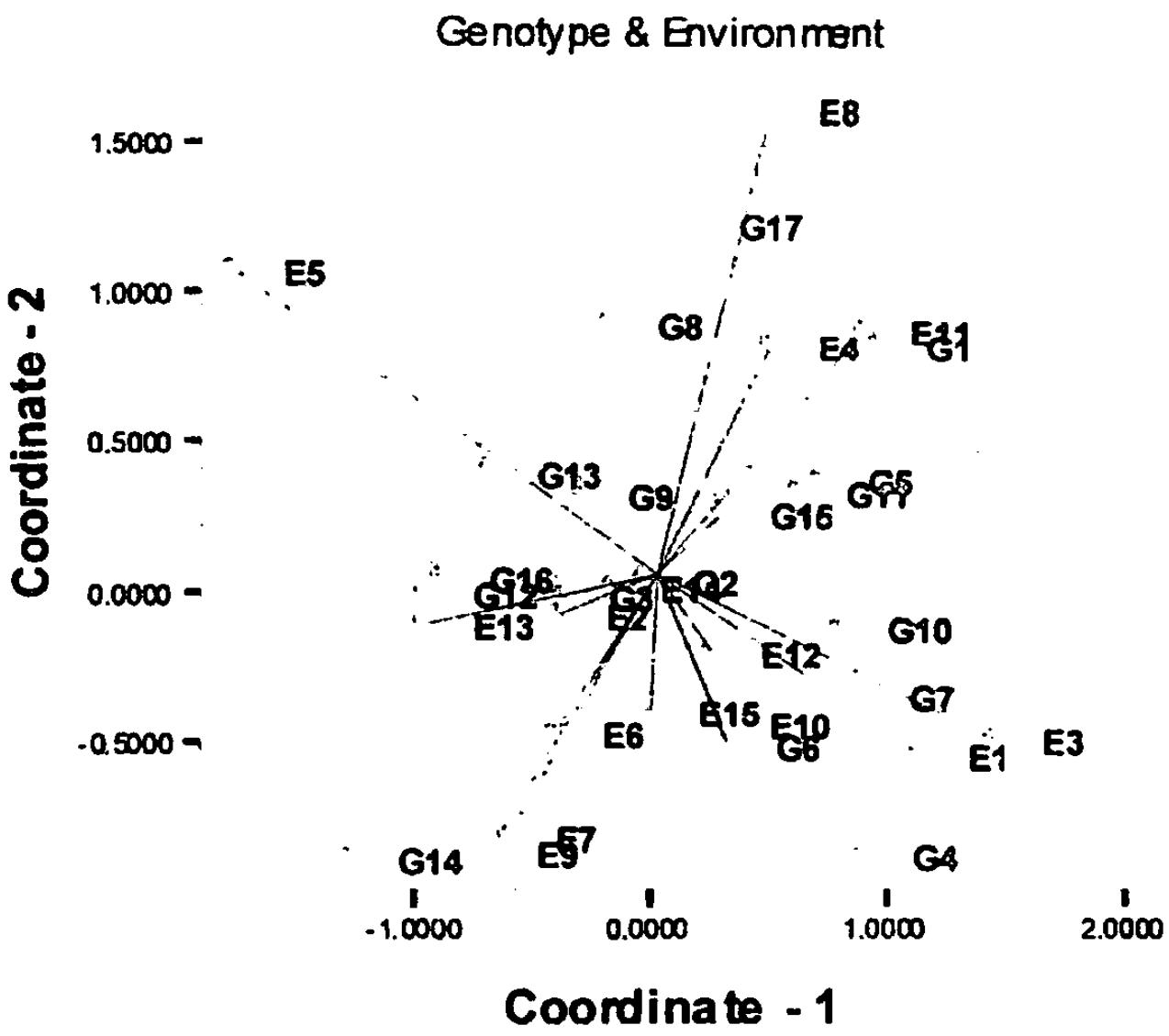


Figure 5: Biplot for Canonical Variate-1 of Residuals from Regression

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